

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 06:14:03 ; Search time 7440 Seconds  
(without alignments)  
13361.329 Million cell updates/sec

Title: US-10-070-489A-1

Perfect score: 18937

Sequence: 1 ggatccgagtggaaggaatca.....cgtgcccgaggagcatggc 18937

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_23Sep04.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	18914	99.9	18940	5 AAA91292	Aaa91292 Insectici
2	2368.8	12.5	37948	2 AAZ06831	Aaz06831 Photorhab
3	2357.8	12.5	110000	10 ACF67367_23	Continuation (24 o
C	2357.8	12.5	110000	10 ACF65386_5	Continuation (5 of
C	2283.6	12.1	110000	10 ACF65386_4	Continuation (5 of
6	1658.8	8.8	38258	2 AAV17876	AAV17876 Cloned to
7	1260.8	6.7	38258	2 AAV17876	AAV17876 Cloned to
8	1108.8	5.9	4431	6 ABS52584	AbS52584 P. lumine
9	1108.8	5.9	4434	12 ADN61378	Adn61378 Photorhab
10	1074	5.7	4431	10 ACF69437	AcF69437 Photorhab
11	1067.6	5.6	4428	10 ACF69428	AcF69428 Photorhab
12	1046.4	5.5	4425	12 ADN61379	Adn61379 Photorhab
13	1046.4	5.5	4425	12 ADP18621	AdP18621 Photorhab
14	969.8	5.1	4458	2 AAV29924	AAV29924 tcac gene
15	968.6	5.1	110000	10 ACF65385_0	AcF65385 Photorhab
16	968.6	5.1	110000	10 ACF67367_29	Continuation (30 o
17	967.8	5.1	4458	10 ACF69896	AcF69896 Photorhab
18	965	5.1	4458	2 AAT68840	Aat68840 Photorhab
19	962.8	5.1	37544	3 AAA50029	Aaa50029 Cosmid cH
20	915.6	4.8	6648	10 ACF69426	AcF69426 Photorhab
21	903.4	4.8	6005	2 AAT68837	Aat68837 Photorhab

22	901.8	4.8	6055	2 AAV29921	Aav29921 tcab gene
23	848.8	4.5	7551	4 AAF58778	Aaf58778 Photorhab
24	848.8	4.5	7551	6 ABS52583	AbS52583 P. lumine
25	848.8	4.5	7551	12 ADP18613	AdP18613 Photorhab
26	845.6	4.5	7551	2 AAV29928	Aav29928 tcda gene
27	832.8	4.4	7551	2 AAT68843	Aat68843 Photorhab
28	815.2	4.3	7577	4 AAF58780	Aaf58780 Modified
29	815.2	4.3	7621	4 AAF58783	Aaf58783 Tcda toxi
30	814	4.3	7578	10 ACF69436	AcF69436 Photorhab
31	797	4.2	4482	12 ADN61356	Adn61356 Xenorhab
32	781.2	4.1	7512	6 ABS52586	AbS52586 P. lumine
33	781.2	4.1	7515	4 AAF58779	Aaf58779 Photorhab
34	779.6	4.1	7515	2 AAV29985	Aav29985 tcba gene
35	776.4	4.1	7515	2 AAT68836	Aat68836 Photorhab
36	771.8	4.1	33521	12 ADN61337	Adn61337 Paenibaci
37	770.8	4.1	6534	12 ADP18617	AdP18617 Photorhab
38	764	4.0	7377	10 ACF69433	AcF69433 Photorhab
39	758.8	4.0	7500	12 ADP18615	AdP18615 Photorhab
40	755.6	4.0	3051	12 ADN61357	Adn61357 Xenorhab
41	748.6	4.0	7541	4 AAF58781	Aaf58781 Modified
42	747.8	3.9	7335	10 ACF69427	AcF69427 Photorhab
43	732	3.9	7146	12 ADP18619	AdP18619 Photorhab
44	725	3.8	3132	2 AAT68850	Aat68850 Photorhab
45	725	3.8	3132	2 AAV29927	Aav29927 tccc gene

ALIGNMENTS

RESULT 1  
AAA91292  
ID AAA91292 standard; DNA; 18940 BP.  
XX  
AC AAA91292;  
XX  
DT 19-JUN-2001 (first entry)  
XX  
DE Insecticidal protein complex gene.  
XX  
KW Insecticidal protein complex; amber disease; insect; Coleoptera;  
KW pesticide; ds.  
XX  
OS Serratia sp.  
XX  
FH Key  
CDS  
FT  
FT Location/Qualifiers  
1860..2295  
/\*tag= a  
/product= "ORF1 protein"  
2416..9546  
/\*tag= b  
/product= "SepA"  
9601..13887  
/\*tag= c  
/product= "SepB"  
13911..14486  
/\*tag= d  
/product= "ORF2 protein"  
14549..17470  
/\*tag= e  
/product= "SepC"

WC200116305-A2.

08-MAR-2001.

04-SEP-2000; 2000MO-NZ000174.

02-SEP-1999; 99NZ-00337610.

(NZPA-) NEW ZEALAND PASTORAL AGRIC RES INST LTD.

Glare TR, Hurst MRH, Jackson TA;

XX

DR WPI; 2001-169009/17.  
DR P-PSDB; AAP97692, AAP97693, AAP97694, AAP97695, AAP97696.  
XX New nucleic acid encoding a polypeptide useful as a pesticide especially  
PT for Coleoptera.  
XX  
XX Claim 1; Page 65-89; 109pp; English.  
XX  
CC This sequence represents the Serratia insecticidal protein complex gene  
CC of the invention. The invention relates to a gene encoding an  
CC insecticidal protein complex or a functional fragment, a neutral  
CC mutation, or a homologue of the complex. The polypeptides and nucleotides  
CC of the invention are used to induce amber diseases or like conditions in  
CC insects, especially to those from the order comprising Coleoptera, useful  
CC as a pesticide  
XX  
SQ Sequence 18940 BP; 4336 A; 4848 C; 5370 G; 4386 T; 0 U; 0 Other;  
  
Query Match 99.9%; Score 18914; DB 5; Length 18940;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 18937; Conservative 0; Mismatches 0; Indels 3; Gaps 2;  
  
QY 1 GGAATCGAGTGAAGGAATCATCGCGCGCTTTATACGTTTCAGGGTGAATACGGTTGGCCG 60  
DB 1 GGAATCGAGTGAAGGAATCATCGCGCGCTTTATACGTTTCAGGGTGAATACGGTTGGCCG 60  
  
QY 61 CAACGTGGCAATCGATGTTGTTGTGTCGTATGAATCGCGCAACGTACTGGTGTCTG 120  
DB 61 CAACGTGGCAATCGATGTTGTTGTGTCGTATGAATCGCGCAACGTACTGGTGTCTG 120  
  
QY 121 ACATACCCAGTCCGATAACTGTGACGAACACTATCAAGATGTGTTCCGTGCACTGA 180  
DB 121 ACATACCCAGTCCGATAACTGTGACGAACACTATCAAGATGTGTTCCGTGCACTGA 180  
  
QY 181 AAGCCAGGATTTATTTTACCAATCGTTGGTGGCTTCTTCTGAACTGGTGCATC 240  
DB 181 AAGCCAGGATTTATTTTACCAATCGTTGGTGGCTTCTTCTGAACTGGTGCATC 240  
  
QY 241 ATTTAGCCGCATCATCAAAAGATGATGGAATACAAATATCATATTTTACGACACCCA 300  
DB 241 ATTTAGCCGCATCATCAAAAGATGATGGAATACAAATATCATATTTTACGACACCCA 300  
  
QY 301 AGTTGATGACCTCTCCGTGAGTTGAAATGCCAGCGGGGAAATCAGCAGCCTTTTCAAC 360  
DB 301 AGTTGATGACCTCTCCGTGAGTTGAAATGCCAGCGGGGAAATCAGCAGCCTTTTCAAC 360  
  
QY 361 TCATGAGCAGGGGAAATCAATCTTCAATAACCCGATGGATATCCTGCCAGTGTGA 420  
DB 361 TCATGAGCAGGGGAAATCAATCTTCAATAACCCGATGGATATCCTGCCAGTGTGA 420  
  
QY 421 TTTAACTTTTATGTTGTTTCTTAAATATCCCAATCGTTGAATCGCTACATACGGCAGA 480  
DB 421 TTTAACTTTTATGTTGTTTCTTAAATATCCCAATCGTTGAATCGCTACATACGGCAGA 480  
  
QY 481 CATTAGTATCTACTTATCATCAAGATTAATCACAACCCGATGCTTAATTTTCAATGAT 540  
DB 481 CATTAGTATCTACTTATCATCAAGATTAATCACAACCCGATGCTTAATTTTCAATGAT 540  
  
QY 541 GAAACGTTCCATTAATAATTTTACAGAACCTTAAACCGGCAATTTTATGCTGATCAGTG 600  
DB 541 GAAACGTTCCATTAATAATTTTACAGAACCTTAAACCGGCAATTTTATGCTGATCAGTG 600  
  
QY 601 AATGATGTTTCTGAAATAATTAATGCACTCTGCCACTTATCAGATAAAACACCCC 660  
DB 601 AATGATGTTTCTGAAATAATTAATGCACTCTGCCACTTATCAGATAAAACACCCC 660  
  
QY 661 ATCGGTAAGTTTTATTTTATTAATGATTTTATTAATGATTTTATTAATGATTTTAA 720  
DB 661 ATCGGTAAGTTTTATTTTATTAATGATTTTATTAATGATTTTATTAATGATTTTAA 720  
  
QY 721 TTAATGATTTTATTAATGATTTTATTAATGATTTTATTAATGATTTTATTAATGATTTT 780  
DB 721 TTAATGATTTTATTAATGATTTTATTAATGATTTTATTAATGATTTTATTAATGATTTT 780

QY 781 TACTCAATTTAATGTTGGTATGACCATGTTTTAGATGAGTGGCAGGATTCATTATTGT 840  
DB 781 TACTCAATTTAATGTTGGTATGACCATGTTTTAGATGAGTGGCAGGATTCATTATTGT 840  
  
QY 841 AAAAAAAGTATCTAAACCTTTAGCAGCAATCCTACTTCAGGATGACCTCGCAGGACTT 900  
DB 841 AAAAAAAGTATCTAAACCTTTAGCAGCAATCCTACTTCAGGATGACCTCGCAGGACTT 900  
  
QY 901 GATTATTGCCATTTTACGAAGGAGATGACGGGTGATAAATAAATAAAAAACAAAAG 960  
DB 901 GATTATTGCCATTTTACGAAGGAGATGACGGGTGATAAATAAATAAAAAACAAAAG 960  
  
QY 961 TATAGCTTAGTATCGCGGATTTACATCCAGTAAACACTTTATTGACTTTTTTTACTTCTA 1020  
DB 961 TATAGCTTAGTATCGCGGATTTACATCCAGTAAACACTTTATTGACTTTTTTTACTTCTA 1020  
  
QY 1021 CCGTTAGCTATAAATATGATATTTAAATCTGATTTTATATAAAACCAAGTTTATGATGC 1080  
DB 1021 CCGTTAGCTATAAATATGATATTTAAATCTGATTTTATATAAAACCAAGTTTATGATGC 1080  
  
QY 1081 TCGATTGGTCATTAAGTCGTTTATATGATCGTTATCTGTCTCATTTGATTTGGTGTAAATC 1140  
DB 1081 TCGATTGGTCATTAAGTCGTTTATATGATCGTTATCTGTCTCATTTGATTTGGTGTAAATC 1140  
  
QY 1141 TTTTATTCTTCAGTGAGGTTTTCAGGGGAATGTTATGGTAAATCATCTCATGTCATTT 1200  
DB 1141 TTTTATTCTTCAGTGAGGTTTTCAGGGGAATGTTATGGTAAATCATCTCATGTCATTT 1200  
  
QY 1201 GTTGTCTGATGTTAAATTAACGTGTTCAATCATTTATGTTTCTACTGTTTCTATTGTC 1260  
DB 1201 GTTGTCTGATGTTAAATTAACGTGTTCAATCATTTATGTTTCTACTGTTTCTATTGTC 1260  
  
QY 1261 CCGAAGCACCATAGACATGTCGCTATGTTAATAGGAATTTTACTGCTGTTATATCGGCC 1320  
DB 1261 CCGAAGCACCATAGACATGTCGCTATGTTAATAGGAATTTTACTGCTGTTATATCGGCC 1320  
  
QY 1321 AAGGGTTATCGCTGCACTCTCTGGGCGATGTTTTCATCATTCACCAAGATAAATTCAT 1380  
DB 1321 AAGGGTTATCGCTGCACTCTCTGGGCGATGTTTTCATCATTCACCAAGATAAATTCAT 1380  
  
QY 1381 TGGTGTGACAGCGGGTGTATTGTTTTTGTGCTTTTTTTTACCTCGGTTTGCATTTTCAGA 1440  
DB 1381 TGGTGTGACAGCGGGTGTATTGTTTTTGTGCTTTTTTTTACTCGGTTTGCATTTTCAGA 1440  
  
QY 1441 GACACAGCTTCCGTTTATCACTTCTATATCCGAATGATATACATATAGGAATGACCT 1500  
DB 1441 GACACAGCTTCCGTTTATCACTTCTATATCCGAATGATATACATATAGGAATGACCT 1500  
  
QY 1501 TGGTGTCTTTGTTTACAGCGCGCTGACCGTGAAGCTTTTTTGTATCATTTATGAGCAAGAT 1560  
DB 1501 TGGTGTCTTTGTTTACAGCGCGCTGACCGTGAAGCTTTTTTGTATCATTTATGAGCAAGAT 1560  
  
QY 1561 AGAGAGAAAATATCTTGGAGATAACCGCATGTTCCAAATCATACTTCTTAATGTTAAT 1620  
DB 1561 AGAGAGAAAATATCTTGGAGATAACCGCATGTTCCAAATCATACTTCTTAATGTTAAT 1620  
  
QY 1621 GCGGTGATTTGCTTGGCTATTGCGCTCAGATTATTCCTGTGGGTATCAATCATATAAATG 1680  
DB 1621 GCGGTGATTTGCTTGGCTATTGCGCTCAGATTATTCCTGTGGGTATCAATCATATAAATG 1680  
  
QY 1681 AAAAAATTTGCTCTCTTTTTATTGCTTTTCTCATTTATPACGGCGTGGCGCTGCTCC 1740  
DB 1681 AAAAAATTTGCTCTCTTTTTATTGCTTTTCTCATTTATPACGGCGTGGCGCTGCTCC 1740  
  
QY 1741 ATCAGAGCATGACGGGGAGTATTATCTATGCGATTTGTCGAGACGATCATTAACCTT 1800  
DB 1741 ATCAGAGCATGACGGGGAGTATTATCTATGCGATTTGTCGAGACGATCATTAACCTT 1800  
  
QY 1801 TCGCTTTTCTCTCTGTTTTATATACGCAATGCGAAATCCTTCGGTGGGGGAG - AAAAA 1859  
DB 1801 TCGCTTTTCTCTCTGTTTTATATACGCAATGCGAAATCCTTCGGTGGGGGAGAAAAA 1860

Qy	1860	ATGAAGATAGTTCCTCCGAGTATCGCAATTAATCAAGAGTTCGAAGTCTGCGCTTACAC	1919	
Db	1861	ATGAAGATAGTTCCTCCGAGTATCGCAATTAATCAAGAGTTCGAAGTCTGCGCTTACAC	1920	
Qy	1920	GCTTATCGCTCGCGCTGACGCTGACGCTGACGCTGCGTTATGCGCCACACCGGCGAGGTTACA	1979	
Db	1921	GCTTATCGCTCGCGCTGACGCTGACGCTGACGCTGCGTTATGCGCCACACCGGCGAGGTTACA	1980	
Qy	1980	AAGGGTGACATCATCAGGTCGATGAAGCCAGACGATGCTGACAAACGATATTAACGGTA	2039	
Db	1981	AAGGGTGACATCATCAGGTCGATGAAGCCAGACGATGCTGACAAACGATATTAACGGTA	2040	
Qy	2040	TTTGAACGGGGGTCAGTCAGCGGTCGCGGTTCTCTGAAATCAGTCGCAATACGATGCC	2099	
Db	2041	TTTGAACGGGGGTCAGTCAGCGGTCGCGGTTCTCTGAAATCAGTCGCAATACGATGCC	2100	
Qy	2100	CTGGTTCTTTGGTTTTTAATATTTGGCCAGGGGAAATTTAAACGCTCTACCTTTGTGAAA	2159	
Db	2101	CTGGTTCTTTGGTTTTTAATATTTGGCCAGGGGAAATTTAAACGCTCTACCTTTGTGAAA	2160	
Qy	2160	AAACTCAACAAACAGGACTATGTCGGCGCCGGGAAACGAGTTTTTACGCTGGACCCCGGCC	2219	
Db	2161	AAACTCAACAAACAGGACTATGTCGGCGCCGGGAAACGAGTTTTTACGCTGGACCCCGGCC	2220	
Qy	2220	AATGGGAAGTCTCTCCCGACTGATTCGCCGACGCGAAGCTGAAACGGGTGTTGTTGAG	2279	
Db	2221	AATGGGAAGTCTCTCTCCCGACTGATTCGCCGACGCGAAGCTGAAACGGGTGTTGTTGAG	2280	
Qy	2280	AAACTGGGTGATTAACCTTTTGGAGTACCCCAAGATGAAGATTAACACCGCGCGTACT	2337	
Db	2281	AAACTGGGTGATTAACCTTTTGGAGTACCCCAAGATGAAGATTAACACCGCGCGTACT	2340	
Qy	2338	GAGCGGTGGCGCAACATGAATAAATGACGTGTGACGGCTGCTCTTCAACACGGATGGG	2397	
Db	2341	GAGCGGTGGCGCAACATGAATAAATGACGTGTGACGGCTGCTCTTCAACACGGATGGG	2400	
Qy	2398	ACCATCAACGTAATGAATGAGGCAAGACATTAATGATAATTAATGATATTTCTGGAGAA	2457	
Db	2401	ACCATCAACGTAATGAATGAGGCAAGACATTAATGATAATTAATGATATTTCTGGAGAA	2460	
Qy	2458	AGTGAATGCTCCAGGACAGCTGTGAGAGAAACGATACAGCGGTGACGTCAGCGGA	2517	
Db	2461	AGTGAATGCTCCAGGACAGCTGTGAGAGAAACGATACAGCGGTGACGTCAGCGGA	2520	
Qy	2518	TTTATTTCTCGGTTCTGTTCCGAGGTCAGAAATCACTGGCGACAGCGCTGTCATGGGG	2577	
Db	2521	TTTATTTCTCGGTTCTGTTCCGAGGTCAGAAATCACTGGCGACAGCGCTGTCATGGGG	2580	
Qy	2578	AGAGGTCGCTATCTGTACAGTCAGGCGCAGCAGCAAGAGAAACCGGCTCACCGA	2637	
Db	2581	AGAGGTCGCTATCTGTACAGTCAGGCGCAGCAGCAAGAGAAACCGGCTCACCGA	2640	
Qy	2638	ATCCGTTATTTGGCCGGGGAATCCCTTACCTGTTGAATGCGGTTCCGCTGGGAATACG	2697	
Db	2641	ATCCGTTATTTGGCCGGGGAATCCCTTACCTGTTGAATGCGGTTCCGCTGGGAATACG	2700	
Qy	2698	GCAGGACGCGGACGTCGAGCTATGATGCTGTTGGCTCCGCGCAGACCGTTTCGC	2757	
Db	2701	GCAGGACGCGGACGTCGAGCTATGATGCTGTTGGCTCCGCGCAGACCGTTTCGC	2760	
Qy	2758	CCGCCCCGGGCTCGGTGGCTTCAATGTTCTCAACCGGCGGCTATCTGACCGAGCTGTACCG	2817	
Db	2761	CCGCCCCGGGCTCGGTGGCTTCAATGTTCTCAACCGGCGGCTATCTGACCGAGCTGTACCG	2820	
Qy	2818	TGAGGCGAAGACCTGTCATCCGACACCTCGCTGTTCCGGCTGGACATCCGGCGTCCCGA	2877	
Db	2821	TGAGGCGAAGACCTGTCATCCGACACCTCGCTGTTCCGGCTGGACATCCGGCGTCCCGA	2880	
Qy	2878	CCTGGCGGCGCTGGCCCTTAGCCAGATAATATGACGACGAGCTCTCCACCTGAGCCT	2937	
Db	2881	CCTGGCGGCGCTGGCCCTTAGCCAGATAATATGACGACGAGCTCTCCACCTGAGCCT	2940	
Qy	2938	GTCCAATGAGCTACTGTATCGCGTATCGGGGACGCGGAGGGGCTTGACGACGACGCGT	2997	
Db	2941	GTCCAATGAGCTACTGTATCGCGTATCGGGGACGCGGAGGGGCTTGACGACGACGCGT	3000	
Qy	2998	CAGGGAGCTGCTCGCGGGTATCGCTGACCGGCTGACCCCTATCCTACCTGGCGGTACGA	3057	
Db	3001	CAGGGAGCTGCTCGCGGGTATCGCTGACCGGCTGACCCCTATCCTACCTGGCGGTACGA	3060	
Qy	3058	GGCGGCGCCCAAGCCATTTCTGGTGAGGACCGGACGCTGATGGGGTTACGCGGTATACC	3117	
Db	3061	GGCGGCGCCCAAGCCATTTCTGGTGAGGACCGGACGCTGATGGGGTTACGCGGTATACC	3120	
Qy	3118	GGATGTGGCGGCTTATGGAACCTGCTCCATGCTGGCCATTTGAAGCCGATATTTCAACC	3177	
Db	3121	GGATGTGGCGGCTTATGGAACCTGCTCCATGCTGGCCATTTGAAGCCGATATTTCAACC	3180	
Qy	3178	GGAGCTGTATCAGATACCTGCGGAGCAAAATTAACGACAGCTTACGAGCAGCTCTGGAG	3237	
Db	3181	GGAGCTGTATCAGATACCTGCGGAGCAAAATTAACGACAGCTTACGAGCAGCTCTGGAG	3240	
Qy	3238	TAAGAAATTTGGTGATATGCTCCCTCCTCCTCTGTTATCTTATGATGCACTTGCAACATTT	3297	
Db	3241	TAAGAAATTTGGTGATATGCTCCCTCCTCCTCTGTTATCTTATGATGCACTTGCAACATTT	3300	
Qy	3298	TTATGATCTTGATTAACGATGAGCTAACTTCTGTTTATTTGTCATTAAGGCTGACCTTTTCAAA	3357	
Db	3301	TTATGATCTTGATTAACGATGAGCTAACTTCTGTTTATTTGTCATTAAGGCTGACCTTTTCAAA	3360	
Qy	3358	TCCAAACAATGATACATTAATGATCAATTAAGTTCGTAATCTGTAATCAAGGACAC	3417	
Db	3361	TCCAAACAATGATACATTAATGATCAATTAAGTTCGTAATCTGTAATCAAGGACAC	3420	
Qy	3418	TGGTTTAAATAACATATACATCACTTATTAAGAACGCTAGGCGGAGACTCACAGCAGATTAA	3477	
Db	3421	TGGTTTAAATAACATATACATCACTTATTAAGAACGCTAGGCGGAGACTCACAGCAGATTAA	3480	
Qy	3478	CCCTGAGCTTATACCTTATGCGGATGGAACATATCTTTTAAATTTAGCGTGTGTCAAC	3537	
Db	3481	CCCTGAGCTTATACCTTATGCGGATGGAACATATCTTTTAAATTTAGCGTGTGTCAAC	3540	
Qy	3538	GATATCAGAGGATGTTTCAAACTAGGCTGTTAGGTTCTTAACAGTAGCAATCTTTACTC	3597	
Db	3541	GATATCAGAGGATGTTTCAAACTAGGCTGTTAGGTTCTTAACAGTAGCAATCTTTACTC	3600	
Qy	3598	TGGGGATTTACAGCTTCAAAAAGGGGTTGCTATAGCATTCCTGTTGAAATAGATGAAGG	3657	
Db	3601	TGGGGATTTACAGCTTCAAAAAGGGGTTGCTATAGCATTCCTGTTGAAATAGATGAAGG	3660	
Qy	3658	AAAGTTAAATGATGGGATCAATAGGATTTAGTAGGAAAGGGGGGGATTTTACTCAAC	3717	
Db	3661	AAAGTTAAATGATGGGATCAATAGGATTTAGTAGGAAAGGGGGGGATTTTACTCAAC	3720	
Qy	3718	AGTAAATTTCACTCTGATGGAATATGATCTGCGATATTCATTTCTTAAATTAATTAAGT	3777	
Db	3721	AGTAAATTTCACTCTGATGGAATATGATCTGCGATATTCATTTCTTAAATTAATTAAGT	3780	
Qy	3778	TATCCGCTTATCAAGCCACCGGATGACACCGCGGAAATATATCAAAATCACCATAT	3837	
Db	3781	TATCCGCTTATCAAGCCACCGGATGACACCGCGGAAATATATCAAAATCACCATAT	3840	
Qy	3838	TCTTAATAACGGTCTCACCATTGACCATGCGGCTCTGAGTAAATCTTCTGCTGGTTCGTTA	3897	
Db	3841	TCTTAATAACGGTCTCACCATTGACCATGCGGCTCTGAGTAAATCTTCTGCTGGTTCGTTA	3900	
Qy	3898	CCTGATGCTCACTATCAGCTTGAATGCGGCTGCTGATATTTGCAACCGAACCAT	3957	
Db	3901	CCTGATGCTCACTATCAGCTTGAATGCGGCTGCTGATATTTGCAACCGAACCAT	3960	
Qy	3958	CAGTGACCGGCTTCAGCGGCGAAACCGGCTGTTCAACCGCTGTTCAACCGCCACC	4017	
Db	3961	CAGTGACCGGCTTCAGCGGCGAAACCGGCTGTTCAACCGCTGTTCAACCGCCACC	4020	
Qy	4018	GCTGAACCGGCGAGCTGTTTCTCAGATGATACCCCTCCTGACTTACGCTCTGAGGACCC	4077	

Db 4021 GCTGAACGGCCAGCTGTTTTCTGCAGATGATACCCCTCGACTTACGCTCTGAAGCACC 4080  
 Qy 4078 GGAGGATGCTTTCCGCTCAGCCTACTGAACCGGCATTAAATCAGCGCTCGGGCT 4137  
 Db 4081 GGAGGATGCTTTCCGCTCAGCCTACTGAACCGGCATTAAATCAGCGCTCGGGCT 4140  
 Qy 4138 TTCCACGCTCTGGCAGTTGGCCAGCGGTGACAGCAGCGCTGGGTTTAACTGCTCTCTCTGA 4197  
 Db 4141 TTCCACGCTCTGGCAGTTGGCCAGCGGTGACAGCAGCGCTGGGTTTAACTGCTCTCTCTGA 4200  
 Qy 4198 CAATATCGCGCACTCTACCGAGTGAACCTCTCGGCTGACATCCAGCACTATCCGCTGG 4257  
 Db 4201 CAATATCGCGCACTCTACCGAGTGAACCTCTCGGCTGACATCCAGCACTATCCGCTGG 4260  
 Qy 4258 TGAGCTGTCAATGTTGCTGCTCGCTCTCCCTTTTTCAGGGGGTGGCCGCGCTCGCTGTC 4317  
 Db 4261 TGAGCTGTCAATGTTGCTGCTCGCTCTCCCTTTTTCAGGGGGTGGCCGCGCTCGCTGTC 4320  
 Qy 4318 CGATAATGAGCTGACGCACTTTCTGTACAGACCACTCTGGCTCACGAGCAGGGCTG 4377  
 Db 4321 CGATAATGAGCTGACGCACTTTCTGTACAGACCACTCTGGCTCACGAGCAGGGCTG 4380  
 Qy 4378 GACGGTCAGCGATGTTTCTGTATGTGACGACGAGTACGGTACCCTGCTGACCCCGA 4437  
 Db 4381 GACGGTCAGCGATGTTTCTGTATGTGACGACGAGTACGGTACCCTGCTGACCCCGA 4440  
 Qy 4438 CATTTGAGAACCTGCTCGCTTCCCTGCGCAACGAGTGTGGGCGGTGAGCTGTTCCCGA 4497  
 Db 4441 CATTTGAGAACCTGCTCGCTTCCCTGCGCAACGAGTGTGGGCGGTGAGCTGTTCCCGA 4500  
 Qy 4498 AACGCTTCCCGCGATGGGCTCCCTTTATTTGCGCGGCCATCGAGCTGGAAGCCACCGA 4557  
 Db 4501 AACGCTTCCCGCGATGGGCTCCCTTTATTTGCGCGGCCATCGAGCTGGAAGCCACCGA 4560  
 Qy 4558 TAGCGGAAGGCGATGCTGACTTTGGGCGGACCACTGATCATCCGAGCAGCGGCTCAGCAG 4617  
 Db 4561 TAGCGGAAGGCGATGCTGACTTTGGGCGGACCACTGATCATCCGAGCAGCGGCTCAGCAG 4620  
 Qy 4618 GGAATTTATTTCTTTGATGATGATGCGCCCAATGAGAGCGAGCGGCGGCGAGTGGC 4677  
 Db 4621 GGAATTTATTTCTTTGATGATGATGCGCCCAATGAGAGCGAGCGGCGGCGAGTGGC 4680  
 Qy 4678 AGGTTTCTGCCAAGCCCTGTGGCACTTGGCACTGATCATCCGAGCAGCGGCTCAGCAG 4737  
 Db 4681 AGGTTTCTGCCAAGCCCTGTGGCACTTGGCACTGATCATCCGAGCAGCGGCTCAGCAG 4740  
 Qy 4738 GCGCGAGCTGACGCTGCTGCTGAGCAGCGGGAAGCTTCCGCAAGATGGACCACTCT 4797  
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 Db 4921 GCTGGCCGCGGCTCTGACAGATGAGCAGGATGAGACCGGCTTGGCGAGGTGAG 4980  
 Qy 4978 GGGGGCGGTGAACAGCAACAGCGTGTTCACCTCTCGGAAGAGGTGACAGGCTGA 5037  
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 Db 5401 GGCCTTTAAACCGAATAGAACTCAGCGCCATGCGCAGAGGTGAGGGGCGCTCAGTTTTTAC 5460  
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Qy 8458 GCTGGCCGTCGGGGCTCCGCTATGGGGCACTATTAAAGCCACCGCCATCGGATCCA 8517  
Db 8461 GCTGGCCGTCGGGGCTCCGCTATGGGGCACTATTAAAGCCACCGCCATCGGATCCA 8520  
Qy 8518 GGTGTCTCTCGGATGCCACCGCATATCAGCGGACAAAATCAGCAGTCGGAAGTGTACCG 8577  
Db 8521 GGTGTCTCTCGGATGCCACCGCATATCAGCGGACAAAATCAGCAGTCGGAAGTGTACCG 8580  
Qy 8578 CCGTCCCGGAGAGTGGGAAATCCAGCGTATAGTGCAGTCTGACGTGGCGAGAT 8637  
Db 8581 CCGTCCCGGAGAGTGGGAAATCCAGCGTATAGTGCAGTCTGACGTGGCGAGAT 8640  
Qy 8638 TGATGCCAGCTGGCGGCATGCGAGTGGCCGGGAAGGGCTGAGCTGCAGAAACTTA 8697  
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Db	10621	TTGCTGAGTACACAGGAAAGTCCTTCACTCAGTCTGCTCGAGAACGTGACCAAGGTGGCT	10680	Qy	11758	TATCGCAGTTCGGTGCAGTTCGGCTGGATGAGAAACCGAGCACTGGCGGCGAGCAGT	11817
Qy	10678	TATGAGTCGACCGGAGCTTTGTGCTTCCCGCACTGCAATTTGGGGTGGCAAACTTT	10737	Db	11761	TATCGCAGTTCGGTGCAGTTCGGCTGGATGAGAAACCGAGCACTGGCGGCGAGCAGT	11820
Db	10681	TATGAGTCGACCGGAGCTTTGTGCTTCCCGCACTGCAATTTGGGGTGGCAAACTTT	10740	Qy	11818	TCCCTCGCTGCTTACCTGCAATTTACATTTGCATACCTGTGGGCTTCGGTGGTGCAGGAT	11877
Qy	10738	ACCCGCGGACATTTGTCCGATGACAGACGCTGACGATATGGCAAGTTGAGTTGCTT	10797	Db	11821	TCCCTCGCTGCTTACCTGCAATTTACATTTGCATACCTGTGGGCTTCGGTGGTGCAGGAT	11880
Db	10741	ACCCGCGGACATTTGTCCGATGACAGACGCTGACGATATGGCAAGTTGAGTTGCTT	10800	Qy	11878	GAGATCACCGGTAAACCGTCTGTGTCAGCAGCTGCTTTATTCGCCACGCGCTTCGGGACGG	11937
Qy	10798	CAACCTTATCAGCTTTAGACCTTAAACGGGAAAGTGTGTGGTATCTCTGTATCAGGAC	10857	Db	11881	GAGATCACCGGTAAACCGTCTGTGTCAGCAGCTGCTTTATTCGCCACGCGCTTCGGGACGG	11940
Db	10801	CAACCTTATCAGCTTTAGACCTTAAACGGGAAAGTGTGTGGTATCTCTGTATCAGGAC	10860	Qy	11938	CAGGAACGGGAGTTTCGGGGGTTTGGTTTGTGAGATCAGGATACCGATACCTTGGCA	11997
Qy	10858	AGCGGTGCTGTGTACCTGTACCGGTACCGGTACCGGTACCGGTACCGGTACCGGTACCGGT	10917	Db	11941	CAGGAACGGGAGTTTCGGGGGTTTGGTTTGTGAGATCAGGATACCGATACCTTGGCA	12000
Db	10861	AGCGGTGCTGTGTACCTGTACCGGTACCGGTACCGGTACCGGTACCGGTACCGGTACCGGT	10920	Qy	11998	AGCCAGGTAACGGGACGGAACTGAGTATGCTTCTGTGAGCGGAACTGCTATGCCACC	12057
Qy	10918	ACCTGGGGGGCGCTGCGGCCCTGCCCAATGCCGCTTTGCATTAACAGCGCATCCTG	10977	Db	12001	AGCCAGGTAACGGGACGGAACTGAGTATGCTTCTGTGAGCGGAACTGCTATGCCACC	12060
Db	10921	ACCTGGGGGGCGCTGCGGCCCTGCCCAATGCCGCTTTGCATTAACAGCGCATCCTG	10980	Qy	12058	GGGTTACCGGCACTAGACGAGCGTCTGCCGGAGACGTATTTGGCAAAACGATGCCGCT	12117
Qy	10978	GGGATCTTAATGGGATGTGCGCTGGAGTGGTCTGTACCGCCCGCTGTGGCGGG	11037	Db	12061	GGGTTACCGGCACTAGACGAGCGTCTGCCGGAGACGTATTTGGCAAAACGATGCCGCT	12120
Db	10981	GGGATCTTAATGGGATGTGCGCTGGAGTGGTCTGTACCGCCCGCTGTGGCGGG	11040	Qy	12118	TTTGCCGATTCGCGACCGTTTCACTGTGCTTCTGAGGAGATGAGGAGATATATCT	12177
Qy	11038	ATGTATGATCGCACCCCGCGCGGACTGTTGATTTTCAACCCCTGTCAGCTTTGCC	11097	Db	12121	TTTGCCGATTCGCGACCGTTTCACTGTGCTTCTGAGGAGATGAGGAGATATATCT	12180
Db	11041	ATGTATGATCGCACCCCGCGCGGACTGTTGATTTTCAACCCCTGTCAGCTTTGCC	11100	Qy	12178	CGCGACGACAGCAAGACATTTCTGGTTGACGAGCGCTTGAAGGCTTCTGCTGCCGAGT	12237
Qy	11098	GTAGAATATCGCATCCAAAGCAGTCTCGCGATATCTTGGGGCTGGTTAAACGGAC	11157	Db	12181	CGCGACGACAGCAAGACATTTCTGGTTGACGAGCGCTTGAAGGCTTCTGCTGCCGAGT	12240
Db	11101	GTAGAATATCGCATCCAAAGCAGTCTCGCGATATCTTGGGGCTGGTTAAACGGAC	11160	Qy	12238	GAGTTATACGGTCCGATGGCAGCAGCGCGGATATCCCTTACAGCGTCACTGAGTCT	12297
Qy	11158	ATGGTCTTATCGGGCCGCGAGTGTTCGCTCTTATTCGGGCAAAACGATGTGGAAT	11217	Db	12241	GAGTTATACGGTCCGATGGCAGCAGCGCGGATATCCCTTACAGCGTCACTGAGTCT	12300
Db	11161	ATGGTCTTATCGGGCCGCGAGTGTTCGCTCTTATTCGGGCAAAACGATGTGGAAT	11220	Qy	12298	CGCCCGCAGTACGGCTAGTCTGAGCGAATGAGACTCCCGTGTGTGGCGGATGGG	12357
Qy	11218	AAAGGGAGACCTGCAGCAAAACGGAAGACTCACTTGCCTGCTCCCGGGTGGACCCA	11277	Db	12301	CGCCCGCAGTACGGCTAGTCTGAGCGAATGAGACTCACTCCCGTGTGTGGCGGATGGG	12360
Db	11221	AAAGGGAGACCTGCAGCAAAACGGAAGACTCACTTGCCTGCTCCCGGGTGGACCCA	11280	Qy	12358	CGCGAAAGCGTACGCTAGTCTGAGCGAATGAGACTCACTCAATGATCCTCAATGCCAACAGCAG	12417
Qy	11278	CGTACCTCTGCGGCTTCACTGATATGGCTGGAGTGAGCAGCAGATTTGACGAGGTG	11337	Db	12361	CGCGAAAGCGTACGCTAGTCTGAGCGAATGAGACTCACTCAATGATCCTCAATGCCAACAGCAG	12420
Db	11281	CGTACCTCTGCGGCTTCACTGATATGGCTGGAGTGAGCAGCAGATTTGACGAGGTG	11340	Qy	12418	GCGGTAATCTCTCAGTGAATGAATACGGTTTCCCACTCGCTCAGTCTGATGTCATTTATCCA	12477
Qy	11338	CGTCTAATCGAGTACGTTACTGCGCAACCTCGGGCAAGCTGCTTTCGGTCAAGCGGTG	11397	Db	12421	GCGGTAATCTCTCAGTGAATGAATACGGTTTCCCACTCGCTCAGTCTGATGTCATTTATCCA	12480
Db	11341	CGTCTAATCGAGTACGTTACTGCGCAACCTCGGGCAAGCTGCTTTCGGTCAAGCGGTG	11400	Qy	12478	CGAGCCCTCCGTCGCGGACCAATCCATATCCGGCTCTTACCGGCGAGCTGTTTCGCC	12537
Qy	11398	AATATTCGCGTTTACCGAGTCACTGACTAGTTTAAACCTGACCAAGATTTGCTGGCC	11457	Db	12481	CGAGCCCTCCGTCGCGGACCAATCCATATCCGGCTCTTACCGGCGAGCTGTTTCGCC	12540
Db	11401	AATATTCGCGTTTACCGAGTCACTGACTAGTTTAAACCTGACCAAGATTTGCTGGCC	11460	Qy	12538	AACAGTTATGACAGCAGCAGCAGATATTAACGCTTCGGGTTGCAACAGAGCAGTGCACAT	12597
Qy	11458	GATACCGACCGTTCCGCTACACCGACCTGATTTATCGGATGAGTGACCGTTTGTGTCATT	11517	Db	12541	AACAGTTATGACAGCAGCAGCAGATATTAACGCTTCGGGTTGCAACAGAGCAGTGCACAT	12600
Db	11461	GATACCGACCGTTCCGCTACACCGACCTGATTTATCGGATGAGTGACCGTTTGTGTCATT	11520	Qy	12598	CACCTTGTTCCTGCTGAGGGGCAATGGTTTGGGTTTGGGTTTGGCGAGGCGTCCGGGAC	12657
Qy	11518	TATTTCAACAGAGTGTAAATTTTCGCGAGCGCATACGCTGCTTTTCCGCAAGGT	11577	Db	12601	CACCTTGTTCCTGCTGAGGGGCAATGGTTTGGGTTTGGGTTTGGCGAGGCGTCCGGGAC	12660
Db	11521	TATTTCAACAGAGTGTAAATTTTCGCGAGCGCATACGCTGCTTTTCCGCAAGGT	11580	Qy	12658	GATGATTCACGTACTCTCGGACCAAGTTCGCGGAGGGGCTGACGCTGGGACACCTG	12717
Qy	11578	GTGGCTATGATCGCACCTGAGTCTGCAAGTGGCGGATATCAAGGGCTGGGGGTGCT	11637	Db	12661	GATGATTCACGTACTCTCGGACCAAGTTCGCGGAGGGGCTGACGCTGGGACACCTG	12720
Db	11581	GTGGCTATGATCGCACCTGAGTCTGCAAGTGGCGGATATCAAGGGCTGGGGGTGCT	11640	Qy	12718	TTGGCCCGGAAAGCCTGCTCGGATAGTTCAGTCTGCTGCGGCTGAGCAGCA	12777
Qy	11638	AGCTGTTACTGAGCGTCCCAATGTCGCGCTCATCATCGGTTGGTGGCAATTTATCGGCA	11697	Db	12721	TTGGCCCGGAAAGCCTGCTCGGATAGTTCAGTCTGCTGCGGCTGAGCAGCA	12780
Db	11641	AGCTGTTACTGAGCGTCCCAATGTCGCGCTCATCATCGGTTGGTGGCAATTTATCGGCA	11700	Qy	12778	GTCTGATCTGGAATTCACAAAGAGTTCGCAAGTTCGCTGCTGCTCCGCCACTTCCCCCAAG	12837
Qy	11698	GACAAACCCCTGGTTGTAATGGCATGAACAAATATGGGGGCCCGGCATGCACTGCAC	11757				

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XX P-PSDB; AAY33728, AAY33729, AAY33730.
XX New nucleic acid from Photorhabdus luminescens encoding insecticidal
XX toxins, used for making resistant transgenic plants.
XX Claim 1; Page 99-130; 148pp; English.
XX This sequence represents an approximately 38kb fragment of Photorhabdus
XX luminescens DNA comprised in the plasmid pNOV2400 (NRRL B-30077). This
XX sequence contains 16 open reading frames (orfs) which encode three
XX insecticidal toxins. This sequence was isolated from a P. luminescens
XX cosmid library which had been screened for insecticidal activity. P.
XX luminescens is a member of the Enterobacteriaceae family and is a
XX symbiotic bacterium of nematodes of the genus Heterorhabditis. The
XX nematodes colonise insect larvae, kill them, and their offspring feed on
XX the dead larvae. However, the insecticidal agents are produced by P.

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CC luminescens rather than the nematodes. The toxins have activity against
CC Lepidopteran insects such as Cabbage Looper (Trichoplusia ni), European
CC Corn Borer (Ostrinia nubilalis) and Fall Armyworm (Spodoptera frugiperda)
CC and also against Coleopteran insects (e.g., Colorado Potato Beetle,
CC Leptinotarsa decimlineata). In addition the toxins are active against
CC strains resistant to known insecticides. This sequence can be used to
CC generate transgenic plants of various species that are resistant to
CC economically important insect pests and also for recombinant production
CC of toxins for use as insecticides
XX Sequence 37948 BP; 11822 A; 8637 C; 7661 G; 9828 T; 0 U; 0 Other;
SQ Query Match 12.5%; Score 2368.8; DB 2; Length 37948;
Best Local Similarity 54.0%; Pred. No. 0;
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Qy	6777	CTCAAGATTTTGGAGTAAAGTCTCATGCGGCACCTTCAGATATATGATTAATCG	6836	17816	GCTGCCGCTCCCGAGACACGCGCGGAAATTCCTGACGGCACTGTTCTCTCCCGCAGCA	7875
Db	7065	TAAACAATTTCTATGATGATGACCGGTGATTTGACATGATGTTTCAGGGATAT	7124	18145	ACTTCTCATCCACAGGCTTAAAGATGAATCAAAACAGATCTTTCTGCGCGCAAGT	8204
Qy	6837	ATGATATCATCTGACATCCGGGTAAATGGGACTGAAATTTAAATCCTGGCCTTCGCTG	6896	17876	GAAAGAGTGTCTCAAAGGCTACTGGCAACCTTTGGCAGCGGCTCCATAAACCTGCGCCA	7935
Db	7125	ATCTATTATACGAACATTAATCATTTCAAAGTTTAAAGTAAATAGTGAAGCCGAGGTAT	7184	18205	CAACGAAAGTGTGCTGAGCTACTGGCAGAAACTAGAAACAACGGTTGTATAAACCCTGCGCA	8264
Qy	6897	AATGGTATATGATAGTGAAGTCTGCAATCCGGGAAT-----AATCTTTTCAACAC	6948	17936	CAACCTCTCCATGACGGCAGCGCTTTCCTCTGCTGCTAGCCACGCGCTCCGAAAC	7995
Db	7185	CACAGAGCAACTTTTGTAGCGAGCGAACAACAGTAATGTCGCCCAATCCGTCGCTT	7244	18265	TAAACCTCTATTGATGTTCAACCTTTTACATTTGCTTATTTTCGAACAACCGAGATCC	8324
Qy	6949	CAAACTCGTGTGTTTACCGTTTAAATACAGTATGTTT-----GAAGA	6993	17996	GTCGCCCTGACAGTGGCGTCTCAACAGCGCGAGGCTGCTGCAGCACTGCGCGCCG	8055
Db	7245	CGAAGAAATGAATATCAGTTTAAAGAGCTTGAATAGATATCTCCACACTGACATTTCA	7304	18325	AAAAGCGTGTCTCAGCGCGCTGTCCCGAGTTTCAAGGTGGAATTAATCTTCCATCAGA	8384
Qy	6994	TGAGTTTGAAGTACGCTTACGTTTCACCGCTGCGATCAGAATAACGCTGCTGGCCG	7053	18056	GGTGATGCGCGTTTACAGTTTCCCGGTCTATGCTGGAGAACGCGCGGGGATGGTAGCCT	8115
Db	7305	TAATAATGAAGCAAGTATGATATCACCCTTATCGCATTTGCTGAGAAATTTGACATAA	7364	18385	ATTTATATCAGTGTGGCGTTTCCCTCATATGCTGGAACACGCCCTGATGATGTCAGTCA	8444
Qy	7054	CGGACGGCGATTAATACCGTCAATCGAAACATTAATATGACACTTCCGTTATCGCAT	7113	18116	GCTGACCGGTTTCGGCAACACACTGCTCGGTATTATCCGAGCGTCAAGTATGCGAGCGCT	8175
Db	7365	TAGTAATGATCGTAACTTAGCGCAAGAACATTTTCAGTATTCGTTATTTATCAAAAAGCGGA	7424	18445	GCTAAACCAATTTCCGCTCCACATTTGCAAAATATTATCGAACTCAAGATGCGGAGCAT	8504
Qy	7114	ACGTAAATACCGTGGCGCGAGTATATTCGTTTCACTGCGGGTAAACGATGTG-----	7168	18176	GGCCAAACTGCTGACAGCCCGGAGTGAATGATACCCAGGCGCTTTCGCCAGCAGGA	8235
Db	7425	AACTGATATGCTGACCTGACCCATATGCAAAACGGGGCGCAATATATGACGTGGGG	7484	18505	AAACAGCTGTTGCAAAATCAGCGCGCAACTGATATTGACCAATCTCAGCATACAGGA	8564
Qy	7169	----GCGCTTATTCGCTCAACACCTCTTTTCCCGCCCACTGGTGCAGCCGGCGCAATAC	7224	18236	TAAAGCTCTCGAGGAAATCGATGCGGATATTCCCGCCTTGGAGGAGAGCGCGCGCGC	8295
				18565	CAAAACCATCCAAGAGCTGGATGCTGAAATAAACTGTGCTAGAAAAAAACCGCGCGGAAC	8624



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Db 15059 ATTACCTACTACAACTATTGTAGAAAAACGA-----ATATA 15094  
QY 14457 GCGGCTACGACGAAGCAGAAAAATAGCGATTTAGCCGTTAAGGAAAAGTGACGGTGT 14516  
Db 15095 TAGAAAAAATACTAACATGCAGATAAAAACTGCGATTGCGAAGACAGATGACACACAAAGCCCC 15154  
QY 14517 TTTCGGGATTAATATTAAACAGAGAGATCAATGAGACATCTTGTTCAGTAGACCCCGT 14576  
Db 15155 AACAAAGAGGTAAAT---CATGAANAACATCGATCTCTAACTTTATCAAAAGACCCCTGT 15211  
QY 14577 CGGTGCGGGTCTCGACAACCGCGGCTGTGTGTGGGAGCTGCAGTACTACCGGCATC 14636  
Db 15212 C-GTCAACATCTACGATACCGAGGTCTAACGATCCGTACAT---CGACTTTCACCGTA 15267  
QY 14637 CGGATACCGGAGGAGACGAGCGGTATACCTGCCATCAGCAGATGAGCGCGGCA 14696  
Db 15268 CCACCGCAAAACGCGGATACCGATATCCGTATTACTCGCCATCAATATGACTCCCTGGGC 15327  
QY 14697 GCTTGTCAAAAGCGCGGACCGCGGTACACGCGCCCGTCTGACA---AATTTCACGT 14753  
Db 15328 ACCTAAGCCAAAGACCGATCCGCGTCTATATGAAGCCAAACAAAATCTAACTTTCTCT 15387  
QY 14754 ACCTGAATAGCTGCACCGGACAGTACTGCAGAGCGTGCAGCGCGGATGCCGTACGTCG 14813  
Db 15388 GGCAGTATGATTGACCGGTAAATTTTGTGTACAGAAAGCGTCGATGCTGTGCGACTG 15447  
QY 14814 TGAATCGAGCGATGCGCGCGGCGGCGGTTCTGCGCGTACCGGGCTGGGAACGAAG 14873  
Db 15448 TCACCTTGAATGATATTGAAGGCGTCCGCTACTGACAGTAAGTAACTGCAACAGG----- 15499  
QY 14874 ACGCGTCAACCGCACTGCGCATATGAAGACATACCTGCCGCGCGCCGCTGAGCA 14933  
Db 15500 ----TGTCATACAAAACCGACAATATGAACGFTTTCCTTACCCTGCTGTGTGTCGTG 15555  
QY 14934 TCACCGAGCAGGTTACCGGTGAAGCGGCCCAATTACGAAACGCTTCGTGTACGCTGGCA 14993  
Db 15556 TTACCGNACAAATACAGAAAAAACATCCGATATACCGAAGCGCTGATTGGGCTGGCA 15615  
QY 14994 ATACGATCCGAGAGATTTCTCAATCTGCTGGCCAGTGTGTGTCAGTCAATTACGATACC 15053  
Db 15616 ATAGCAAGCAGAGAAAAACATAATCTTGCCAGCCAGTGCCTGCCCACTATGACACGG 15675  
QY 15054 CCGGACTGTGCAGACGGACAGCATCGCTGAGCGCGCTGCCCTCGCGCTCAGCGGC 15113  
Db 15676 CGGAGTCAACCGATTAGAGAGTTTGTCACTGACCCGTTACTGTGTTTATCTCAATCCAGCC 15735  
QY 15114 AGTTGCTGCCGACGCGGGGGCCAACTGGATGGGTGAGGATGCCTCGGCCCTGGAATG 15173  
Db 15736 AACTATTGAGCGACACTCAAGAGCTAGCTGGACAGTGATATGAACCGTCTGGCAAA 15795  
QY 15174 ACCTGCTGATGGGAGAGTTCCTTCCACGAGACCCACGCTGATGCGACGCGCGCGCTCC 15233  
Db 15796 ACATGCTGGGTGATGACATCTACAAACCTGAGCGCCTTTGATGCAACGCGCGCTTTAC 15855  
QY 15234 TGAGCATACCGATGCAAAAGGTAATCTGCAGCGTGTGSCATATGATGGCTGGGCTGC 15293  
Db 15856 TCACTCAGACCGGATCGAAAGGGAACATTCAGAGGCTAACCTATGATGTGGCGGCGAGC 15915  
QY 15294 TATCGGGCAGTTGGTTGACGCTGAAGGACGGCAGGAGAGGTCACTGTGGCTCCCTGA 15353  
Db 15916 TAAACGGGAGCTGGTTAAACCTTAAAGAACCAACCGGAACAAGTATCAGATCCCTGA 15975  
QY 15354 CGTACTCGGCGCGGGAAAAAGTTGCGTGAAGAACACCGGCAACGCGGTGTTAACTCGT 15413  
Db 15976 CCTATTCCGCGCGCGCAAAAAATTACGGAGGAACACGCGCATGTGTGTTATCACCGAAT 16035  
QY 15414 ATATTTACGAGCGGAAAAACACGCGCTGCAGCGGATTAAGACGGAACGTCGCTGGGC 15473  
Db 16036 ACGTTATGAAACCGGAACCCAAACAGCTTATCGGTACCAAAACCCACCGTCCGTAGAT- 16094  
QY 15474 ACGTTCGGGACAAAGTGTCTGACGACCTGCGCTATACGTATGACCCGGTAGGCAACG 15533

Db 16095 -----GCCAAAGTGTTCAGATCTACGATTACGATTAGACCCGGTAGGCAATG 16143  
QY 15534 TACTCAGCGCTCAATAACGATCGGAGAGACCCGCTTCTGGCGTAACCAAGAAAGTGGTAT 15593  
Db 16144 TCATCAGTATCCGTATATGACGAGAGCCACCCGCTTCTGGCAATCAGAAAGTGGCGC 16203  
QY 15594 CGGAGATACGTACATCTACGACAGCGCTGTACAGCTGTGTCAGCGCCACGAGCGGTGAGA 15653  
Db 16204 CGGAAAAACATTTATACCTACGACTCCTTGTATCAGCTTATCAGCGCAACCCGGCGCGAGA 16263  
QY 15654 TGGCCAAATCCCGCGCAGCAGGCAAGCACTTACATCCGCTACAGCGCCCGCTTCTTACAG 15713  
Db 16264 TGGCGATATAGGTGAGCAAAAGTAACCAACTTCCCTCC-----CTCACCTTACCTTCTG 16317  
QY 15714 ACAGTCTCTGCTTACCAATTAACGCGCACCTACCGTTTATGACCGTGTGGCAACCTGA 15773  
Db 16318 ATAAACAACCTTACCACTATACCGTACTTATCTTATGACCGTGGCGCAATTTGA 16377  
QY 15774 CGCAGATGCGCCACAGTGCCTGCACGAAACAATAATTTATACGACAGACATCAGGTTA 15833  
Db 16378 CTAAATCCAGCACAGTTTACC CGCGGACGCAAAACAACCTACACCAAAACATCACGGTTT 16437  
QY 15834 GTGACCGCAATAGGCGGTACTGACGACGCTTGGCGGAAGTGCCTGAGATGTTGATA 15893  
Db 16438 CTAAACCGAGCAATCGCGAGTACTCAGCACTCTGACCGAAGATCCGGCGCAAGTAGATG 16497  
QY 15894 TGCTGTTAGTGCAGAGGTCAACGAGCACTGTCAGCGCGGGGCAAGCACTGTGTGTGA 15953  
Db 16498 CTTTATTGATGACGCGGACATCAGAACACCTGTATATCAGGACAAAAACCTGAACTGGA 16557  
QY 15954 CGCCAGTGGAGAACTGCAAAAGGTGACACCGTGTGCTGATGGGGGGC---GGAGC 16010  
Db 16558 ATACACGCGGTGAATACCAATGTGACATTTGGTGAACCGGCAAGGGCGGCAATGATG 16617  
QY 16011 ACAGGAAAGCTATCGGTATGATGGGCGAGTCAGCGTATTATCAAAACCGGACCGCGC 16070  
Db 16618 ATCCGGATGGTATCGCTATAGTACGCGGAGAGGATATTAATAATCAATGACACG 16677  
QY 16071 AAATGGCAACAACTTCAGACACAGCGGTAGTGTACTGCTCGCGGGGCTGGAGTTACGTA 16130  
Db 16678 AGACAGCAGCAACTCTCAACACAGAGAAATACTTATTTGCGGAGCTTAGAACTTCGTC 16737  
QY 16131 TCATGSCAAATGCGGTGACGGAAGAAAGCTCCAGGTTATTACGTTGGCGGAGGCTG 16190  
Db 16738 TAAACAAAACAGCAGATCAACCGAGATTTGCAAGTTATCAGATGAGAGAACGG 16797  
QY 16191 GCGCGGCACAGTGCCTGCTATTGCACTGGGAGATCGCAAGCCGATGACCTCGATGAG 16250  
Db 16798 GTCCGGCACAGGTACAGTATTACATTTGGATAGCGGTCAACCGGAAGATATCGACAA 16857  
QY 16251 ACTCGTGGTTACAGTTACGATAACCTGGTGGGACAGCCAGCTGGAGCTGGACAGAG 16310  
Db 16858 ATCAGTACGTTATAGTACGATAAATCTTATCGGTTCCAGTCACTTGAATTAGACAGA 16917  
QY 16311 AGGTTTACCTTATCAGTGGAGGAGTTCTACCGGTATGGCGGAACGGCTGTTCTGACGG 16370  
Db 16918 AAGGAGAAATTTATGAGGAGAGTACTATCCCTATGGCGGACCGCATTTATGGGCA 16977  
QY 16371 CGCAGGTGAGGTGAGGCTGATCAAAAACCTATCCGATCTCAGCAAGGAGCGGTGAGC 16430  
Db 16978 CAAGGAAGCGGACAGAGCCAGTTATAAACCATCCGTTATTCAGTAAAGACGGGATG 17037  
QY 16431 CGACGGGCTGATTTATTCGTTTATCGGTATTCAGGCATGGGACAGGCGCTGCTCT 16490  
Db 17038 CCACCGGATATATTTATTCGTTTACCGGTATTTATCAGCTTTGGGTGAGGACGATGTTAA 17097  
QY 16491 CCACGACCCCGCAGCAGCGGTGGACGGCTGAACTGTTTCCGATGGTGGCGGAATAATC 16550  
Db 17098 GTGCGATCCGCGACAGACAGTAGATGGTTGAAATTTATTCGATGGTGAAGGAATATC 17157  
QY 16551 CCGTCACGCTGTTGA 16566  
Db 17158 CGTTTACTCTGCTTGA 17173



Db	65478	GTCTGGCAATCTCTACGGCCCTTCAAGCATCACATCTGCGAGGCGCTGCACCTTCATCTG	65537
Qy	8441	CTGCCCAATATTACCGGCTTGGCGCTCGGGGCTCCGCTATTATGGGCACTATTTAAAGCC	8500
Db	65538	GCCCCCAACATCTTTGGCTTCGCTGATGTGTGTAGCCATTGGGGGGCAATCGCCCAAGCC	65597
Qy	8501	ACGCCATCGGCATCCAGTGTCTCCGATGCCACCCGCAATATCAGCGACAAAATCAGC	8560
Db	65598	ACAGGTAAATGTATGGAGTTTTCGCGACGTGTCATGAACACCGAAGCGATAAATTAGC	65657
Qy	8561	CAGTCGGAAGTGTACCGCGTTCGCGGAGAGTAGTGGAAATCCAGGTGTATAGTCGGCAG	8620
Db	65658	CAGTCTGAAGCCCTACCGTCGGCGTCTGAGGAGTGGGAAATTCAGCGTAATAACGCCGAG	65717
Qy	8621	TCTGACGTGGCGCAGATGTATGCCAGCTGGCGGCATGGCAGTGGCGCGGAAGGGCT	8680
Db	65718	ACAGACTGAACAATCGATGCTCAACTTGGTTGCTGTGTAGTGGCGGTGAAGCCGCC	65777
Qy	8681	GAGCTGCAGAAAACTTACCTTGGAGCCAGCAGACCCAGGCACAGCGCAGTTGGCATTC	8740
Db	65778	GTGTTGCAGAAACACGCGCTGAAACGCAACAGGAACAGACTCATGCACTGACCTTC	65837
Qy	8741	CTGCAGAGTAAAGTTCAACAATACGGTCTGTACAGCTGCTCGGGGACAGTGTGTCGCC	8800
Db	65838	CTCAACATTAAGTTCAGCAATCAAGCTTTGTCAACTGGCTCGTGTGGTGTGTCGCC	65897
Qy	8801	ATTATTACAGTTCTATGACCTGGCAGTATCCGCTGCTCATCGCGCAACAGCCTGG	8860
Db	65898	ATTTACTTCAGTTCTATGATTTAAACAGTAGCTCGCTGTTGATGGCTGAATGGCCTAT	65957
Qy	8861	CAGTGGGATAAATTCAGACACTAGGTC---GTTTATCCAGCCGGGGCCTGTGATGGGGCA	8917
Db	65958	CGCTGGGAGACTAACGATGCCGACGACGCTTTATCAAGCCGGTGCCTGSCAGGAACC	66017
Qy	8918	AATGCCGCTCTGTGCGCGGGGAAACCTCTGATCTGAATCTGGCGCAGATGGACGAGCC	8977
Db	66018	CATGCCGGTTTGTGCGCAGAGAAACCTTAATGCTGAATCTGGCAACAATGGAAGACGC	66077
Qy	8978	TGCTGACGGGGATGAGCGGCAATAGAGGTGACCGGACCGTCTGCTGTGCGAGTGC	9037
Db	66078	CATCTGAACAGGAGCAACGCGTACTGGAAGTAGAACGTTACCGTTTCTACTGGCAAAATC	66137
Qy	9038	TATACGAGCCTCGCGGAGTAGCGCATTTCTCTTGGCCGACAAAGTGTGGAATGTGTC	9097
Db	66138	TATAAA-----GAGAAAGTCAATTTCCCTGACTGAGAAATTCAGAACTGATG	66188
Qy	9098	AGTAACGGTTTCGGCAGTTCGGGTACGAAAGCAACGGAATACAGATGGAT-----	9148
Db	66189	AAGAATAAATTAGTCACTGCGGTAGCGAAATAACACCTGAAGTTGGTACCGGAAT	66248
Qy	9149	---CAACAGCAACTCGAGCCACCTGAAACTGGCTGACCTCGGTATCGGCACGATTCAC	9205
Db	66249	GCCCAACGCTCTGCAAGCATCCATTCGTTAGCTGACTTACAAATTCGTCAAGTATAC	66308
Qy	9206	CCGCTCTCC-----TTGSCACCATGAGCGCATCAACAATAAGCGTCAACGCTCCCG	9259
Db	66309	CCAGAAAACAGTCGAGTCGGTAACGTTCCCGGATTAACAGATCAGTGTACCTTGCCA	66368
Qy	9260	CGCTGTGTCGGCCCTATCAGGACGTCCTGCGGTTTCTCAGCTACGCGGGGAATG---	9316
Db	66369	GCATGTTAGTTCCTTATCAGGATGTGCAGCGATTTCTGTCTTACAGCGGAGATGCTACT	66428
Qy	9317	GTCAATGCCCGGGTTGCACGCGCTGGCGGTCTACACGGGAATGAACGACGCGGCAA	9376
Db	66429	GGATTGGCTGAAAGTTGCAAAATCGTTGGCGGTTTCTCATGGGATGAATGACAGCGGCCAG	66488
Qy	9377	TTCCAATCGATTTCATGACCCGCTTACCTGCGGTTTGAAGGACTTCCAGTTGATGAC	9436
Db	66489	TTCCAATCGATTTCACGATGGCAAAATTCCTGCCAATTTGAAGGAATGCAATGAT---	66545
Qy	9437	ACAGGACCTGACACTGAGCTTCCCGATGC-----TGACGGCAAA	9478











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QY	11692	TGGCAGACAAACCCCTGGTGTGATGATGCATGAACAAATATGGGGCCCGCATGCA	11751	GGTCAGCAGCAAGTCTGGTATCTGATTTCAAGACGTTGGCCACGTCGCTCCGCCA	12766
DB	29825	ACACGCGCAAAACCGTGGTTACTCAGCGAAATGAACAAATATGGGAGCCCAACACCC	29766	GGCCAGAAAAAAACCATTTATACCAATGGGAAATATGAGCCCATTCGAAACGCCAAGC	28754
QY	11752	CTGCATCTACGAGTTCGGTTCGAGTTCCTGGCTGGATGAGAAAGCCGAGGCACTGGCGGCA	11811	CTCCCCCACAAGGTAGCTTTTATCGAAACGGCGTGTGGATGAGGGGTATGGTTCAGTTCA	12826
DB	29765	TTGGCTTACCGAGTTCTCCAGTTCTGGCTGGATGAGAAAGCCGCGGCACTGGTTGCC	29706	CGACAAGCGCTAGTTGGCTTTTACCGAGACAACGGTATTTAGTCAATCCACACTATCAGCG	28694
QY	11812	GGCAGTTCCTCGCTGCTACCTGCAATTTACATNTGCATPACCGTGTGGGCTTCGGTGGTG	11871	CTGGCTGCTCTACATTTGTGGATGAACAT-----CTCGACAGACCGGTTACCGG	12886
DB	29705	GGACAAACACCGGTTTGTATCTCCCTTCCCGGTACACACCCATATGGCAACCGAAACA	29646	TTTGATGGGAGCATCCCATCTGCTCAATGTCAACGACGCTGGAACAAGCCGGATACCAA	28634
QY	11872	CAGGATGAGATCACCGGTAAACGCTGTGCTCAGCGAGCTGCTTTATCGCCACCGCTCTGG	11931	CAATCCGGATACCTTTTCCCTCGAGCGAGGGAAGCAGAACAGGCAATTTGTGACCCAGTGT	12934
DB	29645	GCGGATGAATACGCGGCAACAAATTAGTCAACAACACTGCGTTATGCTCGTGGCGCTTGG	29586	CAAAACAATTTATTTCTCGCACC-----GGAGAAGATAAATCTGGGTAGCTCAT	28574
QY	11932	GACGGCAGGAACCGCAGTTTCGGGGTGTGGTTTTGTTGAGATCAGGAGATACCGATACC	11991	CAGGATATGTTACCTATGCGCGGCGCAGAGCATTTCTGGCTACCGCTATCTCTTCGCGGAC	12994
DB	29585	GATGGGGTGAACGGGAATTTCCGGATTTGGTTATGTTGAGCAGACACAGCCCATCAA	29526	CATGGTTATACCGATTACGGTACAGCCGCAAGTTCTGGCGCCGCAAAAACAGAGCAAC	28520
QY	11992	TTGGCAAGCAGGGTACGGGACGGAACCTGATGCTGCTGAGCCGGAACCTGGTAT	12051	AGTATGTTGACCGGCCAGTTTACCGTGAAGCGGTGACGCTGACGCTGATCATCGCAG	13054
DB	29525	CTGGC---CCAGGCAACCGCTCAGAACGCAACCCCAACCGCGATGACCAAAAACCTGGTAT	29469	ACCCAACTCAGCGGCAAAATTACACTCTTGGGATGCAACCTATGCGTTGCTACACAA	28460
QY	12052	GCCACCGGGTACCGGCACTAGACGAGCGTCTGCCGGAGCGTATTTGGCAAAACGATGCC	12111	TGGCAGGATGCCGAGGATTTGTACACAGCCGACTATGACTGGCGCTTCTCTGACGCC	13114
DB	29468	GCCACCGGGCTACCGGTAAATAGATAACAATATCAACAGAGTATTTGGGTGGTATAAT	29409	ACCCGAGATGCTGCTGGGCTGACAACTCAGCCAAATATGACTGGCGTTTCTGACCCCT	28400
QY	12112	GCCGCTTTTTCGCCATTTTCGACCCCGTTTCACCTGTGCTGGTTTCAGGAGAGGATGACGACA	12171	GTGCCACCCCTCGGATTTCTGGGCGACGAGAAATGTTATTTGCCACCGGTTTACAGT	13234
DB	29408	CAGGCTTTTTCGCCGTTTTCACCAACGCTTTACGACTTGGCAAGATGCAAGATATCTG	29349	CCAACTCACACTCCGCTTTTGGGAACTGAAACGCGAAGATGACCGGTTACTTTCACCG	28280
QY	12172	TATATCTCG---GACGACGACAAAGACATTTCTGTTGAGGAGCCCTGAAAGCATCTCG	12228	GTCCAGGTAGCAGTGTCTGTGTATGTACGAGCAGTGTGGGAGATGACGACATGAG	13345
DB	29348	TTAACACCGGAAGATATACAGCCAGTATTTGCTTAAACCGGGCACTGAAAGTCAACTG	29289	CTCCCTGTAGCAGCTGTCAAGTTTACGCACAGAAAGCTGGATGCGCAGTATTAAGTCA	28160
QY	12229	CTCGCAGTGAAGTTATACGGTGGCGATGGCAGCAGCCAGGCGCATATCTCTACAGCTC	12288	AAAAATGCCCCCGCACGCTGGTCTGGCTACCGATCGCTATGACAGT-----GATACCCG	13405
DB	29288	CTAGTGTAGTGTGTACGGATTGGACGACAGTACAATTAACACAGCTTCCCTATCTGTC	29229	AAAGCCCTCAATAGGCTGCGACAGCAAGATCGGCAAAAGTTATACAATCCCGAATCATC	28041
QY	12289	ACTGAGTCTCGCCCGCAGGTACGGC---TAGTTGAAGCGAATGGAGACTACCGGTGGTG	12345	ACAGCAGGTCCGCCAACAGGTGACATTCAGTGAACGCTTTTGGGCGTGAAGTGGCAATCGCG	13520
DB	29228	ACTGAAATTCGTTCCACAGGTACGTCGATTACAGCAGCGCAGATAACCAATACCCGTTACT	29169	ACCGAAGACGGCGCATATGTACACTGGCTATCGCCACTGCTGTCACAAAGTCAAAAGGCA	27981
QY	12346	TGSCCGATGGGCGGGAAGCCGTACGTCAAGTTTATGAACGGTACCAATATGATCTCAA	12405	AACCCGGCAGGCGGAGGCAACGCTTGGCAACGAGGACGCGCAACACTGGTACGCG	13580
DB	29168	TGCTCATCTGTAGTTGAAGCCGACGCTATCATTTACGAGCGTATTCGCCAGCGACCCACAA	29109	ACCC-----TCAACTACTAGCTGTTTAAACAGCGGCCCACTTTACCCCTCACAGC	27927
QY	12406	TGCCAACAGCAGCGGTACTCTCAGTGAATGATACGGTTTCCCACTGCGTCAAGTCACTG	12465	CAGTGAAGGATTCGCGCTCACTGTAGCAACGAATTTCCGCTGGGCGGTCAACGGGAGGCG	13640
DB	29108	TGACGCCAAGATATTACGCTATCAGTGATCTATTTGGCCAAACCGCTTAAACAGTTTCG	29049	CTCACAATGACTACCGATCGTTATGATCAGATCTCTGAGCAACAGATCCGTCAACAGGTA	27867
QY	12466	GTCAATTTATCCAGACCCCTCCGTCGGCGGACAAATCCATATCCGGCGTCTTTACCGGG	12525	GAGTGAAGTATGACAGCAGCAGCAGCATATACGCTGGGGTTGCAACAG	12585
DB	29048	GTACAGTATCCACGCGGAAACCAACAGCAATCAGTCCGCTATCCTGATACGCTGCTGAT	28989	GAATTTGTAGCCAACAGCTATGATGAACAGCAACGCAATTTACGGCTCACCTATCAACAA	28929
QY	12526	ACGCTGTTCCGCAACAGTTATGACGACGACGACAGATATACGCTGGGGTTGCAACAG	12585	AGCAGTGCAATCACCTTGTTCCTCTCTGAGGGGATTTGTTTGGGGTTGGGGGAG	12645
DB	28988	GAATTTGTAGCCAACAGCTATGATGAACAGCAACGCAATTTACGGCTCACCTATCAACAA	28929	TCCAGTTGGCATCATCTGACTGACATAACG-----TTCCGGGTGTAGGATTTACCGAT	28875
QY	12586	AGCAGTGCAATCACCTTGTTCCTCTCTGAGGGGATTTGTTTGGGGTTGGGGGAG	12645	CGCTCGCGGACAGATATTCAGCTACTCGCGGACAACTGCGGGAAGGGGTCTGACG	12705
DB	28928	TCCAGTTGGCATCATCTGACTGACATAACG-----TTCCGGGTGTAGGATTTACCGAT	28875	AGTACCCGCGAGTGATATCTTCACTTATGAAGCTAAAAATGATCTGCTGGTGGTTAAAT	28815
QY	12646	CGCTCGCGGACAGATATTCAGCTACTCGCGGACAACTGCGGGAAGGGGTCTGACG	12705	CTGGAACACCTGTTGGCGCCGAAAGCCTGCTCTCGGATAGTCAAGTCTGCTGCGTGGCG	12765
DB	28874	AGTACCCGCGAGTGATATCTTCACTTATGAAGCTAAAAATGATCTGCTGGTGGTTAAAT	28815	CTGGAACACTACTAGTATTAAGATAGCTGCTGATTCGGGATTAATAACCGCGTGAATCTCT	28755
QY	12706	CTGGAACACCTGTTGGCGCCGAAAGCCTGCTCTCGGATAGTCAAGTCTGCTGCGTGGCG	12765		
DB	28814	CTGGAACACTACTAGTATTAAGATAGCTGCTGATTCGGGATTAATAACCGCGTGAATCTCT	28755		



Db 27689 CAGCCCTATTTCCTCAATGACTGGCGATACGTTAGCAATGACATGTC - CCGG CAGGAAA 27632  
Qy 13881 CTGACTGGAGAGGGGGGACCGGTGATGATCGCTCGCCCTGACAGCGCGTCCCGT 13940  
Db 27631 AAGAACTTATGACAGATACCCATGCTATGATCCCGTTGGTCGAGAAATCAAGGTTATCA 27572  
Qy 13941 ATGAGACAAAGATGAAATACACTATCAGGTTGCGCGGTTGCTGACAGAGTGTATG 14000  
Db 27571 CCGCAAGGTTGTTACCGCGAACCTTGTTCACTCTCTGGTTTACTGTCTAATGAGGATG 27512  
Qy 14001 GTTTGGGGGCTTTCCCATTTGGCGTTACACCGTGGTTACACCGCGGAGATCTCAATGG 14060  
Db 27511 AAAATGACACGGCTGCTGAGGTGAATGAGGTGAATATGTAATCTGATCAATCCCGCCTGC 27452  
Qy 14061 CAACACCGCCAGCGGACAGAACAGGAAGCGCGATCGCTGGCCCTCTCGGAGCAAGAAC 14120  
Db 27451 CTAACGCGGGGAAACAGAGATGAGGTGAAGGTGTTGCTCAATACCGTCAAGTACT 27392  
Qy 14121 CGGAAAGAAAGTGGGAGCAGCAACGACGACTGACATGAACAAGGTGGCTATACATGCT 14180  
Db 27391 CAACCTTATCTGTTGATCATTTGTTTATTCGGCCTGGGCGGCTCGTAAGGTAC 27332  
Qy 14181 GAAGAAGAACTGGCTGCTGCGCGTGACGCTGCCCTGATGCTCAGCGCACTGGTCAGCGC 14240  
Db 27331 CTCATTGATATGCAAAAACAAATATAAATGAGGTTGGATCAACGTTATCTGTCAACTC 27272  
Qy 14241 CTGACGACACCGTTTACCCCTCCAGGCGCACTTCCAGTCTGTAAGAACCCGCGCTT 14300  
Db 27271 ATCATCTCTGCTTTTACCGGTGTTACTAGGAGGATTTGCTGAGTTTGAAGTGGCGGAGT 27212  
Qy 14301 TCC-----GCAGCTACCGCTATCGGTACAGACCACTCGAGGCGCAACCGCGGTTTG 14354  
Db 27211 ATCTATATGACTTTTGCAATTTGACAGTTTATTCGGCAACAGAGGATCGGACTGAAC 27152  
Qy 14355 TTTGCCGAACTGTTCCGCGCGCTGACAGAGAGCGGAGAGCTGGCAGCGTATGCTGAC 14414  
Db 27151 TGGCTCTGGCGCGCCCTCATTTACGTATCATCATGATCATGAGGAAGCAATAAGGCCCC 27092  
Qy 14415 AGGACAGAGTGAATGCGAGGCTCGGCGCGCCTATCAGGCGGCTACGACGAGCA 14474  
Db 27091 ACTGCCAATAAACCATTAGTCTCTAGTTAACTGCAAAATTTATGACTACACTATCGA 27032  
Qy 14475 GAAAAATAAGCGATTTAGCGTTTAAAGAAAAGTGACGGTGTGTTTCGGGATTAATATTA 14534  
Db 27031 CTATCGTAAGAAATTAACATACAGACAACTGCGATTTGCAGAAAGGATTAACACAA 26972  
Qy 14535 -----CAGGAGTACATGACACATCCTGTTTTCAGTAGCACCC 14573  
Db 26971 CAACCCAAACAGAGGTAACCTCATGAAAAAACATTGTATCCAAACTTTTATCAAAAGACTCC 26912  
Qy 14574 CGTCGTTGCGGTGCTCGAACCGCGCCTGTTGGTGGGAGCTGACGTACTACCGCC 14633  
Db 26911 CGTC-GTCAATGTCAGAGAACCGGGTCTGAACATCCGTTAACTGTTTTCACCG-- 26855  
Qy 14634 ATCCGATACACCGGAGAGACGAGCGGTATCAGCTGCATCAGCAGATGAGCGG 14693  
Db 26854 -TACCACTGCAACCGGTGATACCGATACCGGTATTAATGCGCATCAATCACTACTCAG 26796  
Qy 14694 GCAGCTTGTCAAAAGCCGACCCCGGTTTACACGCGCGGTTCTGACAAATTTTCAG- 14752  
Db 26795 GACACCTTAAGTCAAAAGCATCGATCCACGCTATATGAGGCAAGAAAACAGTAGTACGA 26736  
Qy 14753 ---TACCTGAATAGCTGACCGGACAGTACTGACAGCGCTCAGCGCGATGCGGTACG 14809  
Db 26735 TCAACCCCAATTTTCTCTGGCAGTATGATCTGACCGGCAATTCCTCTACGTACAGAGACA 26676  
Qy 14810 TCGCTGAACTGAGCGATGCGCGCGCGGCGCTTTCTGGCGGTCAACGG--GGCTGGGA 14867  
Db 26675 TTGATGAGGTGCGCACTGTCACTTTGATGATGATGAGGCGGCTCCCTGCTGACGTTGA 26616  
Qy 14868 CGGAAGACGCGGTCAACCGCACTTGGCAATATGAAGACGATACCTCTCGCGGCGCGCCCGC 14927

Db 26615 CGGCAACAGGTGTATACAAACCCGCGCAATATGAAACTTCTTCCCTCCCGCGCTCTGT 26556  
Qy 14928 TGAGCATCACCGAGCAGGTTTACCGGTG---AAGCGCCCAAAATTACGGAAGGTTCTGTGT 14984  
Db 26555 TATCTGTTTACCGAAACAAACCCAGAGAAAAACATCCCGTACACCGAGCGCTGATTT 26496  
Qy 14985 ACCTGGCAATACCGATGCGGAGAAGATTCTCAATCTGGCTGGCCAGTGTGTGAGTCAATT 15044  
Db 26495 GGGCGGCAATACCGAAGCAGAGAAAGACCATTAACCTTGGCGGCAAGTGTGGCGCACT 26436  
Qy 15045 ACATACCGCGCACTGGTGACAGCAGCATTCGCCCTTGAGCGGCGTCCGCTCCCGC 15104  
Db 26435 ATGACACGCGCGGAGTTACCGGATTGGAGAGTTCTGCTCACTGACCGTACTGTTTATCGC 26376  
Qy 15105 TCACGGGCGAGTTGCTGCCGACGCGCGGGGGCCCACTGGATGGGTGAGGATGCCTCGG 15164  
Db 26375 AATCCAGCCAACTCTTGTCTGCACTCAAGCAGCTAACTGGACAGGTGATAACGAAACCG 26316  
Qy 15165 CCTGGAATGACCTGCTGGATGGGAGACGTTCTTCAACCCAGAGCCACGCTGATGCGACCG 15224  
Db 26315 GCTGGCAAAACATGCTGGCTGCTGACATCTACACCATCTCTGAGCACCTTCGATGCCACCG 26256  
Qy 15225 GCGCGTCTGAGCATCACCGATGCAAAAGTAACTCTGACGCTGTGGCATATGATGTGG 15284  
Db 26255 GCGCTTTACTGACTCAGACCGATGCGAAAGGCAACATTCAGAGGCTAGCCTATGATGTGG 26196  
Qy 15285 CTGGGCTGCTATCGGCGAGTTGTTGACGCTGAAGNAGCGCACGGAGCAGGTATCTGTGG 15344  
Db 26195 CCGGGCAGCTAAACGGGAGCGGTTAACTAAAGGTTCAGACGGAACAAGTAAATATCA 26136  
Qy 15345 CCTCCCTGACGTACTCGGCGCGCGGAAAAGTTGGTGAAGAACACGGCAACCGCGTGG 15404  
Db 26135 AATCCCTGACCTATTCTGCTGCGGACAAAATAACGGAGGAAACACGGCAATGGTGTGA 26076  
Qy 15405 TAACCTCGTATATTTACGAGCCGAAACACAGCGCTGACGGGATTAATAACGGAAACGTC 15464  
Db 26075 TCACCGAATACAGTTATGACGAGGAAACCCAAAGGTTATCGGTATCAAAACCGCGGTT 26016  
Qy 15465 CGTCTGGCAGCTGTCGCGGAG---CAAAAGTGTGAGGACCTCGGCTATACGTATGACC 15521  
Db 26015 CGTTAGACCAATTCGTGACAGACCAAAAGTGTGCAAGACTTACGCTATGAGTATGACC 25956  
Qy 15522 CGGTAGCAACGCTACTCAGCGTCAATAACGATCGGAAGAGACCGCTTCTGGCGTAACC 15581  
Db 25955 CGGTAGCAATGTATCATGATATCCGTAAACGATCGGAGAACCCCGCTTTGGCACAACC 25896  
Qy 15582 AGAAAGTGTGTAACGGAGAAATACGTATCTACACAGCTGTATACAGCTGGTACGCGCCA 15641  
Db 25895 AAAAAAGTGTGCGGAAAGTACTTATATCTACGACTCCCTGTATCAGCTTATCAGCGCCA 25836  
Qy 15642 CAGGCGTGAGATGGCCCAATGCGCGCAGGCGGCAACGACTTACCATCCGCTACAGCCC 15701  
Db 25835 CCGGCGGAGATGGCGAATATAGGTCAACAAAGTCAACCCATTTCCCTCC-----CCGG 25782  
Qy 15702 CCCTTCTTACAGACAGCTCTGCTTACACCAATTTACACGCGCACCTACCGTTATGACCGGTG 15761  
Db 25781 CTCTACTCTCTGATAACACACCTTACACCACTATACCCGTATATATCTATATGACCGAG 25722  
Qy 15762 GTGGCAACCTGACGAGATGCGCCACAGTGCCCTCTGACGAAACAATAATATATACGACAG 15821  
Db 25721 GCGGCAATCTGACTAAAATCCAGACAGTGTTCACCGGCGACGCAAAACACTACACCAAA 25662  
Qy 15822 ACATACGTTAGTACCGCAGCAATAGGCGGTACTGAGCAGCTGGCGGAGTGCCTG 15881  
Db 25661 ACATACGTTTCTTCCACGAGCAATTCGCGCACTACTCAGCACACTGACCGCAAGATCCGA 25602  
Qy 15882 CAGATGTTGATATGCTGTTTCAAGTGAGGAGTCAACGAGGAGCTTCGACGCCCGGGCAAG 15941  
Db 25601 CACAAGTAGATGCTTTATTTGACGAGCGGCGGACACAGAACACAGTTGATAGCAGGACAA 25542  
Qy 15942 CACTGTTGTGACCGCACGTTGGAGAACTGCAAAAGGTGACACCGGTTGGTGCCTGATGGG 16001  
Db 25541 ACCTGAACCTGGAATCCACGCGGTGAACCTAAACAAAGTGACATTTGGTGAACCGGACAA 25482



QY	16002	GGGC---GGACGACACGAAAGCTATCGGTATGATCGGGGAGTCAGCGTATTATCAAAA	16058	Db	105062	TATGCTGGAGTCCATCCGGTTATATTGTTCA CGGCAGAGTTACAGAACTACCAGTGAAT	105003
Db	25481	GCGCCAATGATGATCGGAATGATATCGTTATAGTGGTACGCGGAGAGATATTAAGA	25422	QY	7481	GTCCGTCGCTGGAGGAGACACCGGTGGAACGACTCGCCGCTGGACTCCATTGACCCC	7540
QY	16059	CCGGCAGCGGCAAACTGSCACAACTGTCAGACACAGCGGGTGTGTACCTCGCGGGC	16118	Db	105002	GTTCGCCGTTACTTGGAAAGACACCAAGTTGGAACTGATTCCTTTAGATTCGTCGATCCT	104943
Db	25421	TCAACGAACACCGGATCCAGCAACACGCTCAATACAAAGAAATACTTATTTGCGGAGTC	25362	QY	7541	GATGCAATAGCCCACTAGACCCCATGATCAAGGTGCGCACCTTTATGTCGTACCTC	7600
QY	16119	TGGAGTTACCTATCATGCGAAATGCGGTGACGGGAAAGAAAGCCCTGCAAGTTATTACGG	16178	Db	104942	GACGGGTAGCACAAACAGATCCATGCACTCAAGTCTCAACTTTATGCTACTCTC	104883
Db	25361	TGAACTCCGCTTAAACGACAGCAATACGACCAACACCGAAGTTTTCGAAGTTATCACCG	25302	QY	7601	GACCTGCTGATTGCGCGCGGTGATCCGCCCTACCGGCTGCTCGAGCGGGAACCCCTTAAC	7660
QY	16179	TGGCGAGGCTGGCGGGGACAAAGTGGCGGTATTGCACTGGGAGATCGGCAAGCGGATG	16238	Db	104882	GATCTGTTGATAGACAGCGCGCATCAGGCTTTACCGCAACTGGAGCGGGAATCGCTTAAC	104823
Db	25301	TAGGAGAAGCGGCGGACAGGTACGGGTATTATCAATTGGGAGAGCGGTAAACCGGAAG	25242	QY	7661	GAGGCCCGATGTGTACGTCAGGCCCTGAACCTTTGSGGAGCGAGCCCTATATTTCC	7720
QY	16239	ACCTCGATGAGGACTCGGTGCGTTACAGTTACGATAACCTGTTGGGACGACGACGCTGG	16298	Db	104822	GAAAGCAAGATGTGTGATATCAAGCGCTGATCTATTGSGGAGCAAAACCTTTACCTACCG	104763
Db	25241	ATATCGACAAATATCAGTTGCGTTATAGTTACGATAATCTTATCGGTTCCAGTCAGCTTG	25182	QY	7721	TTTGACGCGGACTGCTCGCGGTTGACCGGTGACCGAGCAGCGAGGTGACGCGACGC	7780
QY	16299	AGCTGGACAGAGAGGTTACTCTTATCAGTGAGAGAGGTTCTACCCGTATGCGGAACGG	16358	Db	104762	CTGAGTACGATGAATAAATCTCGACTAGACAGAGCCGAGATATTACTACAAAT	104703
Db	25181	AATTAGATACAAAGAGAAATATTAGTGAAGAGAGTACTATCCCTATGTTGGCACGG	25122	QY	7781	GATTACCAAGAGGCTCTGCTGCGCGTGGCGGTTGTCGCCGCTCCCGAGACA---CGG	7837
QY	16359	CTGTTCTGACGGCGGAGTGTAGGCTGACTACAAAATATCCGATCTCAGGCA	16418	Db	104702	GCTCAGCGCAGCTCAATAGTTGCTCTGCGGCGAGAGTACACCAAGCACCTTTAGCATTTGGC	104643
Db	25121	CATTATGGCGGCAAGCAACAAACAGAACCCAGTTTATAAACCATCCGTTATTACAGGCA	25062	QY	7838	ACGGCGAATCCCTGACCGGCACTGTTCTCCGCGAGCAGAAAGAGGTGCTCAAAAGGCTAC	7897
QY	16419	AGGAGCGTGACGCGAGCGGCTGGATTATTACGGTTATCGGTATTACAGCCATGGGCAG	16478	Db	104642	AGCGCAATACCTGACCGATCTCTCTGCGCACAATTAATGAAGTATGATGACTATC	104583
Db	25061	AAGACGGGATGCCACGGGCTATATTATCCGTTACCGATATTACGCTTGGGTAG	25002	QY	7898	TGGCAAACTTTGGCAGACGCGGCTCCATAACCTGCGCCCAACCTCTCTTCAATGACGGCAG	7957
QY	16479	GGCCTGGCTCTCCACGACCCCGCAGGACGCGTGGAGCGGCTGAACCTGTTCCGCAATG	16538	Db	104582	TGGCAGACATTTAGCTCAGAGAGTATACAACTGCTGCTATACCTCTCTATCGACGGTCAA	104523
Db	25001	GACGATGTTAAGCGCGATCCCGCAGGAACAATCGATGGGCTGAATTTATATCGAATGG	24942	QY	7958	CCGCTTTCCTGTCGCTCTACGCAACGCGTCCGAAACGTCGCCCTCGAGAGTCCGCTC	8017
QY	16539	TGGGAATATCCGTCACGCTGTTGACAGCAACGCGGAGTACGACTGTCGTCAGGAG	16598	Db	104522	CCGCTATATCTGCCAATCTATGCCACACCGGCGAGTCCAAAAGCGTTACTCAGCGCCGCC	104463
Db	24941	TGAGGAATATCCAAATTAATATATCATGATCTGATGTTAGGCGCTTGAAATTAAGATG	24882	QY	8018	GTCAACAGCGCGCAGGCTGCTGCAGCACTGCCGCGCGGCTGATGCCGCTTTACAGTTTC	8077
QY	16599	CCAGCAGATTAGTGGGGGAGCATTTGTTTCATC	16631	Db	104462	GTTCGCACTTCTCAAAGTGGAGGCAACTACAGAGTCAATTATGTCCTCTGTCGGCGCTTC	104403
Db	24881	TCGACACACGGTGATATGTTTCAGTCAATC	24849	QY	8078	CCGCTCATGCTGGAGAACCCCGGGGATGTGTGAGCCTGTGACCGGTTTCGGGCAACACA	8137
RESULT 5							
ACF65386 4/c							
Continuation (5 of 7) of ACF65386 from base 40001 (Phototrihabdus luminescens nucleotide							
WP Sequence split into 7 fragments LOCUS ACF65386 Accession ACF65386							
WP	Fragment Name	Begin	End	QY	8138	CTGCTCGTATTACGAGCGTTCAGATGCGGAGCGCTGGCCAAACTGCTGCAGACCCAG	8197
WP	ACF65386_0	1	110000	Db	104342	TTACAAAATATTATCGAGCGTCAGGACGCGGAAGCACTCAATGCGTTATTACAAATCAG	104283
WP	ACF65386_1	100001	210000	QY	8198	GGCAGTGAATGATACCGCGGCTTCGCCAGCAGGATAACGTCCTCGAGGAAATCGAT	8257
WP	ACF65386_2	200001	310000	Db	104282	GCGCGGAGCTGATATTGACTAACCTGAGCAATTCAGGACAAACCAATCGAATTTGGAT	104223
WP	ACF65386_3	300001	410000	QY	8258	GCGGATATTGCGCGCTGGAGGAGAGCCCGCGGCGCGCAGATGGTTTGAACGTTAC	8317
WP	ACF65386_4	400001	510000	Db	104222	GTGAGAAAAACCGTCTGCGAAAAATCCAAAAGCGGAGCCCAATCGCGCTTTGATAGCTAT	104163
WP	ACF65386_5	500001	610000	QY	8318	AAAGTGTGCTAGGCGGAGCGCTCAACACCGCGGAAAAACAGCCCAATGACTTTGACCTC	8377
WP	ACF65386_6	600001	700779	Db	104162	AGCAAGTTGTATGATGAAGCAATCAACGCGGTGTAACCAAGCTATGATGTACGAGCG	104103
Query Match							
Best Local Similarity 55.1%; Score 2283.6; DB 10; Length 110000;							
Matches 5296; Conservative 0; Mismatches 3804; Indels 400; Gaps 33;							
QY	7301	ATGCACTTCTCGGAGCCATGCCCTCTATTCTGGAGCTGTCTATTATACCGCGATG	7360	Db	105182	ATGGAATTCAGCGCGCTAACAGTCTTTATTTCTGGGAACGTGTTCTACTATACCCGATG	105123
QY	7361	ATGGTGTCCAGCGGTTGTTGCAGAAACAGCACTTCCCGGAAGCCACCGCTGCTGCAG	7420	Db	105122	CTGGTGTCAACGTTGTTGATGACAAACAACTTTGATGAGCCAAACCGCTGCTGAAA	105063
QY	7421	TATGTCTGGAACCCGCGCGGACGTTGGTAAACCGGGTGTGCGAGATTTACCTGGAAT	7480	QY	8438	ATGCTGCCAATATTATACGGGCTGGCGTCCGGCTCCGCTATGCGGCACTATTATAA	8497
				Db	104042	TTGGTGCCTAAACATCTTCGCGCTTCGCGCGGTGTGTGCTGCTGGGAGCTATCGCTGAG	103983
				QY	8498	GCCACCGCATCGGCATCAGAGTGTCTCCGATGCCACCCGATATACGCGGACAAATC	8557
				Db	103982	GCAACAGGTTATGTGATGGAATTCCTCCGCTAATGTTATGAAATACCGAAGCGGATAAAT	103923

Qy	8558	AGCCAGTCGGAAGTGTATACCGCGTCGCGGAGGAGTGGGAAATCCACGCGTATAGTGGC	8617	Qy	9605	ATCATCAAGACATGGCCATTACTGCCCCCACCAGCTTGCTTCCGGGGGGCGGTGCGGTACACCG	9664
Db	103922	AGCCATCCGGAACCTACCGTCGTCGCGTACGAGGTGGGAGATCCAACTGATATATGCC	103863	Db	102849	ATTTCACAGACATTCAGTGTGCGAGCTGTCAATCCCAAGGCGCGGGGCAATATACCG	102790
Qy	8618	CAGTCTGACGTGGCGAGATGTATGCCAGTCGCGGCGCCATGAGCAGTGCGCCGGGAAGG	8677	Qy	9665	GGCTCAAGGGTATATCGCGGCGGACGGCCGATGGTGGCGGACCCCTGAGTATTCCTT	9724
Db	103862	GAAGCAGAACTGAAACAACTCGATTCCCACTTCCAACTTAAATCACTGGTAGTACGCCGTGAAGC	103803	Db	102789	GTATGGGTGAAGCATTAACACCAACTGGGCGGATGTATGGCGCGCTTATCCCTGCGCAT	102730
Qy	8678	GCTGAGCTGCAGAAAACCTTACCTTTGACCCAGCAGACCCAGGCGCAGTGGCA	8737	Qy	9725	TGCGCGTTAGCCCCCGGTGCGGGTTAGCCCCCACTGGGGCACTTAATATACAGACCGGT	9784
Db	103802	GCGTATGCAAAAACACGCTGAAACCCAGCAAGACAGACCCCAATCTCAGCTGGCC	103743	Db	102729	TACCCATTTCTGCGGGCGTGGTTACTCCCCATCGCTCACTTGAATTCAGCAGTGGAG	102670
Qy	8738	TTCTGTCAGAGTAAAGTTCAACAATACCGCTCTGTACAGCTGGCTGCGGGGCGAGTTGTCC	8797	Qy	9785	CGGGAAACCGCCCTTTGGCATTGGCTGGGGTATCGCGGTGCTGTGCTCCAGCGTGGTA	9844
Db	103742	TTCTGCAACGTAAGTTCAAGCTTGTGTACAACTGGCTGTGTACAACTGGCTGTGTGCGG	103683	Db	102669	CGGTAACAGCCGTTTGGTCTCGGTTGGGACTGCAACGTTATGACAAATTCGTCGCCGCA	102610
Qy	8798	GCAATTTATACAGTTCTATGACCTGGCAGTATCCGCTGCTGATGGCGCAGATGGCGCAACAGGCC	8857	Qy	9845	CGGCAACAGAGACCACTACTACGATGATCTGATGAAATTCACGGTCCGGACGGTGAGG	9904
Db	103682	GCGATTTACTTCCAAATCTACGATTTGGCTGTGCGCGTTGTTTAAATGGCAGAACAGGCT	103623	Db	102609	CCAGTACTGGCGTACCGAAATACGATGAAACCGATATCTTTCTGGGGCCAGAAAGGTGAAG	102550
Qy	8858	TGGCAGTGGGA---TAAATTCGAGACTAGTCTGTTATCCAGCGGGGCGCTCGATGGG	8914	Qy	9905	TGCTGTGTCGGCAGCTCACGGCTGCTGGCACCCCAAGACCGGACCGCCACTCTACTAC	9964
Db	103622	TACGTTGGGAATCAATGATGCTCTGCAAGTTTCAATTAACCGGGTGCCTGGCAAGGA	103563	Db	102549	TGTTGTCTATAGCATTAATGAGAACGGTCAAGCTGATATCCGAGTGAATCTCATTCG	102490
Qy	8915	GCAATGCCGCTCTGCTGGCGGGGAAACCTGATGCTGATCTGATCTGGCGCAGATGGAGCAG	8974	Qy	9965	TGGGATAAACCCAGCGCGGAAGCTTCAACGTTTACCGTTTACCGTTTACCGTACGAGGGTA	10024
Db	103562	ACCTATGCCGCTCTGCTGGCAGTGAACCTTGTATGCTAGTCTGACACAAATGGAGAT	103503	Db	102489	AGGGCATCAATTTGGGGGAAATCTTCAACGTTTACCGTTTACCGTTTGGAAAGCC	102430
Qy	8975	GCTTGGCTGACGGGGATGACGGGCAATAGAGGTGACGGGACGCTCTGCTGTGCGGAG	9034	Qy	10025	GTCTACGCGCTTGAGCGTTGGCTGCCCGCCGACGAGACAGAAACGGAATTTTGGGTGT	10084
Db	103502	GCCCATCTGAAACGCGATAAACGTGCACTAGAAAGTGGAAACGCGGTGCTGCTAGCCGAA	103443	Db	102429	ACTTTAGCTGGTTGGAATATTGGCAACCCCAAAACACAGGTACACCGATTTCTGGCTGA	102370
Qy	9035	GTCTATACAGCTCGGGAGGATGCGG---CATTTCTCTGCGCGACAGGTGGTGGAA	9091	Qy	10085	TATATACCTCTGACGACAGGTGGCTCTGCTGGCGGAAATGCGAGGCTCGCATCAGCA	10144
Db	103442	GTTTATGCTGGATTGCCACAGATAAAGGTCCATTTCTTCCGTGCTCAGGAAATTTGAGAAG	103383	Db	102369	TATACAGCCCCGACGACGAGGTCCATTTACTGGGAAAAAATCTCAGGCACTGATCAGCA	102310
Qy	9092	CTGCTCAGTAACCGTTCCGGCAGTGGCGGTACGAAAGCAACGATTTACAGATGG---	9146	Qy	10145	ACCCACAGCCCCCAACACAGACGCGGTTTGGCTGATGAGTCTCTCGGTATCTACTTACCG	10204
Db	103382	CTGGTAGTAAAGGCTCAGGAGTGGCGGAGTGGCAGTACATTAATTTGGCATTTGGTGCC	103323	Db	102309	ATCCACTCAATGTTAGCCAAACAGCGCAATGGTTGTTGGAGCTTCGGTATCATCCACG	102250
Qy	9147	-----ATCAACAGCAACTCGAGGCCACCTCGAAATCGGCTGACCTCGGTATGGC	9196	Qy	10205	GGAAACAGATGTATTAACCAATACCGTGGGAGAGATGACGGTTGTGACGAGCGGAGC	10264
Db	103322	GGTACGGACATAAAACCTCTTTGCGAGCATCCATTTCACTAGCTGATTTGAAAAATCGT	103263	Db	102249	GGAAACAGATTTATTAATCAATATCGAGCGGAGATGAAACAAACTCGAAACTGACGAGT	102190
Qy	9197	AAGATTTACCGGTCTCCCTTGGCACCATGAGGGCATCAACAAATAGCGTCAAGCTC	9256	Qy	10265	GGGACGGCACCGCGAGCGCGCCCAACGTTATCCGGTGGCGGCTGTGATGTTGTTAACC	10324
Db	103262	GAGATTTACCGGACATCTTTGGCAAAATTCGACGATATCAAAACAGATCAAGTGTCAACCTG	103203	Db	102189	TCACAGCCCATCGAAACGCAACCGTCCACGCTACTCTGCAAGCGGTCATTACGGTAACC	102130
Qy	9257	CCGCGCTGCTGGCGCCCTATCAGGACGTCGTCGGTTCTCAGCTACGGCGGAAGTATG	9316	Qy	10325	GTACGCGGCTCGGACGCTACCGCGCT---GGTGTGACACCATCAATGGATAGCTGGC	10381
Db	103202	CCGCGCTACTGGGCGCATATCAGGATGTGAGGCAATATGTTTACGGTGTATTAACC	103143	Db	102129	TGACCGCAGCGNAAGTTTTTCCACGCTCAACGGAGATGACCCACTCAATCTGGCTGGT	102070
Qy	9317	GTATGCCCCGGGTTCAGCGGCTGGCGGTCTCACAGGAATGAACGACGCGGCAA	9376	Qy	10382	TGTTTATCCTGGTTTGTATTAATGTTGAGCGTATGCTGGTGTCTGAAGCGCCGCGCT	10441
Db	103142	GGATTAGCTAACGGCTCGGAAGCGCTAGCAGTTTCTCACGCTATGAATGACGCGGCAA	103083	Db	102069	TGTTCTGTTTAGTATTTGATTTACGTTGAACGCAAAACAGCTTATCTGAAATACCGCGT	102010
Qy	9377	TTCCAACTGATTTCAATGACCGCGTTACTGCGGTTTGAAGACTTCCAGTTGATGAC	9436	Qy	10442	GGCAACACACGAGAAAGTGGGAGTGGCTGTGCTCAGGATTTGTTTCCGGGTATGAGT	10501
Db	103082	TTCCAGCTGATTTCAACAGATGCGAAATCTCTGCAATTCGAAGGCACTGCAATGATCA-	103024	Db	102009	TTAAAGCCCTCA-----AGTCTCTGGCTTTGGCGCAAGACCGTTTTTCCGTTATGAAT	101956
Qy	9437	ACAGGACCTGACACTGAGCTTCCCGGATGC-----TGACGGCAACACAG	9484	Qy	10502	TTGGTTTAAACCTGCGGACTCGCGGCTGTGCGGTGAGTTTGTGATTTCCATTAACCTAG	10561
Db	103023	--AGGACGCTGACACTGAGTTTCCCAATATGATTCATGCGGAAGAAGTAAACAGCC	102966	Db	101955	ACGTTTGTGATTTGCGCACCCCGGCTTATGCGCTCAATCTGATGTTTACCGCTTAC	101896
Qy	9485	GCGATGCTCCTCAGTCTGAGCGCATCATCTTCATATCCGTTTACCACTTATCAGCTGA	9544	Qy	10562	GTGTTCTGCGGGAGTTCGGGAGCGAAATGATGCGCAGATTTGATTTCTGCGCTGTTCG	10621
Db	102965	ACTATGCTAAAAACCTGAACGATATCATTTTGTATATTCGCTAGACCAATTAATAACCG	102906	Db	101895	AAACCTGTCTGTCAAGCTAAAGGGGACGATGAACCCGCGTTGGTTTACGCTCTGATAC	101836
Qy	9545	TAGTATCAACATAGCGAGCCCCGAAACGAGGCGCTTCGAGGAGACTGAGCATGCAAA	9604	Qy	10622	TGGACTACAGGNAAGTCTTCACTCAGTCTGCTCGAAGACGTCGACAGCTGCGTTATG	10681
Db	102905	TCCAAACGTAATAA--AACAGGCCCGAATCGGGGCGCTGTAAGAG--TTTTCATGCGAGA	102850	Db	101835	TGGATTAACGATGAAACGCGGTGATCAGCACGCTCGTCTTCTGTCGCGATAGGTCATG	101776
				Qy	10682	AGTCGACGCGGACGCTCTTGTGCTTTCGCGCACTGGCATTTGGGGTGGCAAACTTTTACCC	10741

Db	101775	AGGACAAATACCGTCATCTCACTGCGCAACCACTGGAGTGGCTTACCAAGCCTTTTGAGC	101716	Db	100695	GTAGTCTCTCCAGTTCTTGGCTGGATGACAAAGCCGACGACCTTTGGCGACCGGACAAACAC	100636
Qy	10742	CGCGCAATTTGCGGATGCGGAGACCGGTGACGATATGGGCAAGTTGATTTGCTTCAAC	10801	Qy	11822	CTGCTGTACTGTGCAATTTACATTTGCATACCTGTGGGTTTGGTGGTGGAGGATGAGA	11881
Db	101715	CAGAAACAAAGACGCTGGCAATCAATGATGTACTGGCAAAATTTCAACGCAATTCAC	101656	Db	100635	CGTCTGTACTGTGCTTCCCGGTCCATCTCTGTGGCAACAGAGACCCGAGGATGAAA	100576
Qy	10802	CTATCAGCTTTGAGACCTTAAGCGGAAAGGTGTGGTGGGTATCTGTATACAGGACAGG	10861	Qy	11882	TCACCGGTAAACCGTCTGTGTGACGACGTCTTTATCGCCACGCGCTCTGGGACGGGACGG	11941
Db	101655	GCTGGCACTGCTTGACCTGAAAGAGAAAGGCTACCCGGTGTCTATATCAGGATAGAA	101596	Db	100575	TCAGCGGCATATAAATAGTGACCACTTACGTTACGCTCACGCGCTGGGATGACGCTG	100516
Qy	10862	GTGCTGTGTGATACCGGTACCGCAAGTTCGGGGGATGATCCGGATGTGCTGACCT	10921	Qy	11942	AAACCGAGTTTCGGGGTTTGGTTTGTAGATCAGGATACCGATACCTTTGGCAAGCC	12001
Db	101595	ATGGCTGGTGGTATCGATCTGCCAACGTCAAGCCGGGGAAGATGAATGCGGTACCT	101536	Db	100515	AAACCGAAATTTGCTGGCTTTGGTTATGTGACAGACAGACCACTCAACTCGC---TC	100459
Qy	10922	GGGGGGCGGTGGGCGCTTCGCGACAATGCCCGCTTTTGGATTAACAGCGGCATCTGGCGG	10981	Qy	12002	AGGTTACCGGACGAACTGATATGCCCTTCTGTGACCGGAACTGTGTATGCAACCGGG	12061
Db	101535	GGGGGAAATGCAACTCTCTCTATCACGCCAGCTTTGAGGATTAACGCTCACTGATGG	101476	Db	100458	AAGGCAATGCCCCGGAACGACACACCCGGCACTCACCAGAACTGGTATGCCACCGGAG	100399
Qy	10982	ATCTTAATGGGATGTCGGCTGGAGTGGTCTTACCGCCCGCGGTGGGGGATGT	11041	Qy	12062	TACCGCGAGTAGACGAGGCTCTGCCGGAGACGTATTTGGCAAAACGATGCGCGCTTTTG	12121
Db	101475	ATATTAACGCTGACGGCAACTGGACTGGTTATCACCGACCGGGTTAAGGGGTATC	101416	Db	100398	TCGCCGAGGTAGACAATACGCTATCTGCCGGGTATTTGGCGTGGTATAAACAGCGTTCA	100339
Qy	11042	ATGATCGCAACCCCGCCGCACTGGTTGCAATTTCAACCCCTGTGAGCTTTGCCGATAG	11101	Qy	12122	CCGATTTCCGACCCGCTTCTACTGTGCTTCAAGGATGAGGATGAGCAGACATATATCTCCG	12181
Db	101415	ACAGCCAACACCCGATGGTAGTGACACGCTTTACACCAATTAGATGCTTTGCCGATAG	101356	Db	100338	CCGGTTTACGCGACGCTTACTCGCTGGAAGAGGGCAAGATGTTCCGGCGACACCGG	100279
Qy	11102	AATATCGGATCAAAAGACGTGCTCGCGATATCTGGGGTGGGTTAAGGACATGG	11161	Qy	12182	---ACGACAGCAAGACATTTCTGTTGACGAGCGCTGAAAGGCATCTCTGCTGCCAGTG	12238
Db	101355	AATATTTCTATCCCGTGTCAACTTGGCGATTTAATGGGGCGGGCTGTCCGATTTAG	101296	Db	100278	AAAATGATGATTAATCTGATCTGTTTCAACCGGGCACTAAAGGTCAGCTACTGCGTAGTG	100219
Qy	11162	TGCTTATCGGGCGCGAGTTCGCTCTATTTCCGGCAAAACAGATGTTGGAATAAAG	11221	Qy	12239	AGTTATACGGTCCGATGGCAGCAGCGCCGATATCCCTTACAGCGTCACTGAGTCTC	12298
Db	101295	TACTGATGGCCCCAAAGTGTACGCTTGTATGCTAATTAACCGTGAATGTTTTACCCAAG	101236	Db	100218	AGCTCTACGGCTGTGATGACAGCGAAACAGCAAAATATCCCCCTATACAGTACTGTAATCTC	100159
Qy	11222	GGGAGACCGTGCAGCAAAACGGAAGACTCACTCTGCCGCTCCGGGGTGTGACCCACGTA	11281	Qy	12299	GCCCGAGGTACGGTGTGTAAGCG---AATGGAGACTACCCGGTGGTGGCGGATGG	12355
Db	101235	GGCGGATGTGTGCAATCCGGTGATATCACTCTGCCGTTACCGGGTGGCGATGCCGTA	101176	Db	100158	GTCCCAAGTGGCCAAATTAAGATGGCACTACCGCTTCCCGGTGCTTTGGGCGCTCGG	100099
Qy	11282	CCCTGTGGGTTGAGTGATATGGCTGGCAGTGGAAGAGAGATTTGACGGAGTGGCTG	11341	Qy	12356	GGCGGAAGCCGTACGTCAGTGTATGAACGTACCAATGATCCTCAATGCCAACAC	12415
Db	101175	AGTATGTCGATTTAGTGACGTACTCGGTTTCGGGCCAAACACATCTGTTGAAGTTAGT	101116	Db	100098	TCGTGGAAACCGTGTATCTATGATGAACGTATTTATCGGTGATCTCTAGTCAATCAGG	100039
Qy	11342	CTAATCGAGTACGTTACTGGCAAACTGGGGCAGCGTCTGTTCCGTGACGCGGTGAATA	11401	Qy	12416	AGCGGTACTCTCTAGTGATGAATACGGTTTCCCTACGTGCGTCAGTGTCAATTAATC	12475
Db	101115	CAACTCAAGTCACTGTGGCCAAATCTGGGACATGGCGGTTTGTGTGAGCCAAATACAT	101056	Db	100038	ATATACGCTGTCCAGCGACCAATTCGGGCAACCTCTGAAACAGGTTTCAATGCAATATC	99979
Qy	11402	TTCCCGGTTTACCGAGTCAGTACGTTTAAACCTGACCAAGATTAATGCTGGCCGATA	11461	Qy	12476	CAGACGCGCTCGGTGGGGGACATTCATATCCGGCTCTTACCGGCGACGCTGTTCCG	12535
Db	101055	TGCGGGATTCAGCCAATCTGCCGACAACTTTAATCCGACCGAGTTTCATCTGGCCGATC	100996	Db	99978	CCCGCGCAATCAACCAACCAATCCGTATCCCGATACACTACCGGATACGCTATTTCG	99919
Qy	11462	CCGACGGTTCGGTACCGACCTGATTTATCGGATGAGTACCGGTTAGTCAATTAAT	11521	Qy	12536	CCAACAGTTTACGACGACGACGAGATATTACGCTGGGGTTGCAACAGAGCAGTGAC	12595
Db	100995	TGATGGCAGTGGTCTCGCGATTTGATTTATGTTTCATCTACCTACCGCTCTGGAGATTTC	100936	Db	99918	CAGCAGTTATACCATCAACAACTATTCGGATTAACCTGCCAGCAATCAGTTGCG	99859
Qy	11522	TCAACAGAGTGTAAATTTTCGCGAGCGCATACGCTGCTCTTCCGAAAGGTGTCG	11581	Qy	12596	ATCACCTGTTTTCCTCTGAGGGGCAATGTTGTTGGGGTTGGCGGAGGCGTCCGCGG	12655
Db	100935	AGATGAAGTGTAAACAGCTTTGCAAAACCAATTCACATCCGTTTCTGACGGCTGCG	100876	Db	99858	ACCATCT-----AACCGGTAATGAATCAGAGTGTGCGGATTAACCGGATGTACACGCA	99805
Qy	11582	GCTATGATCGCACTGACGTCTGCAAGTGGCGGATATCCAGGGGCTGGGGGTGCCPAGCC	11641	Qy	12656	ACGATGATTAAGTACTCTCGGACACAGTCCGGAAGGGGCTGTGACGCTGGAACACC	12715
Db	100875	GTTTTGATGATCTTGCAGCTACAAAGTGGCTGATGTTTCAAGGATTAAGGGGCTGTGAGC	100816	Db	99804	GTGATGCTTCTACTTACGATGCAACAGGTCCTGTTGATGCTTTAAATCTGGAAGCCC	99745
Qy	11642	TGTTACTGACGTCCTCCATGTCCGCTCATCTGAGTGGTGTGCCATTTATCGGACACA	11701	Qy	12716	TGTTGGCGCCCGAAAGCCCTGCTCGGATAGTCAAGTGTGAGTGTGCGGGTCAAGCAGC	12775
Db	100815	TGATCTGACGTACCGCATATGGCGCACATCAITTTGGCGCTGCGATCTGACCAATGCGA	100756	Db	99744	TATGTGCTGAAAATAGTCTGATTTGCGATGACAACACCGCGAATACCTTAATCAGCAAA	99685
Qy	11702	AACCTGTTGTTGAAATGGCATGAACAAATATGGGGCCCGGCATGCACTGCACTATC	11761	Qy	12776	AAGTCTGTGATCTGGAATTCACAAGACGTTGCCACCGTCCGCTCCGCTCCGCCCA	12835
Db	100755	AACCGTGGTGTCTCAGTGAATGAACAAATATGGCGCTCATCACACCTGCAATTACC	100696	Db	99684	GAACGTTCTATACCGATGGGAAAAACCAAGCGCCATTTGAAATACCGACACGACAAGCTT	99625
Qy	11762	GCAGTTCCGTGTGAGTTCTGCTCGATGAGAAAGCCGAGGCACTGGCGGACGAGTTCCTC	11821	Qy	12836	AGTGTGCTTTTATCGAAACGGCGCTGCTGGATGAGGGTATGCTGAGTTCAGTTCGCTG	12895
				Db	99624	TAATCGCTTTTACCGAAACCGCGGTATTAACAGAAATCTCTGTTATCCGCAITTTGATGGCG	99565

QY 12896 ACATTGTGATGAACA-----TCTCGAGCAAGCGGTTACCGCAATCCGGAT 12943  
Db |||||  
QY 99564 GTATCACGCCAGATGAATTACCGGCATTCTTGACACAAGCAGGATATCAACAGAGCCTT 99505  
Db |||||  
QY 12944 ACCTTTTCCCTCGAGGAGGAGCAAGAGGATTTGTGACCCAGCTGTCAGGATATG 13003  
Db |||||  
QY 99504 ATCTGTTTCCACGCACC-----GGCGAAACAAAGTCTGGGTAGCAGCTCAAGGCTATA 99451  
Db |||||  
QY 13004 TTACTATGCGGCGCAGAGCATTTCTGGCTACCGCTATCTTTTCGGGACAGTATGTTGA 13063  
Db |||||  
QY 99450 CCGATTACGAACTGAGCGCAATTTTGGGCTCTGTGCGACAAGGTAAACCCCTGTTAA 99391  
Db |||||  
QY 13064 CCGGCCCAAGTTACCGTACGCGGTGACCGGTACGATCGCTGTCATCAGCAGTGGCAGGATG 13123  
Db |||||  
QY 99390 CCGGGAACACGACGCTCAATGGGATACCCACTACTGTGTCACTCAACCCCAAGACG 99331  
Db |||||  
QY 13124 CCGCAGGATTTGTCACACAGCCGACTATGACTGGCGCTTCTGACGCCCGTCCGGGTGA 13183  
Db |||||  
QY 99330 CCGTGGTGTGACTGCTTAGCCAAATTTATGACTGGCGTTTTTCTCACACCTGTGCACTGA 99271  
Db |||||  
QY 13184 CGGACCCCAATGAATCTGAGTCGCTCACTCTGGATGCTCTGGCGCGGTGACCAACC 13243  
Db |||||  
QY 99270 CTGATATTATGATAATGTGCACTCTATAACCTTTGGATGCAATTAGGACGCCCTGTGCAC 99211  
Db |||||  
QY 13244 TGGGATTTCTGGGCGACGAGAAATGGTATTGCCACCGGTTAC-----AGTGATGCCA 13294  
Db |||||  
QY 99210 AACGTTTCTGGGAATCGAAATGGTGTGAACAGGTTACTCTCACCGGAAGAAAGC 99151  
Db |||||  
QY 13295 CGTTTCCGTTTCGGACGCGCGAGACCGCTCTGGCGTTGACGGCGCCCTACCAAGTAG 13354  
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QY 99150 CGTTTCTCACCAATCGATATCAATACTGCCAATGTCTTAAACGGGACCACTCCCTGTGCG 99091  
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QY 13355 CACAGTGTCTGTTGATGTACCGACAGTTGGGGAGATGACGCAATGAGAAA----- 13408  
Db |||||  
QY 99090 CGCAGTGTCTGGTCTATGACCGGACAGTTGGATGGCACTATTTCAGTCAGGAACCTTCA 99031  
Db |||||  
QY 13409 ----- 13408  
Db |||||  
QY 99030 ACATTTAACGAGGAAGACAGACACTGCGTGATTTACGGATTATCACGGAGATT 98971  
Db |||||  
QY 13409 ----- 13408  
Db |||||  
QY 98970 GCGGTATTTGTGCACTGGCTCGCGCGGTTGGTTGCAAGTCAACAGGCTAGTACGCCAT 98911  
Db |||||  
QY 13409 -----TGCCCCGACAGTGGTCTGCTGGCTACCG 13438  
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QY 98910 TGGTTAATCTGTTAACTAACAGCATCGGTTTACCTCCCCATACCTTACGCTGACCCCGG 98851  
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QY 13439 ATCCGTATGACAGTATACCGGACAGCATGGTCCGCCAACAGGTGACATTCAGTGAACGTT 13498  
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QY 98850 ATCCGTATGACCGGATTTCTGGGACGCAATTTATCAGCAAGTTCGCAATTCAGTGTGTT 98791  
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QY 13499 TTGGCGGTGATTTGCAATCGGCAACCCGCGAGCGAGGCAACGCTGCGCAACGAGGAC 13558  
Db |||||  
QY 98790 TTGGCGGTTTGTGCAAGCATCTGTACGGCATGAGGCGAGCGAAGCTTGGCAACGTAACC 98731  
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QY 13559 GCGACGCCAACTGTTGACCGGCCAGTGCAGGATTTGCGGTCACTGTAGCAACGAATTTCC 13618  
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QY 98730 AAGATGGTCTCTGGTGACAAAATGGA-----AGATACCAAAACGC 98689  
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QY 13619 GCTTGGCGGTTCACCGGAGGCGGAGTATGACAAATAAGTCTGCTGTTTCGGGTTATC 13678  
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QY 98688 GCTTGGCGGTTCACCGGACGCACTGAATATGACAAATAGGGACAGAGATACGAATTTATC 98629  
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QY 13679 AGCCGTAATTTTCTGGACAGTTGGCAATATGTCAGTATGACAGTGGCGCGCAGGACCTGT 13738  
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QY 98628 AGCCATTTTCTCAACGACTGGCGATATGTGATGATGACAGCGCCAGAAAAGGGGCT 98569  
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QY 13739 ATCCGACACGCACTTTTACGATCCGACGCAAGGAAATGGAGTTTATTCGGCAAAAG 13798  
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QY 98568 ATCCGATACGCATATTTATGATCCGATTTGGGCGGAAATCCGAGTTTATTCGCAAAAG 98509  
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QY 13799 GTGAACGGCGCAGAGTGTCTGTATATACCCCGTGGTTTGTGGTCAAGTGAAGACGAGATGATA 13858  
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QY 98508 GCTGGCTGCGACAGAGCCCAATATTTCCCGTGGTTTACTGTGAGTGAAGATGAATGATA 98449  
Db |||||  
QY 13859 CCGTTGGGTAAACAGACGCAATCTCTGACTGGGAAGGAGGGGGGACGGTGTAGTCCGTC 13918  
Db |||||  
QY 98448 C-----GGCGCTGAGGTGATTAATGTAATTAATTAATTAATTAATTAATTAATTAATTA 98404  
Db |||||  
QY 13919 GCCCTTGACAGGCGCTGCTGATGGAGACAAAGATGAAGATGAAGATGAAGATGAAGATGA 13978  
Db |||||  
QY 98403 AATGTTAAACAGCGCAATATAAACTACTTGTGAGTTCTTAATAGAGAAACAGGAT----- 98349  
Db |||||  
QY 13979 GGTGTGCTGACAGGTGTTTATGTTTGGGGCTTTTCCCATTTGGCGTTTACACCGTCGTTA 14038  
Db |||||  
QY 98348 -ATTTTGTACCTTTTATTTTATTAAGTAATAAATCCAAATTCCTGTAAATAATCTATCATC 98290  
Db |||||  
QY 14039 CACGGCGCAGTACTCAATATGGCAACAAACCGAGCGGCAACAGAAAGGCGCATGCGTT 14098  
Db |||||  
QY 98289 GGGAGCATAGAGAACTATGTGACCGGGGTGGGTGAGTGACGCCAACAAAGAAAGCAACTTG 98230  
Db |||||  
QY 14099 GGCCTCTCTGGCAGCAGAAACCCGGGAAGAAAGTGGAGCAGCAACGACGACTGACAT 14158  
Db |||||  
QY 98229 AAGATGACAGATATATATCTACTATCCAAAGCTCTCTCGCTTCCCAATGACATATCA 98170  
Db |||||  
QY 14159 GAACAAAGTGGCTATATACATGCTGAAGAAGAACTGGCTGCTGCGGTGACGCTGCGCTGA 14218  
Db |||||  
QY 98169 AGACCATG-----AAATATAGATGAACCAATTTATCATGTAATGTCTACTTGGTG----- 98121  
Db |||||  
QY 14219 TGCTCAGCGCATGCTGTCAGCGCTGACGACACCCGTTTACACCTCTCAGCGGCAACTTTCG 14278  
Db |||||  
QY 98120 -----AAATATTACTAGCTAAACCCAGCCCAATTTAGAAAAATTCG 98083  
Db |||||  
QY 14279 CAGTCTGTGAACCCGCGGCTTTCCGACGACTACCGCTATCGGTACAGACACCTCGGAGG 14338  
Db |||||  
QY 98082 ATACCATCATTTGACATATCAAAATCAGC-----CAACCACTGTTCTCCCAATAGTTGGCC 98028  
Db |||||  
QY 14339 CCAACCGCGGCTTTGTTGCGGAACTGTTCCGCGCTGACAGAGAGCGGAGAGCT 14398  
Db |||||  
QY 98027 GATCACACCGGTTATCTGAACCTTAATTTACCATCAATACAACTCTCAAAATTTACCAAG 97968  
Db |||||  
QY 14399 GGACGCTATGCTGACAGGACCAAGTGAATGGCAGGCTTGGCGGCGGCTTATCAGGC 14458  
Db |||||  
QY 97967 CGTTTGCATTAATAACATCACGATAAATCACTTCTCTTAACTTATTAGTGATATAAGGT 97908  
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QY 14459 GGTACGACGACGAGCAAAAATAAGCGATTTAGCGGTTTAAAGAAAGTGAACGCTGTTT 14518  
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QY 97907 CGTTTATGTTGTCGCGTAATTTAAATTTATTTTGAAGATTAACACCA-----TC 97860  
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QY 14519 TCGCGATTAAATTAACAGAGATCACATGAGCACATCTTGTTCAGTAGCACCCCGCTCG 14578  
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QY 97859 TAAGGATTTAAATATGACGAGTTTATCTGTGAAA-----TTGACAAAAAACACCAATTA 97804  
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QY 14579 GTCCGCTGCTCGAACCCGCGCTGTTGGTTCGGGAGCTGCACTACTACGCCATCCG 14638  
Db |||||  
QY 97803 ATCAGTGTATTGATTAACAGGAGTTAAATGTACGTACTTT---AGAATATCTACGTACT 97747  
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QY 14639 GATACACCGGAGGACGACGAGCTATCACCTGCCATCAGCACGATGAGCGCGGACG 14698  
Db |||||  
QY 97746 CAAGCTGTATGAACAGTATGAATTTGATCACACTCTATGAGTTCAATTTCAAGGATTT 97687  
Db |||||  
QY 14699 TTGTCAAAAGCGCCGACCCCGG---GTTTACAGCGCGGCTCTGACAAATTTCACTGATC 14755  
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QY 97686 GAGGTAAAAGTACTGATCTCTGTAAGAAATAAAATCAGAGCGGCGCCGAAATTTCAATCGC 97627  
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QY 14756 CTGAATAGCCTGACCGGAGCAGTACTGACAGCGCTCAGCGCCGATGCGGTACGTGCTG 14815  
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QY 97626 GTCTTTTAACTCGCGGTGAGGTTCTACGTGAAGAGGGGTGATGCGGTGCAACTATC 97567  
Db |||||  
QY 14816 GAACTGAGGATGCGCCCGGCGGCGGCTTCTGGCGCTCACCGGGCTGGGACGGAAGAC 14875  
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QY 97566 ATCTCAACGATGTTGAAGGTGCGCGGTATTAACCATC-----AATGCAACC 97519  
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QY 14876 GCGGTACCCGACCTGGCAATATGAAGCATACCTTCCCGGCGCCGCTGAGCATC 14935  
Db |||||

Db 97518 GGTGTCGCGCAAGACTATCACTACGAAGATAACATCTACCGGTGCTTACTTGCTATC 97459  
 QY 14936 ACCGACAGGTACCGGTGAGCGGCCCAATATACGGAAGCTTGTGTGACGTGGCAAT 14995  
 Db 97458 ACCGAACAGGTGAGCGCAAA---GAGNAAAATGACCGAGCGCTTATCTGGGCGGCAAT 97402  
 QY 14996 ACGGATGCCGAGAGATTTCTCAATCTGGCTGGCGAGTGTGTCAGTCAATACGATACCGC 15055  
 Db 97401 AGCGCAGAAAAGAGTACAACTTGTGTGTCAGTGTGTCGCACTACGATACCGCT 97342  
 QY 15056 GGACTGGTCAGACGACAGCATTCGCCCTGAGCGGCTGCCCTGCCCTGACGCGCAG 15115  
 Db 97341 GGACTCACTCAACTCAACAGCCTTTCTCTGGCTGGCGTGTGTCATCAAACTCAACAA 97282  
 QY 15116 TTGTCGCCGACGCGCGGGGGCAACTGATGGGTGAGGATGCTCGGCCCTCGAATGAC 15175  
 Db 97281 CTGCTCGTGCATCAAAATGCCAGCTGGACAGGTGAAGATCAAAAGCCTCTGGCAGCAA 97222  
 QY 15176 CTGCTGGATGGGAGAGCTTTCTTACCCAGACCCAGCTGATGCGACCGGCGCGCTCTG 15235  
 Db 97221 AAAGTACGAGTGTCTATACCAACCAAAATAGCACTGATGCCACCGGGCTTTACTT 97162  
 QY 15236 AGCATCACCGATGCAAAAGGTAACTGACGCGTGTGGCATATGATGTGGCTGGCTGCTA 15295  
 Db 97161 ATCCAGACCGATGCCAAAGGCAACATCCAGCGTCTGGCCTATGATGTAGCGGGCAGCTA 97102  
 QY 15296 TCGGCGAGTGTGTGACGCTGAAGACGGCAAGGACAGGTATCGTGGCCCTCCCTGACG 15355  
 Db 97101 AAAGGTGTGTGTTAACTCACTCAAGGTCAAGCGCAACAAAGTGAATCAAAATCGCTGACC 97042  
 QY 15356 TACTCGGCGCGGGAAGATTTGCTGAAGAACACGCGCAACGCGGTGTAACTCGTAT 15415  
 Db 97041 TACTCTGCGCGGACAAATTAATGCTGAAGACAGGTAAACGCGGTATACCGNATAC 96982  
 QY 15416 ATTTACGACCGGAAACACAGCGCTTACGCGGATTAACCGGAACGCTCGTGGGCAC 15475  
 Db 96981 AGCTATGAACCAAGAACCAACCGCTTATTTGGTATCACTACCGCGCTCGTCAGATACC 96922  
 QY 15476 GTTCCGGAGCAAAAGTGTGAGGACCTGCGCTATACGATGACCGGTAGCAACGTA 15535  
 Db 96921 -----AAGGTGTGCAAGACTTACGCTATCAATATGATCCGTTAGCAATGTG 96874  
 QY 15536 CTCAGCGTCAATACGATCGGAAGACCCGCTCTGCGGTAAACAGAAAGTGTGACCG 15595  
 Db 96873 ATCAATATCGTAAACATCGGAGGACCAACCGCTTTTGGGCAATCAGAAAGTGTGCCG 96814  
 QY 15596 GAGAATACGTATCATCTACGACAGCTGTATCCAGCTGGTCAGCGCCACAGCGGTGAGATG 15655  
 Db 96813 GAGATAGCTATCTTACGACTCCCTGTACAGCTTATCAGTGTACTGCGGTGAATG 96754  
 QY 15656 GCCAATGCCGCGCAGCAGGCAACGATTAACATCCGCTACAGCCCCCTTCTCTACAGAC 15715  
 Db 96753 GCCAATATAGGTGAGCAAAATTAATCAACTGCCCTCCCTG-----CGTACCTTCCGAC 96700  
 QY 15716 AGCTCTGCTACACCAATTAACAGCGCACTACGCTTATGACGCTGCGCAACCTGACG 15775  
 Db 96699 AACATACCTACCTAATCTATCTCGCGCTACAGTTATGATCAGACGCGTAACTGACG 96640  
 QY 15776 CAGATGCCGACAGTCCCTTGCAGCAACAAATTAATACGACAGACATCAAGTGTAGT 15835  
 Db 96639 CAAATTCGGCACAGTTTCACTCGGCTACCCAAATAACTACACACGCTATCACTCACTCTCG 96580  
 QY 15836 GACCGCAGCAATAGGCGGTACTGACGACGTTGGCGGAAGTCCGCTCAGATGTTGATG 15895  
 Db 96579 AATCGAGTAACCGCGCGTCTCAGTACGCTGACAAACAGATCCAAATCAAGTGGATACG 96520  
 QY 15896 CTGTTCAAGTCAGGAGGTCAACAGAAAGCACCTGACGCGGGCAAGCACTGTTGTGACG 15955  
 Db 96519 TTATTTGATGCCGTGCTCACCAACAGTTTATACCGGCTCAGACACTGTTCTGGACA 96460  
 QY 15956 CCACTGGAGAACTGCAAAAGGTGACACCGGTTGTCGATGGGGGGCGGACGACAGC 16015

Db 96459 TCACGAGGAGAGTTAAAGCAGGTCAATAACCGTTCCAGAAAT----- 96418  
 QY 16016 GAAAGCTATCGTATGATCGCGGCACTCAGCGCTATTATCAAAACCGCACGCGGCAAACT 16075  
 Db 96417 GAATGGTACCGATACCGCAGCAACGGAATGAGCAACTGAAAGTGAAGTGAACAGCCAACT 96358  
 QY 16076 GCGCAACAGCTTCAGACACAGCGGCTAGTGTACTCTCCCGGGCTGGAGTTAGGTATCATG 16135  
 Db 96357 CAGATATCTACCGCAGCAGCGGCTATCTATCTGCCGGGCTGGAATCTACGCAAACT 96298  
 QY 16136 GCAATATGGCTGACGAAAAAGAAAGCTGAGGTATTATACCGTGGCGGCGGCTGGCGG 16195  
 Db 96297 CAGAACAGCAGCACCAACCAACAGAGATTACACGCTGATCACACTAGGTGAAGCGGCTCGC 96238  
 QY 16196 GCACAAAGTGGCTATTCGACCTGGAGATCGGCAAGCCGATGACTCTGATGAGGACTCG 16255  
 Db 96237 GCACAGGTGCGGCTGCTGACCTGGAGAGCGGTAAACCAAGAGGTATCAACCAATCAG 96178  
 QY 16256 GTGCGTTACAGTTACGATAAATCTGCTGGCAGCAGCCAGCTGGAGCTGGACAGAGAGGT 16315  
 Db 96177 CTACGTTACAGTACGATTAATCTGATCGGCTCAGCCAGCTTGAATGGAACCAAGGG 96118  
 QY 16316 TACCTTATCAGTACGAGAGAGTTCTACCCGTTATGCGGTAACCGGCTTCTGACGGCGCA 16375  
 Db 96117 CAGATTATAGTGAGGAAGATTATTCATTCGCGCGGACAGCGATGTGGCGAGCCAAT 96058  
 QY 16376 AGTGAGTTGAGCTGACTACAAACTATCCGATGCGGTAACCGGCTTCTGACGGCGCA 16435  
 Db 96057 AGCCAAACAGAAAGCAACTATAAACTATTCGCTATTCAGGCAAGAACCGGATACCACT 95998  
 QY 16436 GGGCTGGATTATTCGCTTATCGGTATTACCAAGCCATGGCAGGCGCTGGCTCTCCAG 16495  
 Db 95997 GGGCTGTTATTTACGTTTACCGTTATCAACCGTGGCGGCGAGATGTTAAGCGG 95938  
 QY 16496 GACCGCGCAGGCAAGCGGCTGACCGGCTGAACTGTTCCGATGTTGCGGGAATTAATCCGCTC 16555  
 Db 95937 GATCGCGGAGAACCAATGATGGGCTGAATCTATACCGAATGTTGAGAAATAATCCAGTA 95878  
 QY 16556 ACGCTGTTGACAGCAACGG 16575  
 Db 95877 AGTTTGCAGGATGAAATCG 95858

RESULT 6

AAV17876

ID AAV17876 standard; DNA; 38258 BP.

XX AAV17876;

XX AC

XX DT

XX 23-JUL-1998 (first entry)

XX DE

XX Cloned toxin gene sequence from *Xenorhabdus* strain NCIMB 40887.

XX KW

XX *Xenorhabdus*; toxin; insecticidal; protection; *Pieris brassicae*; crop;

XX *Pieris rapae*; *Plutella xylostella*; Lepidoptera; Diptera; animal; ss.

XX OS

XX *Xenorhabdus* sp.

XX PN

XX WO9808388-A1.

XX PD

XX 05-MAR-1998.

XX PF

XX 27-AUG-1997; 97WO-CB002284.

XX XX

XX 29-AUG-1996; 96GB-00018083.

XX PA

XX (UKAG-) UK MIN AGRIC FISHERIES & FOOD.

XX PI

XX Jarrett P, Ellis DJ, Morgan JAW;

XX XX

XX WPI; 1998-179074/16.

XX DR

XX Orally active insecticidal composition, used for protection of crops or

XX PT

PT animals - contains pesticidal material from *Xenorhabdus* species  
PT optionally synergised with *Bacillus thuringiensis* toxin.

[illegible]

Claim 2; Fig 2; 46pp; English.

XX

This is a toxin gene sequence cloned from a *Xenorhabdus* strain NCIMB 40887. This has insecticidal activity and can be used in an insecticidal composition for oral delivery to an insect. The composition includes material encoded by *Xenorhabdus* strains NCIMB 40886 and 40887.

particularly it contains *Xenorhabdus* cells or culture supernatant. It may also include active materials from other sources, especially *Bacillus thuringiensis* or delta-endotoxins, and is formulated with a carrier, especially an edible material for the pest. Pesticidal agents isolated from *Xenorhabdus* species, especially *X. nematophilus* have oral activity against *Pieris brassicae* or rapae, *Plutella xylostella* and are heat-stable at 55 deg. C. They are resistant to proteolysis by trypsin and proteinase K, and are inactivated by sodium dodecylsulphate or acetone, and by heating to 80 deg. C. The compositions are used to kill Diptera and Lepidoptera, particularly *P. brassicae* or rapae, *P. xylostella* and *Culex quinquefasciatus*, e.g. for crop or animal protection, also for vector control. The isolated pesticidal agent may be expressed in transformed plants to impart protection. *Xenorhabdus* materials show synergistic effects when formulated with *Bacillus thuringiensis* toxins

XX  
SQ Sequence 38258 BP; 10486 A; 8248 C; 8871 G; 10630 T; 0 U; 23 Other;

Query Match 8.8%; Score 1658.8; DB 2; Length 38258;  
Best Local Similarity 53.1%; Pred. NO. 0;  
Matches 4978; Conservative 0; Mismatches 3802; Indels 598; Gaps 44;

Qy	7301	ATGGAC	TTCTCGG	AGCCAA	TGCCCT	CTATTTCTCGG	AGCTGTTCTATT	TACACGCCGATG	7360
Db	10859	ATGGATTT	CAATAGT	GCAGCGC	CTCTATT	TACTGGGA	ATGTTCTATT	TACACGCCGATG	10917

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QY 7361 ATGGTGTTCACGCGTTGTTGCAGGAACAGCACTTCCCGAAGCCACCCGCTGGCTGCAG 7420

Db 10918 ATGTGCTTCCAGCGTTTGCTACAGGAAAAACAAATTCGACGAGCCACACAATGGATAAC 10977

[illegible]

QY /421 TATGTC TGGAAACCGGGCCGGGCACGTGGTAAACGGGGTGC TGCAGAAATACACCTGGGAAT /480

Db 10978 TACGTCATAATCCCGCCGGCTATATCGTTAACGGAGAAATCGCCCCCTGGATCTGGAAC 11037

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QY 7481 GTCCGTCCGCTGGAGGAGGACACCGCTGGAACGACTCGCCGCTGGACTCCATTGACCCC 7540

Db 11038 TGCCGGCCGCTGGAAGAG--ACACTCCTGGAATGCCAATCCGTTGGATGCCATGTATCCG 11095

7541 CZECH REPUBLIC

QY 7541 GATGCAATAGCCCAAGTACGACCCCATGCAATACAAGTTCGCCACCTTTATGTCGTACCTC 7600

db 11096 GATGCCGTCGCACAAATATGACCCGACACACTATAAGTTGCCACCTTTATGGCCGCTGTG 11155

[illegible]

**QY** 7601 GACCTGCTGATTGCCCGCGGTGATGCCGCCCTACCGGCTGCTCGAGCGGACACCCTTAAC 7660

A vertical ruler with a dashed line and horizontal markings. The ruler is oriented vertically, with a dashed line running down its center. Horizontal markings are present along the ruler, with some markings being longer than others, indicating different units of measurement. The ruler is used for measuring the height of the text in the document.

D**b** 11156 GATCAACTTATTCTGCGCGGATATGGCCTATCGCGAACTGACCCGCGATGCGTGAAT 11215

[illegible]

QY 7661 GAGGCCCGGATGTGGTACGTCCAGGCCCTGAACCTTCTGGCGACGAGCCCTATATTC 7720

Db 11216 GAAGCCAAGATGTGGTATGTGCGGTGCCTTGGAA TTGCTGGGTGATGAGCCGAGGATTAC 11275







Db 14745 TTACGCGTTATCGGGCCAAATAGTGTACTGTCTGTGTCAAATAATATCCGCGAGATGGAT 14804  
Qy 11218 AAAGGGGAGACCGTGCAGCAAAACGGAAGAACTCACTCTGCGGTCCCGGGGTTGACCCA 11277  
Db 14805 CGCGCTCAGGATGTTATTCATTTGTCAATAGCCACTGCGGTTCCGGCAAAAATAAG 14864  
Qy 11278 CGTACCCCTGCGGTTCAGTGATATGCGTGGCGAGTGGACAGCAGCATTTTGAACGGAGTG 11337  
Db 14865 CGTCATCTTGTGCGCATTCAGTGATATGACAGGCTCCGGCAATCACATCTGGTGAAGTT 14924  
Qy 11338 CGTGTCAATCGAGTACGTTACTGGCCAAACCTGGGGCACGGTGTGTTGCGTACCGGGTG 11397  
Db 14925 ACGGCAATAGCGGCTACTGGCGAACTTGGGGCATGGAAATTTGGTGAAGCTG 14984  
Qy 11398 AATATTTCCCGGTTTATGCCAGTCACTGACTACGTTTAACTCCGACAGATATTTGCTGGCC 11457  
Db 14985 ATGATAACAGG-CTTCCAAATTACGGGGAACGTTTAAACCCACAGACTGTATATGGTA 15043  
Qy 11458 GATACCGACGGTTCGGGTACCA-CGGACCTGATTTATGCGATGAGTGACCGGTTAGTCAT 11516  
Db 15044 GACCTAAATGGCTCAGGCACACCCGATTTTATTTATGCCCGCAATACTTTACCTTGAAC 15103  
Qy 11517 TTATTTCAACAGAGTGGTAATTTATTCGCGAGCCGCATACGCTGCTCTTGGCGGAAGG 11576  
Db 15104 CTATGCCAATGAAGCGGCAATCATCTGCTGAACCTCAGCGTATTGATCTGCGCGATGG 15163  
Qy 11577 TGTGCGCTATGATCGCACCTCGAGTCTGCAAGTGGCGGATATCCAGGGGCTGGGGTGCC 11636  
Db 15164 GGTACGTTTGTATGATCTTGTGTTTACAAATAGCGGATACACAAGGATTAGGAGTCG 15223  
Qy 11637 TAGCCTGTTTACTGACGGTCCCGCATGTCGGCGCTCATCACTGGGTGTGCCATTTATCGGC 11696  
Db 15224 CAGCATTTTGTACGATCCCCCATATGAAGGTGCAGCACTGGCGATTGATGACCAT 15283  
Qy 11697 AGACAAACCTGTTGTTGATGCGATGAACAACATATGGGGCCCGGCATGCACTGCA 11756  
Db 15284 ATTCAGCCTTGGCTGCTGAATCGGTCATGAACAATATGGGAACAGAAACACGCTGTA 15343  
Qy 11757 CTATCGCAGTTCCGTGCGAGTCTGGCTGGATGAGAAACCGAGCACTGGCGCAGCAG 11816  
Db 15344 TTATCGCAGCTTCCCGAGTTCTGGCTGGATGAGAAATACAGGCTTCTGAATCCGGAT 15403  
Qy 11817 TTCCCTGCTGCTTACCTGCCATTTACATTCGATACCCCTGTGGCGTTTCGGTGTGCAGGA 11876  
Db 15404 GACGGTGTGAGCTACTTACCGTTCCCGGTGCAATGTTGTGGCGCACGGAAGTCTGGA 15463  
Qy 11877 TGAGTACACCGGTAAACGCTGTGTCAGCAGTGTCTTTATGCGCAACGGGCTTGGGACGG 11936  
Db 15464 TGAATTTCCGGTAAACCGATTGACCGCCATTTATCACTCACTGCTGCTGGGATGG 15523  
Qy 11937 GCAGGAACGCGAGTTTCGGGGTTTGGTTTGTGATCAGGATACCGATACCTTGGC 11996  
Db 15524 TCTGGAACGGGAGTTTCTGGTTTGTGGCGGTGACGCAAACTGATATTGATTCACGGGC 15583  
Qy 11997 AAG-----CCAGGATACGGCGACGGAACCTGAGTATGCTCTGTGAGCGCGAATCGSTA 12050  
Db 15584 GAGTGCACACAGGGACATGCTGAACCCACCGCACCTTCGCGCAGGTTAATGGTA 15643  
Qy 12051 TGGCACCGGGTACCGGAGTAGACGAGCGTCTGCGGAGACGATTTGGCAAAACGATGC 12110  
Db 15644 CGGCACCTGGGGTACGGGAAGTCGATATCTTCTGCCACCGCAATATTGGCAGGGGATCA 15703  
Qy 12111 CGCGCTTTTGGCGATTTCCGGACCGGTTTCAC-----TGTGGTTTCAGGAGAGATGA 12164  
Db 15704 ACAGGCATTTCCCAATTTACCCACCGCTTTACCCGTTATGACGAAAAATCCCGTGGTGA 15763  
Qy 12165 GCAGACATATACTCCGACGACAGCAAGACATTCGTGTGCGAGCGCCCTCGAAAGGCAT 12224  
Db 15764 TATGACCGTCAACGCGGAGGACAGGAGAACTACTGTTATCTGATCTGACGCTTAAAGGACA 15823  
Qy 12225 CTGCTCGCAGTGAATTAACGGTGGCGATGGCAGCGCAGCGCGCTTACGCTTACAG 12284  
Db 15824 ACGTTTACGCGAGTGTATGGGATGATGATTCTTATCTACTGCGCGGTACGCGCTTATTC 15883

Qy 12285 CGTCACTGAGTCTCGCCCGCAGGTACGGCTAGTGTGAAGCGAATGGA-----GACTACCCGGT 12341  
Db 15884 AGTGGATGATCCGCGACCAAGTACGTTTGTGTTACCGGTGATGATCGGACGTCCTGC 15943  
Qy 12342 GGTGTGCGCGATGGGCGCGGAAAGCGTACGTACGTTTATGAACGGTACCAATGA-TC 12400  
Db 15944 GGTACTGTTTTCGTTGCGCGCAATCCCGCAATACCGATATGAAGGGGTTGTTACCGATT 16003  
Qy 12401 CTCAATGCCAAACAGCAGGCGGTACTCTCAGTCATGAATCGGTTTCCCACTCGGTGAGG 12460  
Db 16004 CACAGTGCAGCCAAAAGATTGCTTAAATATGATGCTTAGGATTTCCCGAGGACAATC 16063  
Qy 12461 TCAGTGTCAATTTATCCAGCAGCCCTCCGTCGCGGACAAATCCATATCCCGCGCTCTTAC 12520  
Db 16064 TTGAGATTGCCATTTCGAGAGCTCCACAGCTGAGTTCTCGCTTATCCCGATACCTGC 16123  
Qy 12521 CGGCGACGCTGTTGCGCAACAGTTATGACGAGCAGCAGAGATATTACGCTGGGGTTGC 12580  
Db 16124 CCGAAACACTTTTACACGAGCTTCGACGACAGAGATGTTCTCTCGTCT--GACAC 16180  
Qy 12581 AACAGAGCAGTGCACATCACTTGTTCACGTCTGCTGAGGGGCAATGGTTGTTGGGGTTGG 12640  
Db 16181 GCCAGCGTTTCTTATCACCATCTGAATCATGATGATTAATACGTGATCACAGGGCTTA 16240  
Qy 12641 CGGAGCGCTCGCGGACGATGATTTCACGTACTCTCGGACAACTGTCGCGAAGGGGGTGC 12700  
Db 16241 TGGATACCTCACGAGTACGACAGTATTTATCAAGCCGATAAAGTGCAGGACGTTGAT 16300  
Qy 12701 TGACGCTGGAACACCTGTTTGGCGCCGAAAGCCTGCTCGGATAGTCAGGTACGTTACGC 12760  
Db 16301 TTTCCCTTGAATGGTTTCTGC-----CACAGTGCAGGAGCATTTGTTGTGCTG 16351  
Qy 12761 TGGCGGGTACGACAGTCTGCTATCTGGAATTCACAGAGCTTGCACCGTGCCTGCTC 12820  
Db 16352 ATGCCGACCGGATTTCTGGGACATCAGCGTGTAGCATATACCGTCCAGAGAGACAAC 16411  
Qy 12821 CGGCACCTCCCGCCCAAGTAGCTTTTATCGAAACGGCGTCTGGATGAGGGTATGTCATCA 12880  
Db 16412 CGGCTATCTCTCGCTGGTGGCATACATTGAAACCGCAGAGTTTGTAGACGATCGTTGG 16471  
Qy 12881 GTTCACTGGCTGCTACATTTGTGA-----TGAACTCTCGAGCAAGCCGGTTACCG 12932  
Db 16472 CGGCTTTGAGGAGGTGATGATGAGCAGGAGCTGACAAAACAGCTGAATGATCGGGCT 16531  
Qy 12933 GCAATCCGATACCTTTTCCCTCGAGCGGGAAGCAGACAGGCATTTGGACCCAGTGC 12992  
Db 16532 GGAATACGGCAAAAGTGCCTTCAGTGAAGAAG--CAGATTTCCATGCTGCGGTGGGACA 16589  
Qy 12993 TCAGGATATGTTTACCTATGCGCGCGCAGAGCATTTTCTGGCTACCGCTATCCTTTCCGGA 13052  
Db 16590 AAGGAAATTTACAGATATGCGGTGCGAGACGAGTTCTATCGGCCATTGGTGCACCGGA 16649  
Qy 13053 CAGTATTTGACCGGCCCAATTAACGTGACGCGTACGCGTACGAGTACGCTGATACGCA 13112  
Db 16650 AACCAAGCTTACAGGTCAAAACGACAGTACGCTGGGATAGCAATTACTGTTTATCACCGC 16709  
Qy 13113 GTGGCAGGATGCGCGAGGAGTTGTCAACACGCGCATATGACTGGCGCTTCTGACGCC 13172  
Db 16710 AACAGAGGATGCGGCTGGCTTGCATGCAAGCGCATTTACGATTTATGATGTTGTTG 16769  
Qy 13173 CGTCCGGTGAAGGACCCCAATGATATCTGAGTCCGTCACCTGATGCTCTGGGCGC 13232  
Db 16770 GGATAACACCAAGATATCAATGATTAATCTATCACCGTGACGTTTGTATGATCTGGGAC 16829  
Qy 13233 GGTGACCACTCCGATTTCTGGGGCAGCGGAAATGGTATTTGCCACCGGTTACAGTATGC 13292  
Db 16830 GGTAAACAGCTTCCGTTTCTGGGGGACTGAAACGCGTGAAGAAACAGGATATACCCCTGC 16889  
Qy 13293 CAGTTGTCCGTTCCGGAACGCGCAGCGGCTTGGCGGTTGACGCGGCCCTTACCAGT 13352  
Db 16890 G-----GAAATGAAGTGTCCCTTTTATTTGTCGCCCAACAGCGT 16928

Qy	13353	AGCACAGTGTCTGTGTATGTACGGACAGTGTGGGAGATACGACAAATGAGAAAATGCC	13412
Db	16929	GGATGATGTCTTGGCAATTAAGAAACCCGGCATACCTGTGCAGGGCTGATGCTTTATGCCCC	16988
Qy	13413	CCCGCAGCTGGTCTGCTCGCTACCGATCGCTATGACAGTGAATCCGACACGACAGGTCGG	13472
Db	16989	TCCTGAGCTGGATGGTTACAGCCAGCTTTTCTAAATGATGGGAGCTTTATGAGAGCTGAA	17048
Qy	13473	CCAACAGGTGACATTCAGTGAACGGTTTGGGCGTGAAGTTGCAATCGGCAACCCGGCAGGC	13532
Db	17049	ACCGCTGGGATCATCACTGAAGAT	17073
Qy	13533	CGAGGGCAACGCTGCACAGGAGCGACCGCAAACTGGTGACGGCCAGTGACGGATT	13592
Db	17074		17073
Qy	13593	GC CGGTCACTGTAGCAACGAATTTCCGTCTGGCGGTCCCGGGAGGGCGGATGACAA	13652
Db	17074	-----GGTTATCTCTGTCTGTCTTTTCCCGCTGGCATCAAAA	17114
Qy	13653	TAAAGTCTGCCTGTTCGGGTTTATCAGCCGTTATTTCTGGACAGTCTGGCAATATGTCAG	13712
Db	17115	TAAACCTTGGCGTGCATGCCAAAGCAAGTCAATTCACAGAACCCACCCCATGTACTGAG	17174
Qy	13713	TGATGACAGTGC CGCGCACGACCTGTATGCCGACACGCACTTTTACGATCCGACGGCACG	13772
Db	17175	TGTGATCACCGACCGTATGATCCCGATCCGGACAAACA	17213
Qy	13773	GGAAATGGCAGGTTATTACCGGCAAAAGGTGAACGGCGACAGGTGTGTATATACCCGTGGTT	13832
Db	17214	-----ATTACGTCAAACGTTTTA	17230
Qy	13833	TGTGTCAGTGAAGACGAGAAATGATACCGTTCGGCTTAAACGACGATCCTGACTGGGAAG	13892
Db	17231	-----CGTTTTAGTGATGGTTTTGGCGAAACCTTACAAACAGCC	17270
Qy	13893	GAGGGGGGACGGTGTAGTCCGTGCCCTCTGACAGCGCGCTGCCTCATGGAGACAAAG	13952
Db	17271	TACGCCATGAAGTGGTGAAGCCTGGGTACCTGATGAGTATGGAGCCAAATGTGGCTGAAA	17330
Qy	13953	ATGAANAATACACTATCAGGTTGGCGGGTTGTGCTGACAGGTGTATGGTTTTGGGGGCTT	14012
Db	17331	ATCAAGCGCC	17341
Qy	14013	TCCCATTTGGCGTTACACCGTTCGGTTACCAGCGCGCAGATACCTCAATGGCAACAGCCAG	14072
Db	17342	-----CCTGAACGGGCGATTACAAATTTCCGTTGGGCAATTTCCCGGACG---T	17389
Qy	14073	GCGGAACAGAAAGGGCCGATGGTTGGCCCTCTCGGCAGCAGAAATCCGGGAAGAAG	14132
Db	17390	ACAGAATATTAAACGGGAAAGGCAAGCCCTCGCTTACGTTTTCAA	17435
Qy	14133	TGGGAGCAGCAACGACAGACTGCATGAACAAGTGGCTATACATGCTGAAGAAGAACTG	14192
Db	17436	-----ACCGTATTCTGAAATAATTGGGCAACTATGTCAAGTTGACCAAAAAT	17485
Qy	14193	GCTGCTCGCGTGACCGCTGCGCTGATGTCTGACGCGCACTGGTCAAGCCCTGCAGCACACC	14252
Db	17486	GCCCGGAGGATATGATATGCCGATACCCATTACTATGATCCGTTGGGGCGTGAATATCAG	17545
Qy	14253	GTTACACCCCTCCAGCGGCAACTTGGCAGTCTGTGAACCCCGCGCTTTCCGACGCTACC	14312
Db	17546	GTTATACGCCAAAGCGCGGTTGCTGTGATCTCTTATTCACTCCCTGGTT	17594
Qy	14313	GCTATCGGTACAGACGACCTCGGAGGCCAACCGCGGTTTTGTTTGCAGAACTGTTCCGC	14372
Db	17595		17594
Qy	14373	CGCGCTACACGAGACGGGAGAGCTGGCAGCGTATGCTGACAGGACACAGAGTGAATGG	14432
Db	17595	-----TGTTGGTGAATGAAGTTGAAATGACACTCCCGG	17627
Qy	14433	CAGGCCTCGCGGCGGCTTATCAGGCGGGCTTACGCAAGAGCAGAAAAATTAAGCGGATTTA	14492

17628	Db	--TGAATGACAGCATAAAGCTCAGTGATGCGCTGTTCACTGAAACAGACATCACTCCATTTA	17685
14493	Qy	GCCGTTAAGGAAAAGTGACGGGTGTTTTCCGGAATTAATTAACAGGAGATCACATAGCA	14552
17686	Db	GGAAATGA-----TCATGAAGA	17702
14553	Qy	CATCTTGTTCAGTAGCACCCTCGGTGCGGTGCTCGACAAACGGGGCTGTGTGTC	14612
17703	Db	ATTTCTGTTACACAGCAATACGCATCCGTCACCGTACTGGACAACCGTGGTCAGACAGTAC	17762
14613	Qy	GGAGCTGCAGTACTACCGCCATCCGATACACCGGAGGACGGAACGAGCGTATCACCT	14672
17763	Db	GGAAATAGCTGGTATCGGCACCCGATACACCTCAGTTAACCGATGAACGCATACCG	17822
14673	Qy	GCATCAGCAAGATGAGCGCGGACGTGTGTACAAAGCCGACCCGGGTTCACGCGG	14732
17823	Db	GTATCAATATGATGCTCAAGGATCTCTGACTCAGAGTATTTGATCCGCGATTTTATGAAC	17882
14733	Qy	CCGGTCTGACA-----AATTACAGTACTCTGAATAGCC	14765
17883	Db	GCACGACACAGGAGTGACAAAGCCATTACACCAATCTTATCTCTGTGATCAC	17942
14766	Qy	TGACCGGGACAGTACTGACAGACGTGACGCGCGATGCGGTGCTGCGTGAACTGACG	14825
17943	Db	TCAGTAAGAAGCAATTGGCGTACGCAAGGTGTGGATGCCGGAACCGGTGTCGCCCTGCATG	18002
14826	Qy	ATGCCCGGGCGGGCGTTCTTGGCCGTCACCGGGCTGGGACGGAAGACGCGTCAACC	14885
18003	Db	ATGTTGCCGGGCGTCCCGTTTAGCTGTGACGGCCATGG-----CGTTAGCC	18050
14886	Qy	GCACCTGGCAATATGAAGACGATACCTTCGCGGGCGCCGCTGAGCATCACGAGCAGG	14945
18051	Db	GAACGTTTCAGTATGAAGTGATAACCTTCGGGACGATGCTAAACGATTACCAGCAGG	18110
14946	Qy	TTACCGGTGAACCGCCCAATTACGAAACGCTTCGTGTACGCTGGCAATACGGATGCCG	15005
18111	Db	TAAAGGAGAGAACCCCTGTATCACGGAGCAGATTGATTGTGTAGGAATAACGCCGGCAG	18170
15006	Qy	AGAAGATTCTCAATCTGGCTGGCCAGTGTGTCAGTCAATTAGCATACCGCGGACTGGTGC	15065
18171	Db	AAAAAGGCAATAATTGGCCGSCAGTGGTGTTCCATTATGATCCCAACCGAATGAATC	18230
15066	Qy	AGACGAGACAGATTCGCCCTGACGGCGTGCCTGCGCTCACGGCGAGTTGTCGCCG	15125
18231	Db	AAACCAACAGCATATTTGTAAACAGCATACCCCTGTGTCATCACACAGCAATTAGTGAAG	18290
15126	Qy	ACGCGCGGGGCGCAACTGATGGGTGAGGATGCCCTCGGCCTGGAATGACCTGTGGAATG	15185
18291	Db	ATGACAGCAGACCGGATTTGGCAGCGTATGGATGAATTTGGCTGGAAAAACGCGCTGGCG	18350
15186	Qy	GGGAGAGTTTCTTCAACCCAGACCCACGTGTATGACGACGGCGCGCTCTGAGCATCACG	15245
18351	Db	CGGAAAGCTTCACTTCTGTTCAGCAACAACGGATGCTACCGGCACGGTATTAACGAGTACAG	18410
15246	Qy	ATGCARAAAGGTAACTGACAGCGTGGGCATATGATGCTGGCTGGCTGCTATCGGCGAGTT	15305
18411	Db	ATGCTCCGGAAACAAGCAACGATATGCGCTATGATGTGCCGGTCTGTTCAAGGCAGTT	18470
15306	Qy	GGTTGACGCTGAAGGACCGCACGGACAGGTCAATCGTGCCCTCTCTGACGTACTCGGCCG	15365
18471	Db	GTTTGGCGCTGAAGGGGAAAAAAGAAACAAGTTATCGTGAATCCCTGACCTATTTCGGCTG	18530
15366	Qy	CCGGGAAAAAGTTGCGTGAAGAACACGCAACGGCGTGGTAACCTCGTATATTATACGAGC	15425
18531	Db	CCAGCCAGACGCTACCGGAGGAACATGTGTAAACGGGATAGTACTACATATACCTATGAAC	18590
15426	Qy	CGGAAAAACAGCCCTGACGGGGAATTAACAAACGGAACGTCCTGTGGGCACTGTTCGCGAG	15485
18591	Db	CCGAGACGCAACGAGTTATTGGCATAAAAACAGAAGCTCTTCCGGTCAATGCCGCTGGG	18650
15486	Qy	CAAAATGCTGCAGGACCTTGGCGTATACGTATGACCCGGTAGGCAACGTAATCAGCGTCA	15545

Db 18651 AGAAAAATTTTACAAAACCTCGTTATGAATATGATCTCTCGGAAATGTCTGAAATCAA 18710  
QY 15546 ATACGATGCGGAAGAGACCGCTTCTGGCGTAAACAGAAAGTGGTACCGGAGATACGT 15605  
Db 18711 CTAATGATGTAATTAACCGCTTTTGGCGACACAGAAATTTGATCCGGAATACATT 18770  
QY 15606 ACATCTACGACGCTGTACAGCTGTGTAGCGCCACAGCGCGTGAGATGCCAAATGCCG 15665  
Db 18771 ACACCTATGACAGCTGTACAGCTGTGTCCGTCACCTGGCGGTGAATGCGGAATATTG 18830  
QY 15666 GCCAGAGGCGACGATTAACCTACCTACAGCCGCCCTTCTACAGACAGCTGTGCTT 15725  
Db 18831 GCCGACAAAACCACTATAC-----CCATCCCGCTCTGATTTGATGAACAAATATT 18881  
QY 15726 ACACCAATTAACGCGCACCTACCGTTATGACCGTGTGTGCAACCTGACGACAGTGGCC 15785  
Db 18882 ATAGGAATTAATCTGCGACCTTACGACTATGATGTGTGGGGAATCTGACGAGATCGCAT 18941  
QY 15786 ACATGCGCCCTGCCACGAAATAATTAATACGACAGACATCACGGTTAGTGACCGGACGA 15845  
Db 18942 A-----TTACAGATCACCGGTAATACTATACAGGAACATGACCGTTTCAGATCACAGCA 18997  
QY 15846 ATAGGCGGTACTGACGACGCTTGGCGGAAGTGGCTGATGATGATCTGTTGATG 15905  
Db 18998 ACCGGGCTGACTGGAAGAGCTGGCGCAAGATCCCACTCAGGTGGATATGTTGTTCAACC 19057  
QY 15906 CAGGAGTCAACAGAACCTCTGACCGCGGGCAAGCACGTGTGGACGCCACGCTGGAG 15965  
Db 19058 CCGCGGGCATACAGCCCGCTTGTTCGCGTCAGGATCTTTCTGGACACCCCGGTGACG 19117  
QY 15966 AACTGCAAAAGGTGACACCGGTGTGTGATGGGGGGCGGACGACAGCGAAAGTATC 16025  
Db 19118 AATTGCAACAGTGATATGTTCAATAGGGAATAACGACGCTGATCAGGATTTCTACC 19177  
QY 16026 GGTATGATCGGGAGTCAGCTATTAATCAAAACCGGACGCGGCAAACTGGCAACACG 16085  
Db 19178 GTTATGATGACAGACGTCAGCGTGTCTAATTAAGACTCATATTCAGAACACAGGTAACAGTG 19237  
QY 16086 TTCAGACACAGCGGTAGTGTACTCGCGGGCTGGAGTTACGTATCATGCGCAATGGCG 16145  
Db 19238 AGCAATACAGCAACATTAATTTGCGAGCTGGAAATGGCGACGACATATAGCGGCA 19297  
QY 16146 TGACGGAAGAAAGCCTCAGGTATTAACGGTGGCGAGGCTGGCGGGCAACAAGTGC 16205  
Db 19298 ATACATTTAAAGAGTTTTCAGGTCATCACTGTCGTTGAAGCGGTGACGACACAGTGC 19357  
QY 16206 GCGTATGCTACTGGGATCGGACGCGGATGACCTGATGAGGACTCGGTGGTTACA 16265  
Db 19358 GGGTGTCTGCAATGGGAACAGGCAACCGCGGATATCAGCAATGATCAGCTGCGCTACA 19417  
QY 16266 GTTACGATACCTGTGGGACGACGACGCTGGAGCT-GGACAGAGAGGTTACCTTATC 16324  
Db 19418 GTTATGGCAACCTGATTGGCAGTAGCGGCTGGAAATGGGACAGTACGCGGACAGATCA 19477  
QY 16325 AGTGAGGAGGAGTTCTACCGGTATGGCGGAACCGCTGTTCTGACGCGCGCAAGTGAAGTT 16384  
Db 19478 AGTCAGGAAGATTAATACCCCTATGGGGGAACCGCG- TGTGGGCAACCGAATCAGTCA 19536  
QY 16385 GAGGCTGACTACAAAATCTCCGATCTAGGCAAGAGCGGTGACGCGAGCGGGCTGGAT 16444  
Db 19537 GAAGCTTGATTAACAAGCGCGGCTTATTTCTGGCAAGAGCGGATGCAACAGGTTGTAT 19596  
QY 16445 TATTACGGTTATCGGTATTAACGACCATGGGAGGCGCTGGCTCTCCAGGACCGGCA 16504  
Db 19597 TACTACGGCTATCGTTATTAATCAATCTGGACAGGCGGATGGTTGAGTGTAGATCTCGCC 19656  
QY 16505 GGCACGCTGACGCGGCTGAACCTGTTCCGATGCTGGCGGAATTAATCCCGTCACGCTGTTT 16564  
Db 19657 GGTGAGGCCGATGCTCTCAATTTGTTCCGAATGTGCAGGAATTAACCCATCGTTTCTT 19716  
QY 16565 GACAGCAACGGGCGGATC 16582  
Db 19717 GATTCTGATGCTGTTTC 19734

## RESULT 7

AAV17876/c

AAV17876 standard; DNA; 38258 BP.

XX

AC AAV17876;

XX

DT 23-JUL-1998 (first entry)

XX

DE Cloned toxin gene sequence from *Xenorhabdus* strain NCIMB 40887.

XX

KW *Xenorhabdus*; toxin; insecticidal; protection; *Pieris brassicae*; crop;KW *Pieris rapae*; *Plutella xylostella*; *Lepidoptera*; Diptera; animal; ss.

XX

OS *Xenorhabdus* sp.

XX

FN WO9808388-A1.

XX

PD 05-MAR-1998.

XX

PF 27-AUG-1997; 97WO-GB002284.

XX

PR 29-AUG-1996; 96GB-00018083.

XX

(UKAG-) UK MIN AGRIC FISHERIES &amp; FOOD.

XX

PI Jarrett P, Ellis DJ, Morgan JAW;

XX

DR WPI; 1998-179074/16.

XX

PT Orally active insecticidal composition, used for protection of crops or

XX

PT animals - contains pesticidal material from *Xenorhabdus* species

XX

PT optionally synergised with *Bacillus thuringiensis* toxin.

XX

PS Claim 2; Fig 2; 46pp; English.

XX

CC This is a toxin gene sequence cloned from a *Xenorhabdus* strain NCIMB 40887. This has insecticidal activity and can be used in an insecticidal composition for oral delivery to an insect. The composition includes material encoded by *Xenorhabdus* strains NCIMB 40886 and 40887, particularly it contains *Xenorhabdus* cells or culture supernatant. It may also include active materials from other sources, especially *Bacillus thuringiensis* or delta-endotoxins, and is formulated with a carrier, especially an edible material for the pest. Pesticidal agents isolated from *Xenorhabdus* species, especially *X. nematophilus* have oral activity against *Pieris brassicae* or *rapae*, *Plutella xylostella* and are heat-stable at 55 deg. C. They are resistant to proteolysis by trypsin and proteinase K, and are inactivated by sodium dodecylsulphate or acetone, and by heating to 80 deg. C. The compositions are used to kill Diptera and *Lepidoptera*, particularly *P. brassicae* or *rapae*, *P. xylostella* and *Culex quinquefasciatus*, e.g. for crop or animal protection, also for vector control. The isolated pesticidal agent may be expressed in transformed plants to impart protection. *Xenorhabdus* materials show synergistic effects when formulated with *Bacillus thuringiensis* toxins

XX

SQ Sequence 38258 BP; 10486 A; 8248 C; 8871 G; 10630 T; 0 U; 23 Other;

Query Match

Best Local Similarity 6.7%; Score 1260.8; DB 2; Length 38258;

Matches 3921; Conservative 0; Mismatches 3082; Indels 541; Gaps 27;

QY 2511 TGACGGATTTATCTCGCGTTCTGTTTCCCGAGGTCAAAAATCACTGGCGACGCTGT 2570

Db 28349 TGACAAACATTTCTGTTTATGTTCTTTTCAGCGAATTTCTGTCATAGGACAAGTGGAACTCTGA 28290

QY 2571 CATGGGAGAGGTCTCTATCTGTACAGTCAGCGGACGACGACAGAAAGAAACCCGC 2630

Db 28289 CGTGGGAGAAACAGACTTTTATATCAACAGGCTCATCAGGAATCAAAACAGAAATAAC 28230

QY 2631 TCACGGAATCCCGTATTTCTGGCCCGGCGAATCCCTACTGTGGAATGCCGTTGCGCTGG 2690

Db 28229 TTGAAGAACTGGCGATTTTGTCCCGTGCTTAATCCACAACTGGGCTAATATCACTAACCTTA 28170

QY	2691	GAATACGGAGGAGCGCGAGCTATGATGACTGGTTTGGCTCCCGCGAGACC	2750	3761	CTTAAATTAATAAGTTTATCCGCTATACAAGGCGACGGCATGACCACCGCGAAATA	3820	
Db	28169	ATATTACACCGTCAACCCCTAAACAATAGTTTACAACAGTTGGTTTATGGCCGCGCCACC	28110	Db	27089	TTAAAGCTGAATAAAGCGAATTCGTTTGTATAAAGCCACAGGCATATCTCCAGAAGATATC	27030
QY	2751	GTTTCCCGCCCGCGCTCGGTGGCTCCATGTTCTCACCGCGGGGTATCTGACCGAGC	2810	QY	3821	TATCAAAATCACCAATATTTCTTAATAACGGTCTCAACATTTGACCATGCGGTCTCTGAGTAAA	3880
Db	28109	GTTTGTAAACACGGGATCAATTTGCTTCCATATTTTCCACAGCGGCTTATTTAAACAGAT	28050	Db	27029	TGGCAAGTAATAGAAAAGTATTTATGATGACTTAACCATTTGACAGCAATGTGTGGGTAA	26970
QY	2811	TGTACCGTGAGGCGAAGGACCTGSCATCCGGACACCTCGCTGTTTCGGCTTGGACATCCGGC	2870	QY	3881	ATCTTCTGGTGGCTTACTGATGGTGCATCATGAGTTGATGTGGCCGGTCACTGATA	3940
Db	28049	TATATCGGAAGCGAAGATTTTTCATCTTGACAAATTTCTCAATATCACCTGAATAAAGGAC	27990	Db	26969	CTGTTTATGTTCAATATTTATATGAGCACAATAATATTTAGCGTCAGCATGCGCTGTA	26910
QY	2871	GTCCGACCTGGCGGCGCTGGCCCTTAGCCAGAAATATATGACGAGAGCTCTCCACCC	2930	QY	3941	TTGTCAACGGAACCATCAGTGACCGAGCTTCAGCGCGAAACCGGCTGTTTCAACACG	4000
Db	27989	GCCCGACATGCTTCACTGGCACTGACACAGAATAATATGATGAAGAAATTTCCACAT	27930	Db	26909	TTGTGTCAATCAGATAACGCAATATTTCCACTAAACAAACCCAGTCAATTTTACAATG	26850
QY	2931	TGAGCCTGTCCAATGAGCTACTGTATCGCGGTATCGGGCAGCGAAGGCTTGACGAGC	2990	QY	4001	CTGTTCAACACCCCAACCGCTGAAACGGCCAGCTGTTTCTGCAGATGATACCCCTCCGAC	4060
Db	27929	TATCTTTATCTAATGAATTTACTGCTGCATAATTTAGAGCTTTAGAGAAACTGACTATA	27870	Db	26849	CTGTTCAATACACCGCTATTAAATGGCCAAAGATTTTCTGCTGATAATACCAAACTGGAT	26790
QY	2991	ACAGCGTCAAGGAGCTGCTCGCGGGTATCGCTGACCGCCCTGACCCCTATCACTGGG	3050	QY	4061	TTACGCTCTGAAGCAACCGGAGATGCTTTCGTTCTCAGGCTACTGAAACGGCATTTAAC	4120
Db	27869	ACGGTGTATGAATAATTTGTCCACTTACCGCAACCGGCATGACACCTATCATCTGC	27810	Db	26789	TTAACCCCGGTGATCAAAAAACCAATTTTATTTGGGAATAATGAAACGTTCTTCAGA	26730
QY	3051	CGTACGAGCGGCGCGCAAGCCATTTCTGGTGAGGACCGGAGCTGATGGGGTTGAGCC	3110	QY	4121	ATCAGCGCTCGGGCTTTTCCACGCTCTGGCAGTTGGCCAGCGGTGACAGCAGCGCTGGG	4180
Db	27809	CGTATGAGTCAGCCGCTCAGGCAATTTTATTTGCAAGATAAAAAACCTCACCGCATTTAGCC	27750	Db	26729	GTGAATGATATGAACTGTATACATTATGGAACCTGGCTAATGGCGGAACAAATCCAGAA	26670
QY	3111	GTAATCCGATGTGGCGAGCTTATGACCCCTCCATGCTGGCCATTTGAAGCCGATA	3170	QY	4181	TTTAGTCTCTGTGTGACAAATATCCCGCATCTTAACGAGTGAACACTCTGGCTGACATC	4240
Db	27749	GTAAATACAGAGTAGGGAAATTAATGACCCACATCGCTACTGGCTTATTAAGACTGATA	27690	Db	26669	TTTATGTGTCCATCGAGAACCTGTCTCTGCTTTATTCGTTCTGCTGTGTCGACAGCATT	26610
QY	3171	TTTCACCGGAGCTGTATCAGATACTGGCCGAGAAATATACGACAGACAGTTACGAGCAC	3230	QY	4241	CACGACCTTATCCGCTGGTGTGAGCTGCAATGTGCTCGCTCCCTCCCTTTTCAGCGGGTG	4300
Db	27689	TATCGCTGAATTTGTATCAAATCTTTGTAGAGAAATTTACCGGGAATAATCAACAGAAC	27630	Db	26609	CATCATCTGACAGTGAATTAATTCATGTTGTTGTGCGTTTCTCCCTATGTGAAACAGC	26550
QY	3231	TCGGAGTAGAATTTTGGTGATATGCCCTCCCTCCATCTGTTTATCTTATGATGACTTG	3290	QY	4301	GCGCGCGCTCGCTCTCGCATTAATCAGCTGACGCA-----GTTTCTGTACCAGACC	4351
Db	27629	TGATGAAGAAAAATTTGCGTACAGATGATGATCTGATTTTAAAGTATGCTTCTTTGG	27570	Db	26549	AAAAATTGCCCTTTTCTGTATACAGCATTAAGCAATTAATCAGCTTCTGTTCCAATGC	26490
QY	3291	CAACATTTTATGATCTTGATTAGATGAGTAACTTCGTTATTTGTCAATTAAGGCTGGACT	3350	QY	4352	ACCACTGGCTCAGGAGAGGGCTGGAGGCTGAGGTCAGCGATGTCTTCTGATGCTGACGAG	4411
Db	27569	CTCGCTACTACGATTTGCTTATGATGAACCTCAGTTTATTTGTCAATCTCTCCTCGGTA	27510	Db	26489	ACCCAGTGGCTGACACACAGAAATGGTCTGTCTGATGATGTGTTTCTGATGACCAACGAT	26430
QY	3351	TTTCAAAATCAAAACAATGAATATCTAATTAATAGTCAATTAAGTGTGCTGTAATCTGAAATG	3410	QY	4412	CAGTACGCTACCTCTGACCCCGACATTTGAGAACCTGCTCGCTTCCCTGCGCAACGGA	4471
Db	27509	AGAAAAATACAAAATCAACAGTATAAGAAATGAGCAACTGATAACATTTGGTCAATGACGGGA	27450	Db	26429	AAATACAGCAGCTGTCTTACGCCGATATGAAACCTTATCAGACACTAAGTAAATGA	26370
QY	3411	AAAGCACTGGTTTAAATACATATACATCATTTTAAAGAACCTTAGCGGAGACTCACAGC	3470	QY	4472	CTGTGCGGCGGTGAGCTGTTCCCGGAAACGCTCCCGGCGATGGCGCTCCCTTTATGCGC	4531
Db	27449	ATGATACGGCAACGGCAAGATTTGATTAAGCGAACCCCGCAAGATTTCTACGATTCACAT	27390	Db	26369	TTATCAACACTTTTCACTCGGTGATGACGAACCTGATCCGTGACAGTCCCGCGCTGATTGCT	26310
QY	3471	AGATTAACTCTGAGCTTATACCTTATGGGATGGAACATATCTTTTATATTTTCAAGCGTGG	3530	QY	4532	GCGGCATGCACTGGAGCCCAACGGATACGGGAAGGCGATGCTGACTTGGCGGACGAC	4591
Db	27389	TAACTATGAGAGCTAATTTCCAATCAAGAAATGAATGAATAATAATTTTCAAGTAA	27330	Db	26309	GCCAGCATTTCAAATGGATTTTCAAGCAAAACAGCAGAAACATTTTCTGTGGAATTAATCAG	26250
QY	3531	TGTCACGATATCAGAGGATAGTTTCAACTAGGGTCTGTTAGGTTCTTAAACAGTAGCAATC	3590	QY	4592	TTGAACGACAGCGGCTGACGCTGACGGAATTTTCTTTTGGTGAATGATGATGATGATGATG	4651
Db	27329	AAAAACAAGAACCTGACCACTTGGATTTTCTGCTCCAGAAATGGAGATGAAGAAATATAT	27270	Db	26249	ATAAACCAAGAGACTGACATTCGATGATTTTCAATGATTTTGGCGCTAACCGTATCGC	26190
QY	3591	TTTACTCTGGGATTTATCAGCTTCAAAAGGGTTCGCTATAGCATTTCTGTTTGAATAG	3650	QY	4652	AAATGACGACGCGCGGCGAGTGGAGGGTTCTGCCAAGCCCTGTGGCACTGGCACTG	4711
Db	27269	ACCAAGATAAAATTTTCGTCCTCCATTCCTAATACCCATACAGTATTTCCCATTAATATGA	27210	Db	26189	TCAGAGAAATGAACCAACAGCAACATGGTGGCTTTTGTGTCAGTACTGGGGCACTTTCTCTG	26130
QY	3651	ATGAAGGAAAGTTAAATGATGGATCAATAGAGATTGAGTAGGAAA-----GGG	3700	QY	4712	ATCATCCGACGACCGGCTCTAGCAGCGCGAGCTGACGCTGCTGGTCAGCCAGCGGGA	4771
Db	27209	CGACAGAGCAAAATCACCAACGGTATAACATCTCCGCTTATGCGAGTTTAAACCAATCGTC	27150	Db	26129	ATTGTGCGCAATTTTGGACTCAGCGAAACAGAACTGACCTGTGTGTGACAAACCGGAG	26070
QY	3701	GGGGGATATTACTCAACAGTAAACTTCACTCTGATTTGAATATGATCTCTGGATTTTCATT	3760	QY	4772	CGCTTCCGACAGGATGGCACCATCTGCCCATGACCTCCCGCGCTTCCGCACTATTAGC	4831
Db	27149	GGATGCTATCAATGCCCAATGCACACTTTTAAATGATGGAGTTCCCGGTGATATTTCCCTG	27090	Db	26069	AAATTCATGAGAAACACAGCATGCAACATGATCTCCCACTTTTGAAGCGCTGACC	26010
				QY	4832	CGTTTTCATGCGCTGTTTAAACCGCAGCGGACGCCATGCGCGGGAGGTCTCTGACCGCACATT	4891

Db	26009	CGCTTCATCTGTCATCGCTGTGTGAAGCTACGCGACAGAACTCTTAACAGCAATTTGG	25950	24940	TGTGGCTGGAAACAAAGAGCTGAAATAATGAAGTGAAGATGGCAAGATAGATATCAC	24881
Qy	4892	GAGACCGGAGAACTGTCTCAGCCCTGCTGGCCCGGSCCTGTGCACAG--AATGACAGG	4949	5970	AGAGCTACACGCTGAACTGTGCTCCGGCTTACGACGCTACATGAGGTTCCCGGTGT	6029
Db	25949	AACCTTAGGACGCTGACTGCGGAACAAATTTGGCGGTGGCGCTTAAATTTTGTGCTCAGG	25890	24880	AT---TATATATTAATACTGTACATATTCGTTATGATGGCAGCTGAGCTCACCGTTTA	24824
Qy	4950	ATGTGACCGGCGCTTTGGCGCAGGTCAGGTCAGGGGGCCGCTGAACAGGACAAACAGCGTGTTC	5009	6030	CGTTCGACATTAACCGCAACATCGCATTTTCCGG-----AAACGAGGCGCATGCAATG	6082
Db	25889	TTGTGACACAAGCATTTGCAACAGACCGGTTTG-----GGAGTGAATACCTTTAC	25841	24823	ATTTTAATGTGACTGATAAAATAGAAAACTGATCAATAAAAAAGCAGCATTTGGTATGT	24764
Qy	5010	CTCTCTGGGAAGAGGTGGACAGGCTGACAGTGGCTGGCATGAGTGAGACCCCTGTGCC	5069	6083	ACCTGTAATCCCTGCTGAGCAGGCTCTATTGGCGCTTTTACTCGCTCACCACAAGCC-	6141
Db	25840	CAACTGAGAACTTATAGATGTCACTCTGCAATGGCTGGATGTGCTGTCTACATTTGGTA	25781	24763	ATTGTTCTTCTGATTAATGAAAAAGACGTCATTAATGTTTATTTCCATGAGAAAAAGACA	24704
Qy	5070	TTACGCCATCCGCTCTGGCTAGCTGATTTGCCCTGAAGTACATCAATGTGTCGATGACA	5129	6142	-----GGACTTTTGATAACGCTCAGCTGATTTCTGTGGATAATGATATGACGC	6188
Db	25780	TTACCCCGGATGTGTGTCGACTCATATAAAATTAATAATATGTCGGTGAACCGGAACCC	25721	24703	ATTATTTCTTTTAATAGTCTTCTGCAAGAGAAGGATGACCATTAACCTTGATATGACAT	24644
Qy	5130	GTGACCCGTTGTACAGCCAGTCAGGTGGTATCCCGTCTGTGCGAGCCGGCTGAAAA	5189	6189	TAAATGTCATCTCAGATA-----TAGGGATTTTAAAGAGCGTCAGTCACGAAATTTA	6239
Db	25720	CGATGCCAACATTTGATTTGGCAAGCCGACGACTTTTGTGCGAGCGGACTGACAC	25661	24643	TATCCATTCTCAGAAAAATGATTTAGACGCCAATCTGTTAAGACACATATATCAGAACTTG	24584
Qy	5190	GCAGCCAGAGCTCGGCGCTGCACGATTAATCTGAGAGAGGGGACAGCAGCGCCCTTTGTG	5249	6240	ATACGAGCACTG---AGAAATTTTAATAATGTTTTTTCAGACCCCTCCGCTAAATATT	6296
Db	25660	GTCAACAATCCGACAGCTTCAGGCAATGGCTGGATGAAGCCAGCAGCACAGCGGCCAGTG	25601	24583	ATACCAGGACAGAATACAAAGTCAACAATTTGCTACAGATTAATTTGGCCGAAATATA	24524
Qy	5250	CGTATTATCTCGTGAATCTGCGCAGCAACATGTAATCCGGCGCGATGACTCTTCGGGT	5309	6297	TTGTCACTGCAACGAGTGTAAATTGA--TGATGTTATCCACAGCGATTTCTCACTCCTTA	6353
Db	25600	CTTACTACATCAAAAATGGTGCACCTCAACAGATTAAGACCCGGATGAGTTGTACAGCT	25541	24523	AGGATCTATACCAAAAAATAAATTAGCCAGTTTTTACCAGAAATATTTTTGATCTCT	24464
Qy	5310	ATCTGCTGCTGGATAATCAGGTGTGACCCAAAGTGAACACCCCGCATTTGCCGAGGCCA	5369	6354	ATTCTAAAACTCAAGTACTGTTTTTACTAATAAGAAATCTCTCTCTTTTGACGCCAGAGC	6413
Db	25540	ATCTGCTGATTGATAACCAAGTTTCTGCCCAAGTGGAACCAACCCGTGTGCGAGAGCCA	25481	24463	CGTATATATCACAGGAAATGGTCATTAATAATTAACTTCAATCTTCAATGGAATTA	24404
Qy	5370	TCGCCGCGCATACGGCTGTATATCAACCGGCGCTTTAACGGAAATAGAACTCAGCGCCATG	5429	6414	TTCATATTAACAGCAATGTTTCTGTTTGTGTAGTA-----CTG	6452
Db	25480	TTGCCAGCATTCAGTTATATGTCAACCGGCGTGTGAATATGTTGAAGGAAAAAGTATCAA	25421	24403	ATTTTTCAAAAGGCAATATATATAATGATGAGGTTAAATACCTGTTATCGATGTTAGAAG	24344
Qy	5430	CAGAGGTGAGGGGCGTCACTGTTTCTCACTGAGTGGATAGTTCAACAAAGTTACAGCA	5489	6453	CTGGCATCCCATCAATCTACCATAGAAAAATTCGTTCAGGCGAGGATAGAAATTTGAGG	6512
Db	25420	AGCCAGTGAACACCCGTCAGTTCTTCTGCGACTGGGAAACCTACAAATCGACGATATAGCA	25361	24343	ATGAAACGGTTATTTTATTTGATTATGATAGATCATGATGAATGCTTGGAAAGAGAGAG	24284
Qy	5490	CCTGGGCGGCGCTCTCAGAGCTGTTTACTATCCGGAATACTACCTCGACCCGACGCTCC	5549	6513	AAATTAAT-----TTTATGAGCCGAGCCGCGCGGATTTTGACGG	6555
Db	25360	CCTGGGCGGCGTATCTGACTGCGCTTATTCGGBAAACTATATCGACCCACAGATTC	25301	24283	AGGTTTTTTCATATGAACTTTTGGATTTTATTTATTTTCCATCGATCTTAAAAATGCCGAAT	24224
Qy	5550	GTATCGGCGCAGACCGGATGATGACACCTCTGCTGAGTCTGTGACGAGCAGATATCA	5609	6556	ATTTGTGGGAGTGATGTTTCTTAATTCAAAAGTATACAGGTC--GGAAAAGAGCAGTTG	6614
Db	25300	GTATTGCTCAGACAGGTATGATGAACAAACCTGTTACAGCAACTTCCCAAAGTCAGTTAA	25241	24223	ATTTTAGAGTGTTAATGTCATCTAAGAACCAAGGAAAAAATTCCTAGAAAAATCAGAAATG	24164
Qy	5610	ACCGCATACCGTGGAGGATGCTTTTAAACCTATCTGACCAAGTTTGACGATTTGCCA	5669	6615	GTGTCACTGTAAAACTCTTATCCGTCACCTGGCGTTAGTGGTT-----CTGTTGAGTTATT	6669
Db	25240	ATATCGATACCGTTGAAGATAGTTTTTAAATAATATCTGACCGCATTTGAAGATGTGCTA	25181	24163	GAGTTGTTAATAATTAATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATG	24104
Qy	5670	ATCTGAACACTGTGACGGATATCACGATAACCGCAGCATGACGCGGGGACTACATGTT	5729	6670	TATTTGATTCATCAAAATAAATACTTACGCGAAATTTTGTGAGATA---AAATGATAACCGC	6726
Db	25180	ACTTGACGTTGATGCGGATATCATGACAGTATTAATGTCAATGAGGGGCTCACATTAT	25121	24103	TAGTATTTAGATTGGAAGATAACACAGGAGTATGGCATACTATAATGTAATCATTTACTA	24044
Qy	5730	ATGTGGTCCGAGATCACAGATCAGACTAACTGGTACTGCGCAGCGCCCAACACAGCA	5789	6727	TTTAAATAGGGCAGTACATCAAAAGTTAATTAAGTGTGCTCTATTGGCTCTCAAGATTT	6786
Db	25120	TAAATGGTTATAGCAGACAGAACCCAGATAATATTATTGGCGCAATGTGATCACCACAA	25061	24043	ATGATGTTTCAATCAATTAATAACATGGGAAATATTGGGCACCTGTTCTTCGCGAGGATC	23984
Qy	5790	AAATCCNAGACTCAATGATCCCGCGGATGCTTAAACCTATCTGACCAAGTTTGACGATTTGCCA	5849	6787	TTGAGGTGAAGTCCGCTCATGCGGCAC--TTTCAGATATATGAATTAATTCGATGATATC	6844
Db	25060	AGTGCCAGCAGCTCAATTTGCTGCCAATGCCCTGGAGAGATGGAATAATTTGAATATC	25001	23983	CATGGGTGATTTATGTTTCAACAGCCACAGATAATAAATACTGTTCTATCTATGATCGA	23924
Qy	5850	GAATGAATCCGCTGATGATGCTGTGCTCGGTGTTTTTCAACAGTTCGCTTTATGTCG	5909	6845	ATACTGACATCCGCGCTAAATGGGACTGAAATTAATTCCTGGCTTCCGCTGAATGGTAT	6904
Db	25000	CCATCAATGTATGGCAGGAAAAATATCAGACTGTTATTACAGTCTGCTTTGTTATTTAC	24941	23923	ACAGATCCAAGATAAAAAACATTAGTTTTTTTATTAATAAATGGCTCTGATAT--TCTAGTGG	23865
Qy	5910	TCTGGTTCGAGAGAAATCAGTCTGCTGATACGGAGGCGAGAGACAGCAACCAACGACG	5969	6905	AATGATAAGCTGAGTCTGCATCCGGGAATAATCTTTTCAACACCAATTCGCTGAGTTTT	6964
				23864	AGTTAAATGCTGAAGACCATGTGGCATCTAAACCTTTCACACGAATCTGACCCCTATGTTAT	23805

QY 6965 ACCGTTAATACCAGTGATA--TTGTTGAAGATGAGTTTGACGTGACGTTTACGTTTACCG 7022  
DB |||||  
DB 23804 ATGATTTTAAATCAAGTAAAGTTGATATTGAAGGCTATGATATCTCTCTGGTGAGCGAGT 23745  
QY 7023 CTGTGATCAGAAATACGTCGTGTCGCCGCCGAGCGCCATATTAACCGTCATT---- 7078  
DB |||||  
DB 23744 TTATTATTAAAGCAACCCGACGGCGGTTATAACGATATTGTTTGAATCGCAATTCATA 23685  
QY 7079 -----CGAAACATTAATATGACACTTCGTTTATGCAATTAAGTAAATAACGCTGGCG 7133  
DB |||||  
DB 23684 TAAACATAAATCCAAAGATACAGTAACGTTATATCATCTGATTAATAAGTCCATCAGCA 23625  
QY 7134 CGCAGTATATTCGTTTCACTCGGGTAACGATGTGGCGCTTATTCGCTCAACACCTCT 7193  
DB |||||  
DB 23624 CACAATATATGAGATTGGCCCTTACA-----GAACCGGTTAAATACTTTAT 23577  
QY 7194 TTGCCCGCCNACTGGTCGACCGGGCGAATACCGGATTCACACCATCTTCTTCCATGGAGA 7253  
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DB 23576 TTTCCAGAAATTAGCTGAAGAGCCAAATATTGGTATTGATTAATGTTTAAAGTATGGAAA 23517  
QY 7254 CCCAGAGGCTTACCAGAACCGCCCTCGAAGAGGGAGTGATGTGTTTATGACTTCTC-- 7311  
DB |||||  
DB 23516 CGCAAAATTTACCAGAGCCGCAATTAGGTGAAGGTTTATGACATTTAAAGTTGCCCC 23457  
QY 7312 ----- 7311  
DB 23456 CCTACAATAAGAGAGCATGTTGATCAAGTTGTTTAAAGTCCATATTTGGGAATATTG 23397  
QY 7312 ----- 7311  
DB 23396 ATGGCAATCTGCCAGACAACCTTATTACGAAGGAATGTTATCTGATATTGAACACACAG 23337  
QY 7312 ----- 7311  
DB 23336 TAACGCTCTTTGTTCCCTATGCTAAAGGATATTACATACGTGAAGGTGTCAGATTAGGGG 23277  
QY 7312 ----- 7311  
DB 23276 TTGGGTACAAAAAATTAATCTATGACAAATCTCGGAATCTGCTTTCTTTTATTGATG 23217  
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DB 23216 AGAGGAAATCAATTTATATTACTAAATGATCCCGATCATGATTCGGGATGACACAAC 23157  
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DB 23156 AGGGATAGTAAAAAATATCAAAAAATATAAAAGGGGTATTTCAAGTCGTGTCTATGAAAA 23097  
QY 7312 -----CGAGCCCAATGCCCTCTATTTCTGGGAGCTGTCT 7346  
DB 23096 TAACACTGAACCCATGATTTCAACCGGCCCAATGCAATCTATTTCTGGGATTTGTTCT 23037  
QY 7347 ATTAC-ACGCCGATGATGTTTCCAGCGTTGTTGAGGAACAGACACTTCCCGGAAGCC 7405  
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QY 7406 ACCCGCTGGCTGCAGTATGTCTGGAACCCCGCGGACGCTGTGTAACGGGTGCTGCAG 7465  
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QY 7466 AATTACACCTGGAAATGTCGTCGCTGGAGAGGACACCGGCTGGAACGACTCGCGGCTG 7525  
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DB 22918 GATTATTACTGGAACGTCGCCCATTTGGAGGAGATACGTCCTGGAATGCCAATCCGCTG 22859  
QY 7526 GACTCCATTTGACCCGATGCAATAGCCAGTACGACCCCATGCAATTAAGAGTGCACACC 7585  
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QY 7586 TTTATGTCGATCTGACCTGCTCATTTGCCGCGGTGATCGCGCTACCGGCTGCTCGAG 7645  
DB |||||  
DB 22798 TTTATGAAATGCTGGATTGTTGATTACCCCGGAGATAGCGCTATCCCGAGCTTGAA 22739

QY 7646 CGGACACCCCTTAACGAGGCCCGGATGTGTACGTCCAGGCCCTGAACCTTCTTGGCGAC 7705  
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QY 7706 GAGCCCTATATTTCTTGTGACCGCACTGTGTGCGGTGTACCTCTGGGTGACGCAAGCCAGC 7765  
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QY 7766 GAGGTGACGCGACGCGATTTACAGAGGCCCTGTGCGCGTGTGCGCGGTGTGGTCCCGCT 7825  
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QY 7885 GCTCAAAAGCTACTTGGCAAACTTTGGCACACGCGCTCCATAACCTTGGCCCAACCTCTC 7944  
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DB |||||  
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QY 8005 GCAGAGTCCGTCGTCAACAGCGCGCAGGTGTGACGACTGCGCGCGCGGTGATGCC 8064  
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QY 8065 GCTTTACAGTTTCCCGTCATGCTGGAGAACGCCCGGGGATGTTGAGCCTGTGTACCGG 8124  
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DB 22318 GATGTACGTTTTCGCGTATTCTGGAATAATGCCAAGTGGGGGTAAAGCCAGTTGATACA 22259  
QY 8125 GTTCGGCAACACACTGCTCGGTATTACCGAGCTCAGGATCGGAGGCGCTGGCCAACT 8184  
DB |||||  
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DB |||||  
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QY 8365 GGACTTGTAACCTCAGTTGCTCGTGTGCGCATCAACCGCGCGCTCTTTTGGCGCA 8424  
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DB 21778 GGCATAATGCGAAGCTGAGATAAACAATTTGATGCTCAATTAGCCAGCTGGCTGT 21719  
QY 8665 GCGCGGGAAGGGCTGAGCTGCAGAAAACTTACTCTTGAGACCCAGCAGACCCAGGCA 8724  
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QY 9958 TCACTACTGGGATAAACCAGCGGAAGCTTCAACGTTTCAGGTTTACCGTTCACTGACG 10017  
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 QY 10555 TACCTAGGTGTTCTGCGGGGAGTTGCGGAGCGAATGATGCGCGACGATGATTTCTCGC 10614  
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 Db 1375 CTGATGATTTAAACGCTGACGGGCACTGGAGTGGGTGATTTACCGGGCGGGGTAAAG 1434  
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Db 1435 GGGTATCAGCAACACCCGATGGCAGTTGGACGCGTTTACGCCATATACATGCCCTG 1494  
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 Db 1735 GTTAGTGCAACTCAAGTCACTGCTGGCGCAATCTGGGGCATGGCGTTTGGTCAAGCCA 1794  
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 Db 1915 ATTTTCAGCAATGAAGTGGCAACCGTTTTTGAAAAACCAATTCACTCTCTTTCTGCTGAC 1974  
 QY 11575 GGTGTGCGCTATGATCGCACTGCGAGTCTGCAAGTGGCGGATATCCAGGGGCTGGGGGTG 11634  
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 QY 11695 GCAGCAAAACCTGTTGTTGAATGCGATGAACAAATATGCGGCGCCGCGATGACATG 11754  
 Db 2095 AACGGAACCGTGGTTACTCAGTGAACGAACAAATATGGGGCCAAATCACACTTG 2154  
 QY 11755 CACTATCGCAGTTTCGGTTCAGTTCTGGCTGATGAGAAAGCCGAGCACTGGCGGAGGC 11814  
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 QY 11815 AGTTCCGCTGCTGCTACTGTCATTTTACATTTGATGATACCTGTGGGTTCCGTTGGTGCAG 11874  
 Db 2215 CAAACACCGGTCTGTACTGCTGCTTCCGCTTCCATACCTTTTGGCAACAGAAAACCGAG 2274  
 QY 11875 GATGAGATCACCGGTAAACCGTCTGTCAGCAGCTGCTTTATTCGCCACGCGCTCTGGGAC 11934  
 Db 2275 GATGAATACGCGCAATTAAGTTAGTACCATGTTAGTACCTGTTTACGTTTGTCTACGCGCTTGGAT 2334  
 QY 11935 GGGCAGGAACCGAGTTTCGGGGGTTTTGGTTTTTGTGAGATCAGGATACCGATACCTTTG 11994  
 Db 2335 GGACGTGAACGGGAATTTCTGGCTTGTGTTATGTTGAGCAGACAGACGATCACTCACTC 2394  
 QY 11995 GCAACGCGAGGTACGCGGACGGAAGTGTGCTTCTGTGAGCGGGAAGTGTGATGCG 12054  
 Db 2395 GC---TCAAGGCAATTCGCGCGGAACGTACACCCCGGCACTCACCAAAAGCTGGTATGCC 2451  
 QY 12055 ACCGCGGTACCGGAGTACAGAGCGTCTGCGGAGAGAGCTATTGGCAAAACGATGCCGC 12114  
 Db 2452 ACCGATTTACCTGCGGTAGATTAATGCGTTATCCGCGGGTATTTGGCTGGCGATAGCAA 2511  
 QY 12115 GCTTTTGGCGAATTCGCGACCGGTTTCACTGTGCGTTTCAGGAGAGGATGAGCAGCATAT 12174

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Db 2512 CTTTCCGCGGTTTACGCCACGTTTACTCTCTGGAAGAGGCAAGATGTTCCACTG 2571
Qy 12175 ACTCG---GACGACAGCAACATCTCTGTTGACGGAGCCCTGAAAGGCATCCTGCTG 12231
Db 2572 ACACCGGAAGATGACCATATCTATCTGTTTAAACCGGGCGCTAAAGGTCAGCCTG 2631
Qy 12232 CGAGTGAGTTATACGTTGCCGATGCGACGACGAGCCGAGATATCCCTTACAGCGTCACT 12291
Db 2632 CGTAGTGAATCTCTACGGGCTGATGCGACGCGCACAGCAACAGATCCCTATACAGTGACT 2691
Qy 12292 GAGTCTCGCCGACAGGTACGGCTAGTTGCAAGCAATG---GAGTACTACCGGTGGTGG 12348
Db 2692 GAATCCCGTCCACAGGTGCGCAATTAAGATGCGCGCACCGGTTTCCCGGTGCTCTGG 2751
Qy 12349 CCGATGCGCGGGAAGCCGTACGTCACTGTTTATGAAGCGTACCAATGATCCCTCAATGC 12408
Db 2752 GCCTCAGTCTGTGGAAGCGGTAGTTATCACTACGAAGCTATTATCAGTGATCCCGAGTGC 2811
Qy 12409 CAACAGAGGGGTACTCTCAGTGATGAATACGTTTCCACTGCGTCAAGTCAGTGTC 12468
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Qy 12469 AATTATCCAGAGCCCTCCGTGCGGCAATCATATCCGGCTCTTACCGGCAAG 12528
Db 2872 CAATATCCCGCCCAACAAACCAACCAATCCGTATCCCGATACCTACCGGATACG 2931
Qy 12529 CTGTTCCCAACAGTTATGACGACGACGACAGATATTAGCCCTGGGGTTGCAACAGAGC 12588
Db 2932 CTGTTGCGACAGTTATGACGATCAACACAGCTATTGGATTAACTGCCGACATCC 2991
Qy 12589 AGTGCAATACCTTGTTCATCTGTCTGAGGGCAATGGTTTGGGGTTGGCGAGGCG 12648
Db 2992 AGTTGGACCATCTTAIT-----GGTAATGAGCTAAGAGTGTGGGATTACCGATGGC 3045
Qy 12649 TCGCGGACAGTATTAACGACTCTCGGCAACAGCTGCGGAGAGGGGTCTGACGCTG 12708
Db 3046 ACAGCAGTATGCTTTTACTTACGATGCGCAACAGGATCTGTCGATGGCTTAAATCTG 3105
Qy 12709 GAACACCTGTTGGCGCCGAAAGCCTGCTCTCGATAGTCAAGTTCGGTACGCTGGCGGT 12768
Db 3106 GAAACCTGTGTCTGAAATAGCTGATTCGCGATGATAAACCCTCGGAATACCTCAAT 3165
Qy 12769 CAGCAGCAAGTCTGATCTGATCTCAAGAGTTCACACGCTGCTGCTCGGCCACTC 12828
Db 3166 CAGCAACGAAGCTTCTATACCGACGGGAAACCAACACCGCTGAAACACACGACAGCA 3225
Qy 12829 CCCCCAAGTAGCTTTTATCGAAACGCGCTGCTGATGAGGATGCTGATGCTACTG 12888
Db 3226 CAAGCGTTAATCGGCTTTTACCGAAACGCGGTATTAACGGAATCTCTGTTATCCGCGTT 3285
Qy 12889 GCTGCCTACATTTGGATGA-----ACATCTCGAGCAAGCCGGTTACCGGCAA 12936
Db 3286 GATGGCGGTATACCGCAGAGATTAACCGGATATCTGACACAGGCGCGATACCAACAA 3345
Qy 12937 TCGGGATACCTTTTCCCTCGAGGACGGAAGACAGCAATTTGTGACCCACAGTGTGAC 12996
Db 3346 GAGCCTTATCTGTTTCCACGACCGCGGAAACAA-----AGTTTGGGTAGCGCGTCAA 3399
Qy 12997 GGATATGTTACCTATGCGCGGACAGACATTTCTGGTACCGTATCCCTTTCGGACAGT 13056
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Qy 13057 ATGTTGACCGGCCAGTTACCGTGACGCGTGACGCTGACGCTACGCTCATCAGCAGTGG 13116
Db 3460 CTGTTAACCGGGAATGAGCTTAAATGGGATCTCACTATTGTGTCATCACCACCAACC 3519
Qy 13117 CAGGATGCCAGGAGTTGTACCAACAGCCGACTATGACTGGCGCTTCTTGAAGCCCGCTC 13176
Db 3520 CAAGATGCTGCCGCGCTCACCGTCTCAGCCAAATATGACTGGCGTCTTCTCACACCAACG 3579
Qy 13177 CCGGTGACGACCCCAATGATATCTGCACTGCGTCACTCTGAGTCTCTGGGCGCGGTG 13236
Db 3580 CAACTGACTGACATCAACGATAATGTGCTATCTCATCACCTTGGATGCTCTGGGACGCGCT 3639

Qy 13237 ACCACCTCGGATTTCTGGGCAACGAGATGGTATTGCCACCGGTTTACAGT----- 13287
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Qy 13288 GATGCCACGTTGTCGGTTCCGAGCGGCGACAGCCGCTCTGGCGTTGACGCGCCCTTA 13347
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Qy 13348 CCAAGTAGCAGAGTCTGGTGTATGTGTCACGACAGTTGG----- 13386
Db 3760 CCTGTGCAAGTGTCTGGTCTATGCAACCGGACAGTTGGATGCCACTATTTCAGTCAAGAA 3819
Qy 13387 ----- 13386
Db 3820 ACCTTCAACACATTAACGACGAGAGAGGACGCTGCGTATTTCAGTATTATCAGC 3879
Qy 13387 -----GGAGATGACGACAAATGAGAAAA----- 13408
Db 3880 GAAGATTGGCGTATTGCGCACTGACTCGCGCGCTTGGCTACAAAGTCAAAAGATCAGT 3939
Qy 13409 -----TGCCCCGACGCTGGTCTGCTG 13431
Db 3940 ACACCATTAAGTTAACTGTTAACCAACAGCAATGGTTTACTCCCCATAACCTTACCGTG 3999
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Db 4000 ACCACAGACGTTATGACCGGACTCTGACGACGAATTCGCCAACAGTTCGCAATTTAGT 4059
Qy 13492 GACGGTTTGGCGTGAATTCGCAATCGGCAACCGGACGCGGAGGCAACGCTGGCAA 13551
Db 4060 GATGGTTTGGCGTCTGCTTACAAGCGTCTGTACGACATGAGGACGAGCGCTGGCAA 4119
Qy 13552 CGAGGACGACGCGCAACCTGGTGACGCGCAGTACGCGATTGCGGTCATCTGTAGCAAGC 13611
Db 4120 CGTAACCAAGACGGTTCTCTGGTGACAAAAAGTGA-----GAATACC 4161
Qy 13612 AATTTCCGCTGGCGGTCACCGGAGGCGGAGTATGACAAATAAGGTCTGCTGTTTCGG 13671
Db 4162 AAAAAAGTTGGCGGTCACGCGACGCGACCGAATATGATTAAGGGCAACGATACGC 4221
Qy 13672 GTTTATCAGCGTATTTCTGACAGTTGGCAATATGTCACTGATGACAGTGGCCGCGCAG 13731
Db 4222 ACTTATCAGCGTATTTCTCAACGACTGGCGATATGTCACTGATGACGCGCAGAAAA 4281
Qy 13732 GACCTGATGCGCAGACGACATTTTACGATCCGACGCGACGGAATGGCAGGTTATTACG 13791
Db 4282 GAAGCCTATGCGGATACTCATATTTATGATCCAAATTTGGCGGAGAAATCCGGTTATTACT 4341
Qy 13792 GCAAAAGGTGAACGCGGACAGGTTGTTATACCCCGTGGTTTGTGTCAGTGAAGACGAG 13851
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Qy 13852 AATGATACCG 13861
Db 4402 AATGATACCG 4411

RESULT 9
ADN61378
ID ID
ADN61378 standard; DNA; 4434 BP.
XX
AC ADN61378;
XX
XX
DT 01-JUL-2004 (first entry)
XX
DE Photorhabdus strain W14 tcdB1 toxin complex DNA.
XX
XX Cry; toxic; lepidopteran pest; toxin complex; insecticide; strain W14;
XX db; tcdB1.
XX
XX Photorhabdus sp.
XX
```



Db 1498 CCGATAGATATTCCTACCTCCGCTCAACTGCGGATTAATGGGAGCGGCGCTGCC 1557  
Qy 11155 GACATGCTGCTTATCGGCGCGCAGTGTTCGCTCTATTCGCGCAAAACGATGTTGG 11214  
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Qy 11275 CCAGTACCTCGTGGGCTTCAGTGATATGGTGGAGTGACAGCAGCATTTGACGGAG 11334  
Db 1678 GCCCGTAAGTTAGTGGCATTTAGTGAAGTACTGGGTTTCAGGCCAAGCACATCTGGTTGAA 1737  
Qy 11335 GTGCGTCTAATGAGTACGTTACTGGCCAAACCTGGGGCAGGTCGTTTCGGTCAAGCG 11394  
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Qy 11395 GTGAATATCCCGTTTTAGCCAGTCACTAGTCACTAGTTTAAACCTGACCAAGATATTGCTG 11454  
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Qy 11575 GGTGTGCGCTPATGATCGCACCTCGAGTCTGCAAGTGGCGGATATCCAGGGGCTGGGGTG 11634  
Db 1978 GGCCTGCTTTGATGATACCTGCGCAGTTGCAAGTAGCCGATGTACAAAGGTTAGGCGTT 2037  
Qy 11635 CCTAGCCTGTACTGACGGTCCCGCATGTGCGGCTCATCTGCGGTGTCGCAATTTATCG 11694  
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Qy 11695 GCAGACAAACCTGTGTTGTAATGGCATGAACAAATAATGGGGCCCGGATGCACTG 11754  
Db 2098 AACGCGAACCCTGTTACTAGTGAACGAAACAAATAATGGGGCCAAATCACCTTG 2157  
Qy 11755 CACTATCGCAGTTGGTGAGTTCTGGCTGGATGAGAAACCGAGGCACTGGCGGCGAGC 11814  
Db 2158 CATTTACCGTAGCTGTGCCAGTTCTGGCTGGATGAAAGCTGCGGCATTTGGCTACCGGA 2217  
Qy 11815 AGTTCCCTGCTGCTACCTGCCATTTACATTTGATACCTGTGGGCTTCGGTGGTGACG 11874  
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Qy 12409 CAACAGCAGCGGTACTCTCTCAGTGAATACGTTTCCCACTGCGTCAAGTCAGTGTC 12468  
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Qy 12937 TC CGGATACCTTTTCCCTCGAGCAGGGAAGCAGACAGGCAATTTGGACCCAGTGTGAC 12996  
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Qy 12997 GGATATGTTTACCTATCGCGCGCAGACATTTCTGGCTACCGCTATCTTTCCGGACAGT 13056  
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Qy 13057 ATGTTGACCGGCCAGTTTACCGTGACCGGTGACCGCTACGACTGCGTCTATCAGCAGTGG 13116  
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QY 12349 CCGATGGGCGGAAAGCCGTACGTCACTGATTATGAACGGTACCACAAATGATCCTCAATGC 12408  
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QY 12589 AGTGCAATCACTGTTTCACTGTCTGAGGGGCATTTGTTTGGGTTGGCGAGGCG 12648  
Db 2992 AGTTGGCACCATCT-----AACCGGTAATGAATCAGAGTGTGGGATTACCGGATGCT 3045  
QY 12649 TCGCGGAGCATGTTACGTTACTCTCGGCAACGTCGCCGAAGGGGTCTGACGCTG 12708  
Db 3046 ACACGAGTATGCCCTTCACTACGATGCCAAACAGGTGCCTTGTATGTTTAAATCTG 3105  
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QY 13409 ----- 13408  
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QY 13492 GACGGTTTGGCGGTGAGTTGCAATCGGCAACCCGCGAGCGGCGAGGCGAAACGCTGGCAA 13551  
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QY 13732 GACCTGTATCCGACACGCACTTTTACGATCCGACGCGCAATGGCAGGTATTACG 13791  
Db 4282 GGGGCTATGCCGATACGCAATTTATGATCCGATTTGGCGGGAATCCGAGTTATTACC 4341  
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Db 4342 GCAAAAGGCTGGCTGCGACAGAGCCAATATTTCCCGTGGTTTACTGTGAGTGAGGATGAA 4401  
QY 13852 AATGATACCG 13861  
Db 4402 AATGATACCG 4411

## RESULT 11

ACF69428

ID ACF69428 standard; DNA; 4428 BP.

XX ACF69428;

AC ACF69428;

DT 20-NOV-2003 (first entry)

XX Photorhabdus luminescens nucleotide sequence #7895.

DE Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;

KW detection; food; gene expression; plant; animal; microorganism; toxin;

KW antibiotic; biopesticide; virulence factor; disease model; plague;

KW whooping cough; gene; ds.

XX Photorhabdus luminescens.

XX WO200294867-A2.

XX PD 28-NOV-2002.  
XX PF 07-FEB-2002; 2002WO-IB003040.  
XX PR 07-FEB-2001; 2001FR-00001659.  
XX PA (INSP ) INST PASTEUR.  
XX PA (CNRS ) CNRS CENT NAT RECH SCI.  
XX PI Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;  
XX PI Buchrieser C;  
XX DR WPI; 2003-148459/14.  
XX PT Genomic sequence of Photorhabdus luminescens and encoded polypeptides,  
XX PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.  
XX PS Claim 2; SEQ ID NO 7895; 1205pp; French.  
XX CC The invention relates to the isolation of genes and their encoded  
CC proteins from Photorhabdus luminescens. The isolated sequences are  
CC sources of probes and primers for detecting the genome of P. luminescens  
CC and related species; to study polymorphisms; for gene analysis and for  
CC detection/amplification of the genes. Antibodies (Ab) raised against the  
CC polypeptides encoded by the genes are used for detection/identification  
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that  
CC carry a gene-containing vector are used to select compounds that  
CC modulate, regulate, induce or inhibit expression of the genes in plants,  
CC animals or microorganisms other than P. luminescens and are able to alter  
CC response or sensitivity to toxins and antibiotics produced by P.  
CC luminescens. Cells transformed to express the genes are useful for  
CC recombinant production of the proteins, particularly toxins and  
CC antibacterials useful as insecticides, bactericides and fungicides. The  
CC genes, proteins, vectors containing the genes and Ab are also useful  
CC therapeutically (to treat microbial infection by bacteria or fungi that  
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as  
CC biopesticides. Other uses of the genes and the proteins are as virulence  
CC factors and for identifying targets of human diseases for which P.  
CC luminescens is a model (particularly plague and whooping cough). This  
CC sequence represents one of the isolated P. luminescens genes  
XX SQ Sequence 4428 BP; 1220 A; 1142 C; 1043 G; 1023 T; 0 U; 0 Other;  
Query Match 5.6%; Score 1067.6; DB 10; Length 4428;  
Best Local Similarity 57.0%; Pred. No. 4e-243;  
Matches 2187; Conservative 0; Mismatches 1584; Indels 69; Gaps 10;  
QY 9598 ATGCAAAATCATCAAGACATGGCCATTAATGATTTACAGAACTATCATTTGCCAAAGGAGGCGCT 9657  
DB 1 ATGCAAAATTCACAAAGATTTAGTATTACAGAACTATCATTTGCCAAAGGAGGAGGCGCT 60  
QY 9658 GTACCGGGCTCAAGGTGATATCGCGCGGAGGCGCGGATGGTGGGAGCCCTGAGT 9717  
DB 61 ATACCGGAATGGGGGAAGCGTTAAACCCCGCGGACCGGATGGTATGGCGCGCTATCT 120  
QY 9718 ATTCCCTTGGCGGTAGCCCGGTTACGCGGTTACGCGGCTTACGCGGCTTAAATATCAC 9777  
DB 121 CTACCATTAATCTTCTGCGGCGGCGGTTATGCGCGGCTTACGCGGCTTAAACTAAC 180  
QY 9778 AGCCGCTCGGGGAACCGGCCCTTTTGGCAATGGCTGGGGTATCGCGGCTGCTGCTCCAG 9837  
DB 181 AGCGGTGCGGTTAACTCCATTTGTTGCTGGGTTGGGATTCGAACTGATGACCATCCGC 240  
QY 9838 GTCTGTACGGCAACGAGACCTTACCTACGATGATCTGATGAAATTCACCGTCCGGAC 9897  
DB 241 CGCCGCAACCCATTTTGGTGTCCGCCATTAACGAAACCGATATCTTCTTGGCGCGGAA 300  
QY 9898 GGTGAGGTGCTGGTCCGGCACTCACGGCTGTGGCACCCCAAGACAGCGGAGCCACC 9957  
DB 301 GCGGAAGTACTGGT-----AGTCGCGGATCAACCGGCTGATGATCG 342  
QY 9958 TCACACTCTGGGATAAACCAGCGGGAAGCTTCAAGTTTACGGTTTACCGTTTCACTGAC 10017

DB 343 ACATTACAGGGTATCAACCTAGGCGCTACCTTACCGTTACCGGATACCGTCCCGCTCG 402  
QY 10018 GAGGGTAGTCTCAGCGCGCTTGGCGCTTGGCTCCCGCGGACGAGACAGAAACGGAATTT 10077  
DB 403 GAAAGTCATTTTCAGCGGATTTGGAATATTTGGCAGCCCAAGACAAACAGGCAAAACAGATTTT 462  
QY 10078 TGGGTGTTATATACCCCTGACGACAGGTGGCTCTCTGGGCGGAAATGCGAGGCTCGC 10137  
DB 463 TGGCTGATATATAGCCAGATGGGAGGTACATTTATTGGGTAATACCCGCAAGACCG 522  
QY 10138 ATCAGCAACCCACAGCCCAACACAGACGCGGTTTGGCTGATGGAGTCTCTCGGTATCA 10197  
DB 523 ATCAGCAACCCATCCCAACAGCACAAACAGCAAACTGGTTGCTGGAAGCTTCTGTATCA 582  
QY 10198 CTTACCGGCGAAGATGATTTACCAATACCGTGGCGAAGATGATACGGTGTGACGAG 10257  
DB 583 CCACATGGTGAGCAAAATTTATTATCAGTACCGGCGGCAAGATACTTAGATTGTGAAACT 642  
QY 10258 GCGGAGCGGACGCGCACCGCGGCGGCGCAACGTTTATCCGTTGGCGGCTCTGGTAT 10317  
DB 643 AATGAATTAACGCTCCATCCAGGCCACAGCAACGTTATTATATAGTGTATTAC 702  
QY 10318 GGTAAACCGTCAGCGGCTCGGACGTTACCGGCGCTG---GTGTCGACACCATCAATGGAT 10374  
DB 703 GGCACCGGACAGCGGCAAGGTTTACCGGCTCTGAATGGTCTGCGGCCCATCACAAGCA 762  
QY 10375 AGCTGCTGTTTATCTGCTGTTTATGATGATGTCGAGCTAGCTCGGTCGTCTGAAGCG 10434  
DB 763 GACTGGTGTCTTACCTGTTTATGATTTACCGGCAACGCACTGAAATGCGCA 822  
QY 10435 CGGCGCTGCAACACACAGGAGTGGGAGTGGCTGTCGTCAGGATTTGTTTCCGG 10494  
DB 823 CCAGC-----ATTACAGCAACGGTAATGCTGTTGCTGAGGACCGTTCCTCCGT 876  
QY 10495 TATGATTTGGTTTAACTCGGAGCTCGCGGCTGTCGCTGAGTGTGATGTTTCCAT 10554  
DB 877 TATGAATATGGCTTTCATTAATGCTGCTGCGGCTTATGCGCTGAGTGTATCAC 936  
QY 10555 TACCTAGTGTCTGCGGCGGAGTTCCGGAGCGAATGTCGCGCAGCATGATTTCTCGC 10614  
DB 937 TGCCTCAAGCGCTGGATTAATAGATATAAAGAAACACACGCAACGCTGTTTCCACGC 996  
QY 10615 CTGTTCTGCACTACAGGGAAGTCTTCACTCAGTCTCTCGAGAACGTCGACCAAGTG 10674  
DB 997 CTGATACTCAATATGACGAAGCGCAATCGCAGACGCTGTTATGTTCTCGAGTA 1056  
QY 10675 GCTTATGATCGGACGGGACGCTTGTGCTTTCGCGGCACTGGCATTTGGGGTGGCAACC 10734  
DB 1057 GGACATGAGCAAGAGCGGTACTGCGGTCACCTGCCACCATTAGAATTTGGCGTATCAAGAT 1116  
QY 10735 TTTACCCCGCGACATTTGTCGATGCGGATGCGGATGAGATATGGCAAGTTGAGTTTG 10794  
DB 1117 TTTTCAACCGCAACATAACACTGACTGSCAACCGATGGATGTGCTGGCAAACTTCAATGCC 1176  
QY 10795 CTTCAACCTTATCAGCTTGTAGACCTTAACGCGGAAGGTGTTGGTGGTATCTCTGATCAG 10854  
DB 1177 ATTCAGCGTGGCAGCTAGTTCGATCTAAAGGGAAGGATTTACCCGCGCTGCTATATCAG 1236  
QY 10855 GACAGCGGTGCTTGGTGGTACCGTGAAACCGGTACGCGAGTCGGGGGATGATCCGATGCT 10914  
DB 1237 GATAAAACCGTGTGTTGGTACCGTTCGCGCACAGCGCTCTGGGTGAAATTTGGCTCAGATACC 1296  
QY 10915 GTGACCTGGGGGCGGCTCGGCCCTCGCGCAAAATGCGCGCTTTTGATTAACAGCGGATC 10974  
DB 1297 GTCACTTGGGAAAAAATACAGCCTTTGCTGTTATCCCTTCTCTTGAAGCAACGCGCTCG 1356  
QY 10975 CTGGCGGATCTTAAATGGGATGCTCGGCTGGAGTGGTCTGTACCGCCCGGCTGGCG 11034  
DB 1357 CTGGTGGATATCAACGGAGACGCGCAACTTGAATGGGTTATCACCGGACCGGATTTACCG 1416  
QY 11035 GGGATGTATGATCGCACCCCGCGCGGACTGCTGTCATTTTACCCCTTGTGAGGCTTTG 11094

Db 1417 GGATATCATAGTCAACGTCAGATGCGAGTTGGACAGCTTTTACCCCACTCAATGCTCTG 1476  
Qy 11095 CCGTAGAATATCGGATCAAAAGCAGTGTCTCGCCGATATCCTGGGGGCTGGTTAACG 11154  
Db 1477 CCGGTGGAATATACTCATCGTGGCAACTCGCCGATTTAATGGGAGCCGGCTCTCT 1536  
Qy 11155 GACATGGTCTTATCGGGCGCGCAGTGTTCGCTCTATTCGGGCAAAACAGATGTTGG 11214  
Db 1537 GATTAGTCTGATCGGCCCTTAATAGTGTGCGTTTATATGCCAATATCTCGTACGCGCTTC 1596  
Qy 11215 AATAAAGGGGAGACCGTGCAGCAAAACGGAAGACTCACTCTCGCGTCCCGGGGTTGAC 11274  
Db 1597 GCCAAGGAAGAATGTGGTGAATCCGGTGATGTCACGCTGCCAGTACCGGGTCCGAT 1656  
Qy 11275 CCAGTACCCCTCGTGGCGTTAGTGATATGGCTGGCAGTGGAGCAGCAGCATTTTGACGGAG 11334  
Db 1657 CCGCGTAAGCTGGTGGCGTTTAGTGATGTAATTGGGTTCGGGTCCGGCAGCACAATCTGGTTGAA 1716  
Qy 11335 GTGCGTCTAATGGAGTACGTTACTGGCCAAACCTGGGCAAGCTCGTTTCGGTCAAGCCG 11394  
Db 1717 GTGAGCGCAACTAAGTCACTGCTGGCCTAATCTGGGGCATGGACGTTTGGTCAACCC 1776  
Qy 11395 GTGAATATTTCCCGGTTTTAGCCAGTCAGTCACTGTTTAAACCTGACCAGATATTGCTG 11454  
Db 1777 ATTACCCCTCGGGATTACGCCAGCCAGAGGCTATATTTAAACCGGCTCAAGTTTATCTG 1836  
Qy 11455 GCGGATACCGAGGTTCCGGTACACGGACCTGATTTATTCGATGATGAGTACCGGTTAGTTC 11514  
Db 1837 GCGGATCTGGATGGCAGCGGCCAACCGGATCTGATTTATGTTTACACCAACCGCTCGGAC 1896  
Qy 11515 ATTTATTTCAACAGAGTGTATTTATTTTCGCGAGCCGATACGCTGCTTTCGCCGAAA 11574  
Db 1897 ATCTTCTGAATAAAGTGGCAACGGTTTTTCCGCAACGATGACATGCGCTTCCAGAA 1956  
Qy 11575 GGTGTGCGTATGATCGACCTGTCAGTCTGCAAGTGGCGGATATCCAGGGGCTGGGGGTG 11634  
Db 1957 GGCTTGGTTTTGACCATACCTGTCAAGTTACAAGTGGCGGATATACAAGGGTTAGTGTC 2016  
Qy 11635 CCTAGCCTGTACTAGGTCCTCCCATGTGCGGCTCATCATCTGGGTGGCATTTATCG 11694  
Db 2017 GCCAGCCTGATAGTACGCTGGCCACATATGACCCCCATCACTGGCGTTGTGATCTAAC 2076  
Qy 11695 GCAGACAAACCTGGTTGTAATGGCATGAACAAATATGGGGCCCGGGATGCACCTG 11754  
Db 2077 AGCGCAAAACCGTGTACTCAGCGAATGAACAAATATGGGAGCCACACACCTTG 2136  
Qy 11755 CACTATCGAGTTCGGTGCAGTTCGGCTGGATGAAAGCCGAGGCACTGGCGGAGGC 11814  
Db 2137 CGTTACCGCAGTTCCTCCAGTTCCTGGTGGATGAAAGCCGCGCACTGGTTGCCGA 2196  
Qy 11815 AGTTCCCTCGCTGCTACCTGCCATTTACATTCATACCTGTGGGTTTCGGTGGTGCAG 11874  
Db 2197 CAACACACCGGTTTGTATCTCCCTTCCCGGTACACACCTATGGCAAAACGGAACAGCG 2256  
Qy 11875 GATGATCACCGGTAACCGTCTGGTCAGCGCTGCTTTATCGCCACCGGCTCTGGGAC 11934  
Db 2257 GATGAATCAGCGGCAAAATAGTACAACTGCTTATGCTCGTGGCGCTTGGAT 2316  
Qy 11935 GGGCAGGAACGCGAGTTTCGGGGTTTGGTTTTGTTGAGATCAGGGATACCGATACCTTG 11994  
Db 2317 GGGCGTGAACGGGAATTCGCGGATTTGGTTATGTTTGGACAGACAGACGCAATCACTG 2376  
Qy 11995 GCNAGCAGGTTACGGGACGGNACTGAGTATGCTTCTGTGACCGGAACTGGTATGCC 12054  
Db 2377 GC---CCAAAGGCAACCGCTCAGAACGCCACCCACCGGATGACCAAAACTGGTATGCC 2433  
Qy 12055 ACCGGGTACCGGCACTAGACAGCGTCTCGCGGAGACGTTATGGCAAAACGATCCGCC 12114  
Db 2434 ACCGGCTACCGGTAATAGTAACAATATCAACAGATATTGGCGTGGTGAATACAG 2493  
Qy 12115 GCTTTTGGGATTTTCGGACCCGTTTCACTGTGCGTTTCAGGAGAGGATGAGCAGACATAT 12174  
Db 2494 GCTTTTGGCGGTTTTTCAACCACGTTTTTACGACTTGGCAAGATGGCAAGATATTTCTGTTA 2553

Qy 12175 ACTCGGACGACAGCAAGACA---TTCTGGTTGCAGCGAGCCCTGAAAGGCATCCTGCTG 12231  
Db 2554 ACACCGAAGATGATAACAGCAGTATTGGCTAAAACCGGGCACTGAAAGGTCAACTGCTA 2613  
Qy 12232 CCGAGTGTAGTTATACGGTGCAGTGGCAGCAGCCAGGCGGATATCCCTTTACAGCGTCACT 12291  
Db 2614 CGTAGTGTAGTGTACGGATTGGACACAGTACAAATAAACAGTTCCTTATCTACTGTCACT 2673  
Qy 12292 GAGTCTCGCCCCCAGGTACGGC---TAGTTGAAGCGAATGAGAGACTACCCGCTGGTGTG 12348  
Db 2674 GAATTTGGTCCACAGTACGTGATTTACAGCAGGAGATAACCAATACCCGGTACTTTGG 2733  
Qy 12349 CCGATGGGGCGGGAAGCGGTAGCTAGTTTATGAAACGATACCAATGATCCTCAATGC 12408  
Db 2734 TCATCTGTAGTTTGAAGCGCAGCTATCATTTACGAGCGTATCGCCAGCGACCCACAATGC 2793  
Qy 12409 CAACAGCAGGCGGTACTCCTCAGTGTATGAATACGGTTTCCCACTGCGTCAGGTCAGTGTC 12468  
Db 2794 AGCCAGATATTTACGCTATCCAGTGTATCTNTTTGGCCAAACCGCTAAACAGGTTTCGTA 2853  
Qy 12469 AATTATCCACGACGCCCTCCGTGCGGGAACAATCCATATCCGGCGTCTTTACCGGCGAG 12528  
Db 2854 CAGTATCCACGCGGAAGCAACAGCAATCAGTCCGTATCTCTGATACGCTGCTGATGAA 2913  
Qy 12529 CTGTTGCGCAACAGTTTATGACGAGCAGCAGCAGATATTACCGTGGGTTGCAACAGAGC 12588  
Db 2914 TTGTAGTCAACAGCTATGATGAACAGCAACGCCAATTTACGGCTCACCTATCAACAATCC 2973  
Qy 12589 AGTGACACATCACCTTGTTCACCTGTGAGGGGCAATGGTTTGGGGTTGGCGAGGGG 12648  
Db 2974 AGTTGGCATCATCTGACTGACATACCGT-----TCGGTGTAGGATTACCGGATAGT 3027  
Qy 12649 TCGCGGACGATGTATTCAGTATCTCTGCGGAACAAGTCCCGGAAGGGGTCTGACGCTG 12708  
Db 3028 ACCCGCAGTGATCTTCACTTATGAAGCTAAATAATGTACTGCTGCTGGTGTGTTAAATCTG 3087  
Qy 12709 GAACACCTGTTGGCGCCGGAAGCCTGGTCTCGGATAGTCAAGTCCGTGCTACGCTGGCGGT 12768  
Db 3088 GAACACTGTAGTATTAAAGATAGCCTGATTCGGGATATATAAACCGGTGAATATCTCGGC 3147  
Qy 12769 CAGCAGCAAGTCTGGTATCTGATTTCAAGAAGCTTGCACCGCTGCTCTCGCCACATC 12828  
Db 3148 CAGAAAAAACCATTTATACCAATGGGAAAAATGCAGCGCCATTCGCAACGCCAACGCGA 3207  
Qy 12829 CCCCCAAGGTAGCTTTTATCGAAAACCGCGCTGTGGATGAGGGGTATGCTAGTTCACTG 12888  
Db 3208 CAAGCGCTAGTTGCGCTTTACCGAGACACCGGTATTTAGTCAATCCACACTATCAGCGTTT 3267  
Qy 12889 GCTGCTACATTTGTGGATGAACA-----TCTCGAGCAAGCCGGTTTACCGGCAA 12936  
Db 3268 GATGGAGATCCCATCTGCTCAATTTGTCAACGAGCTGGAAACAGCCGGATACCAACAA 3327  
Qy 12937 TCCGGATACCTTTTCCCTCGAGGAGGAAAGCAGAAACAGGCAATTTGTGACCCAGTGTGAG 12996  
Db 3328 ACAATATCTATTTCTTCGACCCGGAAG-----ATAAATCTGGGTAGTCTCAT 3381  
Qy 12997 GATATGTATCCTATGTCGGCGCAGAGCAATTTCTGGCTACCGCTATCCTTTTGGGACAGT 13056  
Db 3382 GGTATATCCGATACGGTACAGCCGACAGTTCTGGCGCCGCAAAAAACAGAGCAACACC 3441  
Qy 13057 ATGTTGACCGGCCAGTTTACCGTACGCGTGAAGCGGTACGCTGCTCATACGCAAGTGG 13116  
Db 3442 CAACTCAGGGCAAAATTAATCACTCACTTGGATGCACTATTTGCTGTGTGACACAAACC 3501  
Qy 13117 CAGGATCGCGCAGGATTTGTCCACAGCCGATATGACTGCGCTTCTCTGACGCCGCTG 13176  
Db 3502 CGAGATGCTGCTGGCTGCAACACCTCAGCAAAATATGACTGGGTTTTCTGACCCCTGTG 3561  
Qy 13177 CCGGTGACGGACCCCAATGATTAATCTGAGTCCGTCACCTCTGATGCTCTGGCGCGGTG 13236  
Db 3562 CAACTCAGAGATATCAATGACAATCAGCACCTTATCATGCTGATGCACTGGCGCGGCCA 3621

QY 13237 ACACCCCTGCGATTCTCGGGCAGCGGAGATGGTATTGCCACCGGTTACAGT----- 13287  
Db 3622 ATCACACTGGCGTTTGGGAACTGAAAAACGCAAGATGACCGGTTACTCTTACCCGAA 3681  
QY 13288 GATCCACGTTGTCGGTTCGGAGCGCGCAGCAGCGCTCTGGCGTTGACGGGCCCTTA 13347  
Db 3682 AAGACACCGTTTCTCCACCGTCCGATGTGAACCTCCCGCTATTGAGTTAAAAAACCGCTC 3741  
QY 13348 CCAGTAGCACAGTGTCTGGTGTATGTCAACGACAGATTGGGAGATGACGACAAATGAGAAA 13407  
Db 3742 CCTGTAGCACAGTGTCAAGTTTACGACACCAAGAGCTGGATGCCAGTATTAAAGTCAGAAA 3801  
RESULT 12  
ADN61379  
ID ADN61379 standard; DNA; 4425 BP.  
AC ADN61379;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Photorhabdus strain W14 tcdB2 toxin complex DNA.  
XX  
KW Cry; toxic; lepidopteran pest; toxin complex; insecticide; strain W14;  
KW ds; tcdB2.  
XX  
OS Photorhabdus sp.  
XX  
PN W02004002223-A2.  
XX  
PD 08-JAN-2004;  
XX  
XX 27-JUN-2003; 2003WO-US020082.  
XX  
XX 28-JUN-2002; 2002US-0392633P.  
PR 21-JAN-2003; 2003US-0441647P.  
XX  
XX (DOWC) DOW AGROSCIENCES LLC.  
XX  
XX Bintrim SB, Bevan SA, Zhu B, Merlo DJ;  
XX WPI; 2004-082821/08.  
XX  
PT Screening a culture of Paenibacillus isolate for Cry protein or toxin  
PT complex protein, useful for controlling lepidopterans, comprises  
PT obtaining DNA or protein from the culture and assaying the presence of  
PT the gene or protein.  
XX  
XX Example 12; SEQ ID NO 43; 220pp; English.  
XX  
XX The invention relates to a novel method for screening a culture of a  
CC Paenibacillus isolate for a gene encoding a protein selected from a Cry  
CC protein that is toxic to a lepidopteran pest and a toxin complex protein.  
CC The method comprises obtaining DNA from the culture and assaying the DNA  
CC for the presence of the gene or obtaining a protein produced by the  
CC culture and assaying the presence of a protein that indicates the  
CC presence of the gene in the isolate. The method of the invention has  
CC insecticide applications and may be useful for screening Paenibacillus  
CC sp. for toxin complex (TC)-like genes and proteins which may themselves  
CC be used to enhance or potentiate the activity of a stand-alone  
CC xenorhabdus toxin protein. The method may also be useful for screening  
CC Paenibacillus sp. and others for insecticidal thiaminase genes and  
CC proteins for controlling insects, particularly lepidopterans. The current  
CC sequence is that of the Photorhabdus strain W14 tcdB2 toxin complex DNA  
CC of the invention.  
XX  
SQ Sequence 4425 BP; 1207 A; 1157 C; 1050 G; 1011 T; 0 U; 0 Other;  
Query Match 5.5%; Score 1046.4; DB 12; Length 4425;  
Best Local Similarity 56.4%; Pred. No. 4.6e-238;  
Matches 2166; Conservative 0; Mismatches 1606; Indels 66; Gaps 9;  
QY 9598 ATGCAAAATCATCAAGACATGGCCATTACTGCCCCACGTTGCTTCCGGGGGGGCG 9657

Db 1 ATCAAAATTCACAAAGATTTTAGTATTACGAAACTGTCACTGCCCCAAAGGGGGGGCGCT 60  
QY 9658 GTCACCGGGCTCAAGGGTGNATATCGCGCGGAGGGCCGATGGTGGCGGACCCCTCAGT 9717  
Db 61 ATCAGCGGAATGGTGAAGCAITTAACCCCACTGGACCCGATGGTATGGCGCGGCTATCT 120  
QY 9718 ATTCCCTTGGCGGTATAGCCCCGGTTCGCGGGTTACGCCCCCACTGGGGCACITTAATATCAC 9777  
Db 121 CTACCATTTGCTATTTCTGCCGGCGGGTTATGCTCCCGCATTCCTCTGAATTACAAC 180  
QY 9778 AGCGGTTCGGGGAACCGGCCCTTTTGGCATTTGGGTGGGTTATCGCGGTGTCTGTCTCAG 9837  
Db 181 AGCGGGCGCGGTAAACAGTCCATTTGGTCTGGGTGGGATTCACACGTTATGACTATCCGC 240  
QY 9838 CGTCGTACGCGCAACGAGGACACCTACTACGATGATACTGATGAATTCACCGGTCCGAC 9897  
Db 241 CGCCGACCCCATTTTGGCGTCCCCCATTAATGACGAACCGATACCTTTTGGGGGCCAGAA 300  
QY 9898 GGTGAGGTGCTGTGCGCGCACTCAGCGGTGCTGGCACCCCAAGACACGCGAGGCCACC 9957  
Db 301 GCGGAAGTGTGCTG-----GTAGCGGATCAACTCTCGGACGATCC 342  
QY 9958 TCATACTGGGATAAACCAGCGGAAGCTTCAACGTTTCAGGTTTACCGTTTCACTGATCG 10017  
Db 343 ACATTACAGGGTATCAATTTAGCGGCCACCTTTACCGTTTACCGGTACCGTTCGCGTCTG 402  
QY 10018 GAGGGTAGTCTAGCGCGCTTGGCGTTGGCTGCCCGCCGACGACGACGAGAAACGGAATTT 10077  
Db 403 GAAAGCCATTTTCAGCCGATTTGGAAATATTTGGCAACCCCAAAACAAACAGGTAAACAGATTTT 462  
QY 10078 TGGGTGTATATACCCCTGACGACAGGTGGCTCTGCTGGCGCCGAAATGCGAGGCTCGC 10137  
Db 463 TGGTTGATATATAGCCAGATGGGAGGTGATCTACTTGGGTAAATCACCGAAGCGCGG 522  
QY 10138 ATCAGCAACCCACAGCCCCCAACACAGACGGCGGTTTGGCTGATGGAGTCTCTCGGTATCA 10197  
Db 523 ATCAGCAACCCATCCCAACAGCACAAACAGCAACAATGGCTGTGGAGGCTCTGTATCA 582  
QY 10198 CTTACCGCGCAACAGATGATTTACCAATACCGTGGGAGATGATGACGGTTGTGACGAG 10257  
Db 583 TCACGTGGGGAACAAATTTATTAATCAATATCGCGCCGAAAGATGACACAGGTTGCGAAGCA 642  
QY 10258 GCGGAGCGGACGCGCACCGCGAGCGCGGCCCAACGTTTATCCGTTGGGGGTCTGTAT 10317  
Db 643 GATGAATTTACGACCATTTTACAGGCTACAGCCAAAGCTTTATTTACATCGTGTATTAC 702  
QY 10318 GGTAAACCGTCAGCGGCTCGGACGCTACCGCGCTGCTGTGTCGA---CACCATCAATGGAT 10374  
Db 703 GGCACCGGTACAGCCAGCGAACAATTTACCGGTCTGGATGGCAGCGCCCATCACAAAGCA 762  
QY 10375 AGCTGCTGTTTATCTGTTGTTGATTTATGGTAGCGTAGCTCGGTGCTGTCTGAAGCG 10434  
Db 763 GACTGTTGTTCTATCTGTTGTTGATTTGATTAAGCGGAACGCAAGTAACACCTCAAAACGCCA 822  
QY 10435 CCGGCTCGCAACACACAGGAAGTGGGAGTGTCTGTCTGTCAGATTTGTTTTCCGGG 10494  
Db 823 CCAAGATTTTGGTACAGTAG-----CTGCTTTTCCGTGAGGACCGTTTTTCCCGT 876  
QY 10495 TATGAGTTTGGTTTTAACCTGCGGACTCGCGGCTGTGCGGTGAGGTTTGTGTTCCAT 10554  
Db 877 TATGAATATGGCTTTGAGATTCGTACCCCGCTTATGCCGTGAGGTTATGATGTACCAT 936  
QY 10555 TACTAGGTGTTCTGGGGGAGTTTCGGGAGCGAATGATGCGGCAGCATTTGATTTCTCGC 10614  
Db 937 CACCTCAAGCACTGGATAGTAAGATAACAGAAACACACGACCAACGCTGGTTTTACGC 996  
QY 10615 CTGTGCTGACTACAGGGAAGTCTTCACTCAGTCTGCTCGAGAACGTCACGAGGTG 10674  
Db 997 CTGATCTCAATTTACAGGAAGCGGATAGCAGCACGCTAGTATTCTGTTCCCGGAGTG 1056  
QY 10675 GCTTATGAGTCGACGGGACGCTCTTGTGCTTCCCGCACTGGCATTTGGGGTGGCAAC 10734

Db 1057 GGACACGACAGATGGTAATGTCGTCAACCTCCGCCCAATTAGAAATGGCATATCAGGAT 1116  
QY TTTTACCCGCGGACATTTGTCGGCATGCGACAGCCGTGACGATATGGGCAAGTTGAGTTTG 10794  
Db 1117 TTTTACCCGCGACATCAGCTCACTGGCAACCAATGGATGTAAGTACTGGCAAACTTCAATGCC 1176  
QY CTTTCAACCCCTATCAGCTTTPAGACTTAAACGGCGAAGGTGTGGTGGGTATCTCTGTATCAG 10854  
Db 1177 ATTTCAGCGCTGGCAGCTAGTCGATCTAAAGGCGAAGGATTTACCCGGCCTGTTTATATCAG 1236  
QY GACAGCGGTGCTGTGGTGTACCGTGAACCGGTACGCGAGTGGGGATGATCCGGATGCT 10914  
Db 1237 GATAAAGGCGCTTGGTGTACCGCTCCGACACGCTGTGGGCAAAATTTGGCTCAGATGCC 1296  
QY GTACCTTGGGGGCGGCTGGCGCCTCGCCGACAAATGCCCGCTTTGCAATAACAGCGGCATC 10974  
Db 1297 GTCACTTGGGAAAGATGCAACCTTTATCGGTATTCTCTTTTGGCAAGTAAATGCTCG 1356  
QY CTGGCGGATCTTAAATGGGATGTCGGCTGGAGTGGGTGTTACCGCCCCCGGTGTGGCG 11034  
Db 1357 TTGGTGGATATCAATGGAGACGCCCACTTGACTGGGTTATCACCGGACCGGATTAACGG 1416  
QY GGGATGTATGATCGCACCCCGCGGACTGGTTCATTTTACCCCTGTGTCAGCTTG 11094  
Db 1417 GGATATCATAGTCAACCGCCGGATGGCAGTTGGACACGTTTACCCCACTCAACGCTCG 1476  
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Db 1477 CCGGTGAATACACCCATCCACGCGGCAACTCGAGATTTAATGGGAGCGGGCTATCC 1536  
QY GACATGGTCTTATCGGCGCGCAGTGTTCGCTCTATTCGGGCAAAACGATGTTGG 11214  
Db 1537 GATTGGTGTGATCGCCCTTAAGAGCGTGGTATTATATGCCAATACCCGCGACGGCTTT 1596  
QY AATAAAGGGAGACCTGTCAGCAAAACGGAAGACTCACTCTGCCGTCCCGGGTTGAC 11274  
Db 1597 GCCAAAGGAAAGATGTGGTGAATCCGGTGATATCACATGCGGTGCGGGCGCGGAT 1656  
QY CCACGTACCCCTCGTGGCTTCACTGATATGGCTGGCAGTGGACAGCAGCATTTGACGGAG 11334  
Db 1657 CCACGTAAAGTTGGTGGCTTTAGTATGATGATTGGGTTCAAGTCAAGCCCATCTGGTTGAA 1716  
QY GTGCGTCTAATGGAGTACGTTACTGGCAAAACCTGGGCAAGTGTGGGTGACGCC 11394  
Db 1717 GTAAGCGCACTAAAGTCACTCTGCGCTTAATCTGGGGCGGAGCGTTTGGTCAACCC 1776  
QY GTCAATATTCGCGTTTACCGAGTCACTGACATACGTTTAAACCTGACAGATTTGCTG 11454  
Db 1777 ATTACCTTACCGGATTCAGCCAGCCAGCAACCGAGTTTAAACCGGCTCAAGTTTATCTG 1836  
QY GCCGATACCGAGCTTCCGGTACACGGACCTGATTTATGCGATGATGACCGGTTAGTC 11514  
Db 1837 GCCGATCTGGATGGCAGCGGTCAAACGGATCTGATTTATGTTATCATACAAACCGTCTGGAT 1896  
QY ATTATTTCAACAGAGTGGTAATTTATTCGCGAGCCGCAATACGCTGCTTTGCGGAAA 11574  
Db 1897 ATCTTCTGAACAAAAGTGGCAATGGCTTTGTGTAACCAAGTGAATTTAGCTTCCCGGAA 1956  
QY GGTGTCGGCTATGATCGCACTTCAGTCTGCAAGTCGCGGATATCCAGGGCTGGGGTG 11634  
Db 1957 GGTCTGCTTTTATATACCTGTCAAGTACAATATGGCCGATGTAACAAGATTAGGCGTC 2016  
QY CTAGCTGTGTACTGAGCGTCCCGCATGTGCGGCCCTCATCACTGGGTGGCCATTTATCG 11694  
Db 2017 GCCAGCTGATCTGAGCGTGGCGATATGCTCTCCCATCATCTGGCGCTCGCATCTGACC 2076  
QY GCAGCAAAACCTGTTTGAATGGCATGAACAAACATATGGGGCGCGGATGACATG 11754  
Db 2077 AACATGAACCGTGGTTACTCAATGAATGAACAAACATATGGGGGTCCATCACACTTG 2136  
QY CACTATCGAGTTTCGGTGCAGTTCTGGCTGGATGAAGAACCGAGGCACTGGCGGAGGC 11814  
Db 2137 CGTTACCGCAGTTCTCCCAATTTCTGGCTGGATGAAAAAGCCCGCGGCTGACTACCGGA 2196

QY 11815 AGTTCCTCTGCTGCTACTGCTGCAATTTTCAATTCATACCTGCTGGCGTTTCGGTGTGCAG 11874  
Db 2197 CAAACACCGTTTGTCTATCTCCCTTCCGATCCACACCTATGGCAACGGAACAGAA 2256  
QY 11875 GATGATATCACCGTAACCGTCTGTGACGAGCTGCTTTATTCGCCACGCGCTCTGGGAC 11934  
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QY 11935 GGGCAGGACGCGAGTTTCGGGGTTCGTTTTGTTGATCAGGATACCGTACCTTG 11994  
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QY 12055 ACCGGGTACCCGGAGTAGACAGCGTCTGCGGAGACGTTATGGCAAAACGATGCCGC 12114  
Db 2434 ACCGACTGCGCGTGATAGATAACGATTTATCAACCGAGTATTGGCGTGTATCAGGCT 2493  
QY 12115 GCTTTTCCGATTTCCGCGACCGTTTCACTGTCGTTTCAAGGAGAGATGAGCAGATAT 12174  
Db 2494 TTTGCCGTTTCTCACCGGCTTTACGACTTGGCAAGATAACAAAGATGTCCCGTTAAACA 2553  
QY 12175 ACTCCGCGACGACAGCAAGACATTTCTGTTTGCAGCGAGCCCTGAAAGGCACTCTGCTGCCG 12234  
Db 2554 CCGGAAGATGATAACAGTCTGTTACTGTTTCAACCGCGCTTGAAGGTCAACTGTACTGT 2613  
QY 12235 AGTGAATTATACGGTCCGATGGCAGCAGCGCGGATATCCCTTACAGCGTCACTGAG 12294  
Db 2614 AGTGAATGTATACGGATTTGACGATAGTACAAATAAACACGTTTCCCTATATCTGCTCACTGAA 2673  
QY 12295 TCTCCCGCGAGTACGCG---TAGTTGAAGCAATGGAGACTCCCGTGTGTGGCCG 12351  
Db 2674 TTTGTTTACAGGTACGTGATTACAGCATACCGACGCGGATACCTCTGTTTGGTCA 2733  
QY 12352 ATGGCGCGGAAAGCGTACGTGTTTATGAACGAGTACCAATGATCCTCAATGCCAA 12411  
Db 2734 TCTGTGTTGAAAGCGCAACTATCACTACGAACGTATCGCCAGCGACCCGCAATGCACT 2793  
QY 12412 CAGCAGCGGTACTCTCTGATGATGAATACGGTTTCCCTGCTGCTGAGTCACTGAT 12471  
Db 2794 CAAAATATTACGCTATCCAGTGTATGCTGATTCAGCGCTAAAACAGCTTTTCGGTACAG 2853  
QY 12472 TATCCAGCAGCGCTCCGTCGCGGACCAATCATATCGGCGTCTCTTACCGCGACGCTG 12531  
Db 2854 TACCGCGCGCGCAGCAGCCAGCAATCAATCTGTATCTGTATACATTGCTCTGATATGTTG 2913  
QY 12532 TTCGCCAACAGTTATGACGAGCAGCAGATATTACGCTGGGGTTGCAACAGAGCACT 12591  
Db 2914 TTAGCCACAGCTATGATGACCAACAAACGCAATTTACGGCTCACCTATCAACAATCCAGT 2973  
QY 12592 GCACATCACTTGTCTCTGCTGAGGGGCAATGGTTGTTGGGTTGGCGGAGGCTGCG 12651  
Db 2974 TGGCATCACTTCAACCAACAAATACCG-----TTCGAGTATTGGGATTTACCGATAGTACC 3027  
QY 12652 CCGGACGATGATTACAGCTACTCTCGGACAACTGCGGAAAGGGGTCTGACGCTGGAA 12711  
Db 3028 CCGAGTATCTTTACTTATTCGCGCTGAAATGTCCTGCTGCTGCTGTTGTTTAAATCTGGAA 3087  
QY 12712 CACTGTTTGGCGCCGAAAGCTGCTCGGATAGTCAAGTCCGTTGCTGAGTCCGCTGGGCTCAG 12771  
Db 3088 CTTCCTGAGTGATAAAAAATAGCCTGATCGCGGACGATAAACACCGTGAATACCTCGGCTCAG 3147  
QY 12772 CAGCAGTCTGTTATCTGGAATTCACAGAGTTGCCACCGTCTGCTCGGCACTCCCC 12831  
Db 3148 CAAAAAACCGCTTATACCGGATGGAACAAATACACCGCGTTGCCAAACACCAACAGGCA 3207  
QY 12832 CCCAAGGTAGCTTTTATCGAAACGCGGCTGCTGGATGAGGGTATGGTCACTGTTCACTGGCT 12891  
Db 3208 GCGCTGATTGCTTTTACCGAACAACAGGTATTCAACCACTCCACCATTTACAGGGTTTAC 3267



Qy 12892 GCCTACATTTGGTGAAGA-----TCTCAGCAGAACCGGTTTACCGGCAATCC 12939  
Db 3268 GGAAGCATCCCGTCCGATAAATATCAACGACGCTGGCAAGCTGATATCAGCAACA 3327  
Qy 12940 GGTACCTTTTCCCTCAGGAGGAGCAGACAGGCAATGTGGACCCAGTCTCAGGA 12999  
Db 3328 AATTATCTATTTCCCTCAGCTGGAGAAG-----ATAAGTTTGGGTAGCCCATCAGCGC 3381  
Qy 13000 TATGTTACCTATGCGCGGAGACATTTCTGGCTACCGCTATCCTTTCCGGGACGATG 13059  
Db 3382 TATACCGATTATGTACAGCGGCACAGTTCTGGCGCCGCAAAACAGACACACCCAA 3441  
Qy 13060 TTGACCGGCGCAGTTACCGTACCGGTGACCGGTACGACTGCTGTCATCAGCAGTGGCAG 13119  
Db 3442 CTCACCGGTAAATCACCCTCATCTGGGATGCAAACTATTGCGTTGGTACAAACCCGG 3501  
Qy 13120 GATGCCCGAGGATTGTACACAGCGCATATGACTGGCGCTCTCTGACGCGCGTCCGG 13179  
Db 3502 GATGCTGCTGACTGACAACTCAGCCAAATATAGTGGCGTTTCTGACCCCGGTGCAA 3561  
Qy 13180 GTGACGACCCCAATGATATCTGCAGTCCGTCACTCTGGATGCTCTGGCGCGGTGACC 13239  
Db 3562 CTCACCGATTATGATACATCAGCACTTATCAGCTGGATGATGGCGCGACCAATC 3621  
Qy 13240 ACCCTGCGATTCTGGGCGACGAGATGGTATTGCCACCGGTTA-----CAGTGTAT 13290  
Db 3622 ACATTGCGCTTTTGGGAACTGAAACCGCAAGATGACAGGTTATTCTCACCAGAAAAA 3681  
Qy 13291 GCCAGTTGTCGGTTCGGAGCGGCGAGCAGCGCTCTGGGTTGACGGCGCCCTACCA 13350  
Db 3682 GCATCATTTTCTCCACCATCCGATGTTAATGCCGCTATTGAGTTAAAAAACCCTCCCT 3741  
Qy 13351 GTAGCAGATGCTGGGTGTGTCAACGACAGTTGGGAGATGACGACAATGAGAAAA 13408  
Db 3742 GTAGCAGATGCTAGGTTCTACGACCAAGAAAGCTGGATGCCAGTATTAAAGTCAGAAA 3799

RESULT 13  
ADP18621  
ID ADP18621 standard; DNA; 4425 BP.  
XX  
AC ADP18621;  
XX  
XX 12-AUG-2004 (first entry)  
XX  
XX Photorhabdus luminescens W-14 tcdB2 encoding DNA SEQ ID NO:9.  
DE  
XX tcd; Photorhabdus luminescens W-14; transgenic plant; Toxin A;  
KW orally active insect toxin; insect toxin; tcdB2; gene; ds.  
XX  
XX Photorhabdus luminescens.  
XX  
FH Key Location/Qualifiers  
CDS 1..4425  
FT /\*tag= a  
FT /product= "tcdB2"  
XX  
XX WO2004044217-A2.  
XX  
XX 27-MAY-2004.  
XX  
XX 12-NOV-2003; 2003WO-IB005553.  
XX  
XX 12-NOV-2002; 2002US-0425672P.  
XX  
XX (UYBA-) UNIV BATH.  
XX  
XX Ffrench-Constant RH, Waterfield NR;  
XX  
XX WPI; 2004-411735/38.  
DR P-PSDB; ADP18622.  
XX  
XX New isolated Photorhabdus luminescens nucleic acids, useful for

expressing orally active insect toxin or for generating transgenic plants with enhanced resistance to insects.

Claim 2; SEQ ID NO 9; 118pp; English.

The present invention describes DNA sequences from the tcd genomic region of Photorhabdus luminescens W-14. Also described: (1) a transgenic monocol or dicot cell having a genome comprising a nucleic acid sequence that encodes SEQ ID NO:4, 6, 8, 10, 12, 14, or 16; (2) a transgenic plant with a genome comprising a nucleic acid sequence that encodes SEQ ID NO:4, 6, 8, 10, 12, 14, or 16; (3) a seed of the transgenic plant; (4) a progeny of seed; (5) a method of producing toxin A of Photorhabdus luminescens W-14 in a heterologous host; and (6) a method of producing an orally active insect toxin. The nucleotide sequences are useful for heterologous expression of orally active insect toxin. They can also be used for generating transgenic plants with enhanced resistance to insects. The present sequence encodes Photorhabdus luminescens W-14 tcdB2, which is used in the exemplification of the present invention.

XX Sequence 4425 BP; 1207 A; 1157 C; 1050 G; 1011 T; 0 U; 0 Other;

Query Match 5.5%; Score 1046.4; DB 12; Length 4425;  
Best Local Similarity 56.4%; Pred. No. 4.6e-238;  
Matches 2166; Conservative 0; Mismatches 1606; Indels 66; Gaps 9;

Qy 9598 ATGCAAAATCATCAAGACATGGCCATTACTGCCCCCACCAGTTGCTTCCGGGGCGGTGCG 9657

Db 1 ATGCAAAATTCACAGATTTAGTATTACGAACTGTCACTGCCCAAGGGGGGGCGCT 60

Qy 9658 GTCACGGGCTCAAGGTGATATCGCGGGGCGAGGCGCGATGGTGGCGGACCTGAGT 9717

Db 61 ATCAGCGGAATGGGTGAAGCATTAACCCCACTGGACCGGATGATGGCGCGCTATCT 120

Qy 9718 ATTCCTTCGGGTTAGCCCCGGTTCAGCCCCCACTGGGACACTTAATATATCAC 9777

Db 121 CTACCATTTGCTATTTCTGCCGGGCGGTTATGCTCCCGCATTTCACTGGAATTAAC 180

Qy 9778 AGCCGGTTCGGGGAACCGCCCTTTTGGCATTTGGCTGGGGTATCGCGGCTGCTGTCAG 9837

Db 181 AGCGGCGCGTAAACAGTCAATTTGGTCTGGTGGATTGCAACGTTATGACTATCGC 240

Qy 9838 CGTCTGACGCGCAACGAGACCTACTACGATGATACGATGAATTCACCGGTCGGAC 9897

Db 241 CGCGGACCCCATTTTGGCGTCCCCCATTTATGAGAAACCCGATACCTTTTGGGGCCAGAA 300

Qy 9898 GGTGAGGTGCTGGTCCGGCACTCAGCGTCTGGCACTCCCAAGACACGCGAGCCACC 9957

Db 301 GCGAAGTGTCTGTG-----GTAGCGGATCAACCTCGGACGAATCC 342

Qy 9958 TCACTACTGGGGATAAACCCAGCGGAAGCTTCAACGTTTACCGTTTACCGTACG 10017

Db 343 ACATTACAGGATCAATTTAGGCGCACCTTTACGTTACCGGTACCGTTCCCGTCTG 402

Qy 10018 GAGGGTAGTCTCAGCCGCTTGAGCGTTGCTGCCCGCAGACAGAAACGGAATTT 10077

Db 403 GAAAGCCATTTACGCGGATTGGAATATTGGCAACCCCAAAACACAGTAAACAGATTTT 462

Qy 10078 TGGGTTATATACCCCTGACGACAGTGGCTCTGCTGGCGCGGAATATGCGAGGCTCGC 10137

Db 463 TGGTTGATATATAGCCAGATGGGCGAGTCTACTTGGGTAAATCACCAGCGCGCG 522

Qy 10138 ATCAGCAACCCACAGCCCAACACAGACGCGGTTTGGCTGTGATGGAGTCTCTCGGTATCA 10197

Db 523 ATCAGCAACCCATCCCAACAGACACAAAGACACATGGTGTCTGGAGCTCTGTATCA 582

Qy 10198 CTTACCGCGCAACAGATGATATTACCAATACCGTCGGAAGATGATACGGTTGTGACGAG 10257

Db 583 TCACGTGGCGAACAATTTATTATCAATATCGCGCGAAGATGACACAGGTGCGAAGCA 642

Qy 10258 GCGGAGCGGACCGGACCGCGCGCGCGCCCAAGCTTATCCGGTGGCGGCTGTGAT 10317

Db 643 GATGAAATTAACGCCACCATTTTACAGGCTACAGCGCAACGTTATTATACATCGTGTATTAC 702



Db 2854 TACCCGCGCCGAGCAGCAGCAATCAATCTGTATCTCTGATCATTTGCTGATAGTTG 2913  
 Qy 12532 TTGCCAACAGTTATGACGAGCAGCAGATATTACGCTGGGGTTGCAACAGACAGT 12591  
 Db 2914 TTAGCAACAGTATGATGACCAACAGCCATTAAGGCTCACCTATCAACATCCAGT 2973  
 Qy 12592 GCACATCACCTTTTTCACGTCTGAGGGGCAATGTTGTTGGGGTTGGCGGAGCGTGC 12651  
 Db 2974 TGGCATCACCTGACCAACAATACCG-----TTCCGAGTATTGGGATTTACCGGATAGTACC 3027  
 Qy 12652 CGGACCATGATTTTACGCTACTCTGCGGACAACTGCGGAGAGGGGTCTGACGCTGGAA 12711  
 Db 3028 CGCAGTATATCTTTTACTTATGCGCTGAAATAGTCTGCTGCTGTTTAAATCTGGAA 3087  
 Qy 12712 CACCTGTTGGCGCCGAGAGCTGCTCGGATAGTCAGGTCTGCTGAGTGGCGGGTCCAG 12771  
 Db 3088 CTTCGAGTGATAAATAATAGCTGATCGCGGACGATAAACAACGATACCTCGGTCCAG 3147  
 Qy 12772 CAGCAAGTCTGGTATCTGGAATTCACAAGAGCTTGCCACCGTCTGCTCGGCCACCTCCC 12831  
 Db 3148 CAAAAAACCGCTTATACCGATGGAACAAATACAAACGCGTTGCAAAACCAACACGCGCA 3207  
 Qy 12832 CCCAAGTACTTTTATCGAAACGCGCTGCTGATGAGGTATGTCAGTTCACTGGCT 12891  
 Db 3208 GCCCTGATTCCTTTACCGAAACACCGTATTCAACCAAGTCCACATTATCAGCGTTTAA 3267  
 Qy 12892 GCCTACATTGTGATGAACA-----TCTCGAGCAAGCGGTTTACCGCAATCC 12939  
 Db 3268 GGAAGCATCCGCTCGATTAATATCAACAGCGTGGAGCAGCTGATATCAGAAACA 3327  
 Qy 12940 GGAATACCTTTTCCCTCGAGCAGGAGCAAGCAGCAATGTGGACCCAGTGTCAAGGA 12999  
 Db 3328 AATTATCTATTCCTCGCACTGGAGAG-----ATAAAGTTTGGGTAGCCCATCAGGC 3381  
 Qy 13000 TATGTTACCTATGCGCGGAGAGCAATTTCTGGTACCGTATCTTTCGGGACAGTATG 13059  
 Db 3382 TATACCGATTATGTTACAGCGGCACAGTTCTGGCGCCCGCAAAACAGACCAACCCAA 3441  
 Qy 13060 TTGACCGCCGCGAGTTACCGTGACGCGTGACGCGTACGCTACGCTACGCGAGTGCAG 13119  
 Db 3442 CTACCGGTAATACCTCATCTGGGATGCAAACTATTCGTTGTTGGTACAAACCCGG 3501  
 Qy 13120 GATGCCGACGAGTATGTCACACAGCCGACTATGACTGGCGCTTCTGACGCGCCGTCGG 13179  
 Db 3502 GATGCTGCTGACTGACAACTCAGCCAAATATGACTGGCGTTTCTGACCCCGGTGCAA 3561  
 Qy 13180 GTACGACCCCAATGATATCTGCACTCGTCTGATGCTCTGGGCGCGGTGACC 13239  
 Db 3562 CTCACCGATATCAATGACAACTGACACCTTATCACACTGGATGCAITGGGCGGACCAATC 3621  
 Qy 13240 ACCTGCGATTCTGGGCGCAGGAGATGGTATTGCCACCGGTTA-----CAGTGAT 13290  
 Db 3622 ACATTGCGCTTTTGGGAACTGAAACCGCAAGTACAGTTATTCCTCACCGGAAAAA 3681  
 Qy 13291 GCCAGTGTGCTGCTCGGACGCGGACGAGCGCTCTGGCGTTGACGCGCCCTTACCA 13350  
 Db 3682 GCATCATTTTCTCCACCATCGATGTTAATGCGGCTATTGAGTTAAAAAACCGCTCCCT 3741  
 Qy 13351 GTAGCAGAGTCTGTGTTATGTCACGGAAGTTGGGAGATGACGACAAATGAGAAA 13408  
 Db 3742 GTAGCAGAGTCTGAGGTCTACGACCAAGAGTGGATGCCAGTATTAAAGTCAGAAA 3799

## RESULT 14

AAV29924

ID AAV29924 standard; DNA; 4458 BP.

XX

AC AAV29924;

XX

DT 07-AUG-1998 (first entry)

XX

DE tcaC gene from the tca genomic region encoding protein TcaC.

XX

KW TcaA; Photorhabdus luminescens W-14; nematode; symbiotic;  
 KW Heterorhabditis; tca; tcb; tcc; tcd; insecticidal activity; toxin;  
 KW Lepidoptera; Coleoptera; Hymenoptera; Diptera; Dictyoptera; Acarina;  
 KW Homoptera; Southern; Western corn rootworm; Colorado potato beetle;  
 KW mealworm; boll weevil; turf grub; beetle armyworm; black cutworm;  
 KW cabbage looper; codling moth; corn earworm; European corn borer;  
 KW Tobacco hornworm; budworm; ds.  
 XX  
 OS Photorhabdus luminescens.

Key Location/Qualifiers  
 CDS 1..4458  
 FT /\*tag= a  
 FT /product= "TcaC"

WO9808932-A1.

05-MAR-1998.

05-MAY-1997; 97WO-US007657.

28-AUG-1996; 96US-00705484.

06-NOV-1996; 96US-00743699.

06-NOV-1996; 96WO-US018003.

(DOWC ) DOWELANCO.

(WISC ) WISCONSIN ALUMNI RES FOUND.

PA Ensign JC, Bowen DJ, Petell J, Fatig R, Schoonover S;

PI Firench-Constant RH, Rocheleau TA, Blackburn MB, Hey TD, Merlo DJ;

PI Orr GL, Roberts JL, Strickland JA, Guo L, Ciche TA, Sukhapinda K;

XX WPI; 1998-179427/16.

DR P-PSDB; AAW56546.

XX Isolated toxins from Photorhabdus luminescens strains - useful for  
 control of insect pests.  
 PS Claim 38; Page 190-196; 321pp; English.

XX The present sequence encodes a protein named TcaC of the bacterium

CC Photorhabdus luminescens (W-14). This is a symbiotic bacterium of the  
 CC nematodes of the Heterorhabditis genus. The bacterium has at least 4  
 CC distinct genomic regions, tca, tcb, tcc, and tcd. Peptide products are  
 CC produced from these regions that are associated with insecticidal  
 CC activity. The native toxins are secreted proteins. The proteins are toxic  
 CC to insects upon exposure and especially when ingested. The nucleic acid  
 CC sequence can be used to produce transgenic plants, baculoviruses or  
 CC microbial hosts for toxin production. They can be used to control insects  
 CC pests from the Lepidoptera, Coleoptera, Hymenoptera, Diptera,  
 CC Dictyoptera, Acarina or Homoptera orders, especially the Southern or  
 CC Western corn rootworm, Colorado potato beetle, mealworm, boll weevil,  
 CC turf grub, beetle armyworm, black cutworm, cabbage looper, codling moth,  
 CC corn earworm, European corn borer or tobacco hornworm or budworm  
 XX  
 SQ Sequence 4458 BP; 1199 A; 1181 C; 1088 G; 990 T; 0 U; 0 Other;

Query Match

Best Local Similarity 53.8%;

Matches 2395; Conservative 0; Mismatches 1857; Indels 201; Gaps 11;

Qy 9598 ATGCAAAATCATCAACACATGGCCATTACTGCCCCCAGCGTTCCTTCGCGGGCGGTGCG 9657  
 Db 1 ATGCAAGATTCCACCAAGATATCGATTACACCTGTCTCTCCCAAGGTGGCGGTGCT 60

Qy 9658 GTCACCGGGGTCAAGGGGTGATATCGCGGGCGGAGCGGCGGATGGTGGCGGACCCCTGAGT 9717  
 Db 61 ATCAATGGCATGGAGAACACACTGAATGCTGCGGCGCTGATGGAATGGCTCCCTATCT 120

Qy 9718 ATTCCCTTGGCGGTAGCCCCGGTTCGGGGTTAGCCCCCAGCTGGGGACCTTAATATCAC 9777  
 Db 121 CTGCCATTACCCCTTTTCGACCCGCGAGAGGACGGCTCCTGGATTATCGCTGATTACAGC 180



Db 2338 TGGGATGTTAAAGACGGGAATTCAGAGGATTTGGCTGCAATCAAAACAGACAGATACCACA 2397  
Qy 11989 ACCTTGCAAGACCAAGGTACGGCAGCGAACTAGTATGCTTCTGTGAGCCGGAACCTGG 12048  
Db 2398 ACGTTTTC---TCAGGCAACGCCCCGAAACAGCGGCAACGCTGCTGAGTATTAGCTGG 2454  
Qy 12049 TATGCCACCGGGTACCGGAGTAGACGAGCGTCTGCCGAGAGCTATTGGCAAAACGAT 12108  
Db 2455 TTTGCCACCGCATGGATGAAGTAGACAGCAATTAGCTACGGAATATTGGCAGGCAGAC 2514  
Qy 12109 GCCGCCGTTTGGCGATTTCCGACACCGGTTTCACTGTGG-----TTCAGAGAGGAT 12162  
Db 2515 ACGCAAGCTTATAGCGAATTTGAACCCGTTATACCGTCTGGGATCACCAACACGACA 2574  
Qy 12163 GAGCAGACATATACTCCCGGACGACAGCAAGACATTTCTGTTGACGAGCGCTTGAAGGC 12222  
Db 2575 GACCAAGATTTACCCCAATGACACACAGGTAACCTGCTGAGCGAGCGCTTAAAGC 2634  
Qy 12223 ATCTGTGCGCACTGAGTTATACGGTGGCGATGGCAGCAGCGCCGATATCCCTTAC 12282  
Db 2635 CAACCTGCTACGCACTGAGCTCTACGGTCTGACGGAACAGATAAGCAACAGTGCCTTAT 2694  
Qy 12283 AGCGTCACTGAGTCTCCCGCAGGTAGCGGTAGTTGAAGGAATGGAGA---CTACCG 12339  
Db 2695 ACCGTCACTGAGTCACTGAGTCACTGAGTCACTTATCCCGTAAATAAGAAACTGTAATTA 2754  
Qy 12340 GTGTGTGGCGGATGGCGGGAAGCGGTACGTGAGTTTATGAACGTTACCAATGAT 12399  
Db 2755 TCTGCTGGGTGACTGCTATTGAAATCGCAGCTACCACTATGAACGTATCATCACTGAC 2814  
Qy 12400 CCTCAATGCCAAACAGCGGGTACTCCTCAGTGATGAATACGGTTTCCCACTGCGTCAG 12459  
Db 2815 CCACAGTTACGCCAGAGTATCAAGTTGCAACAGATATCTTTGCTCACTCACTGCAAGT 2874  
Qy 12460 GTCACTGCTCAATTTATCCAGAGCCCTCCGTCGGCGGACAAATCATATCCGGGTCCTTA 12519  
Db 2875 GTCGATATTGCTGGCCGCGCGGAAACACAGCAGTGAATCCCTACCGGCTTACCCTG 2934  
Qy 12520 CCGCGACGCTGTTGCGCAACAGTTATGACGCGACAGCAGATATTACCGTGGGGTTG 12579  
Db 2935 CCGGAAACGCTATTGACGAGCTATGATGATCAACAACTATTACCTCTGGTGAGA 2994  
Qy 12580 CAACAGACGAGTGACATCACTTGTTCATGCTGCTGAGGGCATTTGGTTGGGGTTG 12639  
Db 2995 CAAATAATAGCTGCGATCACTGACT-----GATGGGAAACTGGCGATAGGTTTA 3048  
Qy 12640 GCGAGCGCTGCGGGACGATGATTTACGTAATCTGCGGACAACTGCGGGAAGGGGT 12699  
Db 3049 CCGAATGCACAAACCGCGTATGTTTATCTTATGACCGGAGCAAAATTCACCGAAGGG 3108  
Qy 12700 CTGACGCTGGAACACCTGTTGGCGCCGAAAGCTGCTCGGATAGTCAAGTCTGCTACG 12759  
Db 3109 ATTTCCCTTGAATCTTGTGTAAGATGATGGCGCTGCTAGCAGATGAANAAGCGCGCT 3168  
Qy 12760 CTGCGGGTCAGACGAAGTCTGATCTGATTCACAAAGCTGTCACCGCTGCTGCT 12819  
Db 3169 TATCTGGGAACAACAGAGCTTTTACCGCGGTCAAGGGAAGTCACTCTAGAAAAA 3228  
Qy 12820 CCGCACTCCCGCCCAAGGTAGCTTTTATCGAAACCGCGTCTGATGAGGATGATGCT 12879  
Db 3229 CCCACGTTACAAGCACTGGTCCGCTTCCAAAGAACCGCCATGATGGACGATACCTCATTA 3288  
Qy 12880 AGTTCACTGCTGCTACATTTGGATGAACATCTCGAGCAAGCCGTTTACCGCAATCC 12939  
Db 3289 CAGCGGTATGAAGCGGTGATTTGAAGACGAAGATGTAATACCGCGCTGACACAGCGCGT 3348  
Qy 12940 GGATACCTTTTCCCTCGAGGACGGA-----AGCAGAACAGGCATTTGTGGACCCAGT 12993  
Db 3349 TATCAGCAAGTCGCGCGGTGTTTAAATACAGATCAGAAAGCCCGGTATGGCGGACCG 3408  
Qy 12994 CAGGATATGTTACTATGCGCGGACAGCATTTCTGGCTACCGCTATCTTTTGGGAC 13053  
Db 3409 CAAGGTTATACCGATTACGTTGACCGCGCACAGTCTTCTGGCGGCTCAGGCTCAGCGTAA 3468

Qy 13054 AGTATGTTGACCGGCCAGTTACCGTGACGCGTGACGCGTACGACTGCGTCAACGACG 13113  
Db 3469 TCGTTGCTGACAGGGAACACACACTGACTGGATACCCATCATTTGTGTAAATAACAG 3528  
Qy 13114 TGGCAGGATGCCGACAGGATTTGACCAACAGCGACTATGACTGGCGCTTCTCTGACGCC 13173  
Db 3529 ACTCAAGATGCGCTGGATTAACGACGCAAGCCATTACGATTATGTTCTTCTTACACG 3588  
Qy 13174 GTCCGGGTGACGACCCCAATGATTAATCTGCACTGCTGCTGATGCTGATGCTGCGCGG 13233  
Db 3589 GTACAACTGACAGATTAATGATTAATCAATTTGTGACTCTGACGCGCTAGTGTGCG 3648  
Qy 13234 GTACCAACCTGCGATTTCTGGGGCAGCGAATGTTATGCCACCGGTTACAGTGATGCC 13293  
Db 3649 GTAAACCAACAGCGGTTCTGGGGCAGAGGAGGACAGCCGAGGCTATTCACACGAG 3708  
Qy 13294 ACCTTGTGCGTTCGGAACGCGCAGCGCTCTGCGTTGACGCGCGCCCTTACCACTA 13353  
Db 3709 CCCTTCAACACCGGACTCCGTAGATAAAGCGCTGGCATTAAACCGGCGCACTCCCTGTT 3768  
Qy 13354 GCACAGTGTCTGCTGATGTCACGAGCAGTTGGGAGA-----T 13391  
Db 3769 GCCCAATGTTAGTCTATGCGGTTGATGCTGATGCGCTGCTGTTATCTTTGCTCAGCTT 3828  
Qy 13392 -----T 13392  
Db 3829 TCTCAGTCAACAGAGGACGAGGCTATGGGCGCACTGCTGCGCTCATATGATT 3888  
Qy 13393 GACGACAATGAGAAAATG----- 13410  
Db 3889 ACCGAAGATGGGAAAGTGTGCTGTTAAGCGGAAACAGAGAAACAGCCATCAGAACCTG 3948  
Qy 13411 -----CCCGCGACGTGGTCTG 13428  
Db 3949 ACGATTCAACTTATTTGCTATTGGCAAGTATTTCCCGCTTTTACCGCACATGACTGGG 4008  
Qy 13429 CTGGCTACCGATCGCTATGACAGTGATACCGGACAGCGTCCGCCAACAGGTGACATTC 13488  
Db 4009 ATCACCCTGATCGCTATGATAGCGATCCGCAACAGAGACCAACAGACGGTGAAGCTTT 4068  
Qy 13489 AGTACGCGTTTTGGGCGTGAGTTGCAATCGGCAACCGGACGCGCGGCAACGCGCTGG 13548  
Db 4069 AGTGACGTTTTGGCGGTTACTCCAGAGTTCACTGCTCATGATCAGTCAAGTGCCTGG 4128  
Qy 13549 CAAACGAGGACGCAACGCGCAAACTGGTGACGCGCAGTGACGAGTTCGCGTCACTGACGA 13608  
Db 4129 CAACTGTAAGAGGATGGCGGCTGGTCTGCTGATGCAAAATGGCGTTCTGCTCAGTGGCCCT 4188  
Qy 13609 ACGAATTTCCGCTGGGCGTCAACGCGGAGGCGGAGTGATGACAAATAAAGCTGCTGCTGTT 13668  
Db 4189 ACAGACCCCGATGGGCGGTTTCCGCTGCGACAGAAATATGACGACAAAGCCCAACCTGTG 4248  
Qy 13669 CGGGTTTATCAGCGCTTATTTCTGGCAGTTGGCAATATGTCAGTATGACAGTGCCTGG 13728  
Db 4249 CGTACTTATCAACCTTATTTCTAAATGACTGGCGTTACGTTAGTAGTACAGCGCAGCA 4308  
Qy 13729 CAGGACTGTATGCCGACAGCACTTTTACGATCCGACGCGCAAGGAAATGGCAGGTTATT 13788  
Db 4309 GATGACTGTTTCCCGATACCCACTTATGATCCATTTGGGACGCGGAATACAAAGTCACTC 4368  
Qy 13789 ACGGCAAAAGGTGAACGCGGACAGGCTGCTATACCCCGGTTTGTGCTGCTGCTGAGAC 13848  
Db 4369 ACTGCTAAGAAATATTTGGAGAAAAGCTGTACACCCCGGTTTATTTGTCAGTGAGGAT 4428  
Qy 13849 GAGAAATGATACCG 13861  
Db 4429 GAAAACGATACAG 4441

RESULT 15  
ACF65385 0  
WP Sequence split into 7 fragments LOCUS ACF65385 Accession ACF65385

WP Fragment Name Begin End  
 WP ACF65385\_0 1 110000  
 WP ACF65385\_1 100001 210000  
 WP ACF65385\_2 200001 310000  
 WP ACF65385\_3 300001 410000  
 WP ACF65385\_4 400001 510000  
 WP ACF65385\_5 500001 610000  
 WP ACF65385\_6 600001 618776  
 ID ACF65385 standard; DNA; 618776 BP.  
 XX  
 AC ACF65385;  
 XX  
 XX 20-NOV-2003 (first entry)  
 DT  
 XX  
 XX Photorhabdus luminescens nucleotide sequence #38.  
 DE  
 XX Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;  
 KW detection; food; gene expression; plant; animal; microorganism; toxin;  
 KW antibiotic; biopesticide; virulence factor; disease model; plague;  
 KW whooping cough; gene; ds.  
 XX  
 XX Photorhabdus luminescens.  
 OS  
 XX WO200294867-A2.  
 PN  
 XX 28-NOV-2002.  
 PD  
 XX  
 XX 07-FEB-2002; 2002WO-IB003040.  
 PF  
 XX 07-FEB-2001; 2001FR-00001659.  
 PR  
 XX (INSP ) INST PASTEUR.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 PA  
 XX Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;  
 PI Buchrieser C;  
 PI WPI; 2003-148459/14.  
 DR  
 XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,  
 PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.  
 PT  
 XX Claim 1; SEQ ID NO 38; 1205pp; French.  
 PS  
 CC The invention relates to the isolation of genes and their encoded  
 CC proteins from Photorhabdus luminescens. The isolated sequences are  
 CC sources of probes and primers for detecting the genome of P. luminescens  
 CC and related species; to study polymorphisms; for gene analysis and for  
 CC detection/amplification of the genes. Antibodies (Ab) raised against the  
 CC polypeptides encoded by the genes are used for detection/identification  
 CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that  
 CC carry a gene-containing vector are used to select compounds that  
 CC modulate, regulate, induce or inhibit expression of the genes in plants,  
 CC animals or microorganisms other than P. luminescens and are able to alter  
 CC response or sensitivity to toxins and antibiotics produced by P.  
 CC luminescens. Cells transformed to express the genes are useful for  
 CC recombinant production of the proteins, particularly toxins and  
 CC antibacterials useful as insecticides, bactericides and fungicides. The  
 CC genes, proteins, vectors containing the genes and Ab are also useful  
 CC therapeutically (to treat microbial infection by bacteria or fungi that  
 CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as  
 CC biopesticides. Other uses of the genes and the proteins are as virulence  
 CC factors and for identifying targets of human diseases for which P.  
 CC luminescens is a model (particularly plague and whooping cough). This  
 CC sequence represents one of the isolated P. luminescens genes  
 XX  
 SQ Sequence 618776 BP; 181854 A; 139249 C; 125634 G; 172037 T; 0 U; 2 Other;  
 Query Match 5.1%; Score 968.6; DB 10; Length 110000;  
 Best Local Similarity 53.9%; Pred. No. 1e-218;  
 Matches 2405; Conservative 0; Mismatches 1859; Indels 201; Gaps 12;  
 9586 AGGAGACTGAGCATGCAAAATCATCAAGACATGGCCATTACTGCCCCACGTTGCTTCC 9645

Db 26544 AGGAGTACTTTTATGACAGGATTCACAGAGATGATGATTAACCGTGTCTACTTCCAAA 26603  
 QY 9646 GGGGGCGGTGCGGTACCGGGGTCAAGGGGTGATATCGCGCGCGCAGGGCGGATGTTGG 9705  
 Db 26604 GGTGGCGGAGCTATCAATGGCATGGAGAGCGTAAGTGTCTGCGGCCCTGATGAATG 26663  
 QY 9706 GCGACCTGAGTATTCCTTGGTCCGGTTCAGCCCGGTTCGGGGTTACGCCCCCACTGGGGCA 9765  
 Db 26664 GCCACTCTATCTGCGCGTGGCCCTTTCGACTGGCAGAGGACTGCGCTGGATATCG 26723  
 QY 9766 CTTAATTATCACAGCGGTTCGGGGAACGCCCTTTTGGCATTTGGCTTGGGATTCGGCGGT 9825  
 Db 26724 CTGCTTTACAGCAGTAGTCAGGTAAACGGGCTTTTCGGTATCGGCTTGGCAATGTGCGCT 26783  
 QY 9826 GCTGCTGTCCAGCTGTACGCGCAACGAGAGCACCTTACCTACGATGATATCTGATGAATTC 9885  
 Db 26784 ATGACTATTAGCGGACGACCAACATGSCATTCCACAATACGTAATGACGACACGTTTC 26843  
 QY 9886 ACCGGTCCGACGGTGTGCTGTGCGGCACTACGCGTGTGCGGCACTGCGGCAACCAAGACA 9945  
 Db 26844 TTATCTCCACAAGGCGAAGTCATGAATATTTGCCCTTAATAACCAAGGCGCAACGATATC 26903  
 QY 9946 CGGCAGGCC--ACCTCACTACTGCGGATATAACCCAGGCGGAAGCTTCAACGTTCAAGTT 10002  
 Db 26904 CGTCAAGAGTTAAGACGCTGCAAGCGTGACCTTGGCCATCTCTATACGTTGACCCGC 26963  
 QY 10003 TACCGTTACGTPACGAGGGTGTCTCAGCCGCTTGAGCGTTGGCTGCCGCCGACGAG 10062  
 Db 26964 TATCAAGCCGCGCAGATGTTGAGTTCAGCAGAAATCGAATACTGGCAACCGGCTCCGCT 27023  
 QY 10063 ACAGAA---ACGGAATTTGGTGTATATACCCCTGACGAGCAGGTGCTCTGTGGGC 10119  
 Db 27024 CAAGAAGGACGCGCTTTCTGGCTGATATCGTACCAGCGGCAATGTCACATCTTAGGG 27083  
 QY 10120 CCAATGTGCGCAGGCTCGCATCAGCAACCCACAGCCCCAACACAGACGCGCGTTGGCTG 10179  
 Db 27084 AAAACGACAGGCTGTCTGCAATTCGCAAAATGATCAACAATGCGCCAGTGGTTG 27143  
 QY 10180 ATGGAGTCTCGGTATCACTTACCGCGCAACAGATGTATTACCAATACCGTCGGAAGAT 10239  
 Db 27144 CTGGAAGAAACCGTGCACCAACCGGTGAACATGTCACTTATCAATACCGAGCCGAAGAT 27203  
 QY 10240 GATGACGGTTGTACGAGCGGAGCGGACCGCGCGCTACCGCGCTACCGCGCGCTGTGTCG 10299  
 Db 27204 GAAACCCATTGTGACGCAATGAAAAAACCCGCTACCCCAATGCTACCGCACAGCGCTAT 27263  
 QY 10300 CCGGTGCGGCTCTGTTATGTTAAACCGTACGCGCGCTCGAGCGCTACCGCGCTGTGTCG 10359  
 Db 27264 CTGGTACAGGTGAATACGTTAAACATCAACCGCAACACGAGCTGTTCGTACTGGATAAC 27323  
 QY 10360 ACA---CCATCAATGATAGTGTGTTTATCTGGTGTGTTTATGTTATGTTGAGCGTAGC 10416  
 Db 27324 ACACCTCGACACCGGAGAGTGGCTGTTTCACTCTGTTTGAACACCGTGAACCGCAT 27383  
 QY 10417 TCGGTGCTCTGTAAGCGCGGCTCGGCAACACGAGGAGTGGGAGTGGTGTGCTG 10476  
 Db 27384 AGCTCACCTTCAACCGTCCGAAATGGGA---TGACAGGTACAGCAATGGCTGTGACGC 27440  
 QY 10477 CAGGATTTGTTTTCGGGTATGAGTTTGTGTTTAACTTCGCGACTCGCGCTGTGCGCT 10536  
 Db 27441 CAGGATATCTCTCTCGTATGAATACGGTTTGAAGTACGTACTCTGCGCTTATGCCAA 27500  
 QY 10537 CAGGTTTGTATGTTTCATTACCTAGTGTTCGCGGGGAGTTCGGGAGCGAATGATGG 10596  
 Db 27501 CAACTACTGATGTTTTCACCGTACCGGCTCATGGCGGAGAGCGGTACCACTGACGCC 27560  
 QY 10597 CCAGCATTTCTCGCTGTGCTGGACTACAGGGAAGTCTTCACTCACTGCTGCTC 10656  
 Db 27561 CCGGAACCTGGTGGACGCTTAATACTGGATTACGATAGAAATGCCAGCGTCAACCATG 27620  
 QY 10657 GAGAACGTGACAGGTGCTTATGAGTCGGAAGCGTCTTGTGCTTTCGCGGACCTG 10716



Db 27621 ATTCCCGCCCGCCAAATTGAGTCAAGAACCGGATGCGAGCCCAATCACTCTGCCACCAATTA 27680  
Qy 10717 GCATTGGGGTGGCAAACTTTACCCCGGACATTTGTCGGCATGCGCAGACGCGTGACGAT 10776  
Db 27681 GAGTTGGCTTGGCAGCGGTTCACTAGAGAGATGCCAATGCGCAACGTTTGTATGCA 27740  
Qy 10777 ATGGGCAAGTTGAGTTTCTTCAACCCCTATCAGCTTGTAGACCTTAAACGCGAAGGTGTG 10836  
Db 27741 CTAGATAATTTTAACTCGCAGCAACGTTTATCAATTTGGTTGATCTGCGAGGAGAAGGGTTG 27800  
Qy 10837 GTGGGTATCTGTATCAGGACAGCGGTGCTGCTGGTGTACGTTGACCGGTACGCCAGTCG 10896  
Db 27801 CCGGGTATGCTGTACCAAGATCGCGGTGCTTGGTGTATAAAGCGCCGCAACGTCAGGAA 27860  
Qy 10897 GGGGATGATCCGATGCTGTGACCTGCGGGCGGCTGCGGCCCTGCGCAAAATGSCCGCT 10956  
Db 27861 GACGGGATAGTAAATGCGGTCACTTACGACAAATTCGCCCACTGCTTACCCTACCT 27920  
Qy 10957 TTGCATTAACAGCGCATCTCTGGCGGATCTTAAATGGGATGGTGGCTGGAGTGGTCTGTT 11016  
Db 27921 TTGCAGGATAATGCTCATTTGATGATGATATCAACGAGACGCGCAACTGGATTGGGTAATC 27980  
Qy 11017 ACCGCCCGCGTGTGGCGGATGTATGATGCGACCCCGCGCGGCTGCTGGTGTGATTC 11076  
Db 27981 ACCGCTCCGGTATTCGCGGATACCATAGCCAGCAACCCGATGGAATAATGCAAGCACTTT 28040  
Qy 11077 ACCCCCTGTGAGCTTCCCGTGAATATGCGATCCAAAGCAGTGTGCGCGATC 11136  
Db 28041 ACGCAATCAATGCTTCCGAGTGAATATTTTCAACCAAGATCCAGTTCGCTGACCTT 28100  
Qy 11137 CTGGGGCTGGGTTAAGCGCATGCTGCTTATCGGGCGGCGAGTGTTCGCTCTATTC 11196  
Db 28101 ACCGGGCGAGCTTATCCGATTTAGTGTGATCGGGCGGAAGCGTGTCTGACGCC 28160  
Qy 11197 GCGAAACAGTGTGGATTAAGGGAGACCGGTGAGCAAAACGGAAGACTCACTCTG 11256  
Db 28161 AACAGCGAAACCGCTGGCTGTAAGGACAAAGATGCCCCAATCCACAGGTATCACTCTG 28220  
Qy 11257 CCGTCCCGGGTGTGACCAAGTACCTCTGTGCGTTCAGTGATATGGCTGGCAGTGA 11316  
Db 28221 CCGGTTACTGAAACCGACCGCCGCAAACTGGTGGCTTTCAGCGATATGCTCGGTTCGGT 28280  
Qy 11317 CAGCAGCATTTGACGAGAGTGTGCTTAATGGAGTACGTTACTGGCCAAACCTGGGGCAC 11376  
Db 28281 CAACAGCACCTAGTGGAAATCAGGGCTAATCGCGTCACTTGTGGCTTATCTGGGACAT 28340  
Qy 11377 GGTGTTTGGTCAAGCGGTGAATATTCGCGTTTATGACGAGTCACTAGCTTTAAC 11436  
Db 28341 GGGCGTTTCGGTCAACCACTGACCTGCGAGGATTTAACAGCCCGGAACTAGCTTCAAT 28400  
Qy 11437 CCTGACAGATATGCTGGCGGATACCGAGGTTCCGGTACCAAGGACCTGATTTATGG 11496  
Db 28401 CCGGAAACGGCTGTTTGGCGGATATCGAGGCTCCGGCCACCTGACATATCTATGCG 28460  
Qy 11497 ATGAGTGACCGGTAGTCAATTTATCAACAGAGTGTGAATATTTTCGCGAGCCGAT 11556  
Db 28461 CAATCCGGCTTTGCTCAATTTATCAACCAAGTGTGAATCAATTTGATGCCCGCTG 28520  
Qy 11557 ACGTGTCTTGGCGAAGGTGTCGCTATGATCGACCTGCACTGTGCAAGTGGCGGAT 11616  
Db 28521 ACGTTAGCTTGGCAGAAGGTGTAATTTGACAATCTTGGCAACTCCAACTGCTGTAT 28580  
Qy 11617 ATCAGGGGCTGGGGTGCCTAGCCTGTACTGACGCTCCCGATGTCGGCTCATCAC 11676  
Db 28581 ATTCAGGGCTTAGGGATAGCCAGTCTGATCCTGACGTGCCATATGCGCACCATCAC 28640  
Qy 11677 TGGGTGTCCATTTATCGGACAGAAACCTGTTGTTGATGTCATGAACAAATATG 11736  
Db 28641 TGGCGTTGCGATTTGCTGCTAACCAACCTTGGTTGCTTAATGTGATGAACAATACCGG 28700  
Qy 11737 GGGCCCGGATGCACTGCACTATCGGAGTTCGGTGTGAGTTCTGGCTGGATGAGAAAGCC 11796  
Db 28701 GGTGCACATCACACTTACATTTATCGTAGCTCCGCGCAATTTCTGTTGGATGAGAAATTA 28760  
Qy 11797 GAGGCACTGCGCGCAGGCACTTCCCTGCTGCTACTGCTCAATTTACATTTGCATACCTG 11856  
Db 28761 CAATCAACAAACAGGCAATCTCCAGCTTGTGTTACTGCGGTTTCAATGCTATGCTG 28820  
Qy 11857 TGCGTTTCGGTGTGAGAGATGAGTACACCGGTAAACCGTCTGCTGACGACGCTGCTTAT 11916  
Db 28821 TGCGCATACCGAAATTCAGGATGAAATCAGCGGTAAACCGGCTCAGAGTGCAGTCAGCTAC 28880  
Qy 11917 CCGCAGCGGCTTGGGACCGGAGGAAACCGAGTTCGGGGGTTTGGTTTGTGATC 11976  
Db 28881 AGCCACCGGTTTGGGATGTTAAAGACGCGGAATTCAGAGGATTTGGTTCGCTCAACAG 28940  
Qy 11977 AGGGATACCGATACCTTTGGCAACCGAGGTACCGCGACGGAATCTGAGTATGCTTCTGTG 12036  
Db 28941 ACAGATACCAACATTTTC---TCAGCGCACCGCCCGCAACAGCGGACCGTCAATTG 28997  
Qy 12037 AGCGGAACTGTGATGCCACCGGGTACCGGAGTAGACGAGCGTGTGCGGAGACGTAT 12096  
Db 28998 AGCATTTAGCTGTTTGGCACCGGATAGAGTACGAGTACAGCAATTTAGCCACAGAAATAT 29057  
Qy 12097 TGSCAAAACGATCCCGCGCTTTTGGCGATTTCCGACCCGTTTCACTGTCGG-----T 12150  
Db 29058 TGSCAGGCAATACTCAGGCTTATAGCGATTTTGAACCCGTTTATACCGTCTGGGATAAC 29117  
Qy 12151 TCAGGAGAGGATCAGCAGACATATCTCCGACGACAGCAAGACATTTCTGTTTGCAGCGA 12210  
Db 29118 GCTAACAGACAGTCAAGCATTCACCCCAATGAGACACACAGTAACTGGCTGACGCGG 29177  
Qy 12211 GCCTTAAAGGCACTGCTACGACCGAGCTCTACGGTCTGACGCAACGAGTCAAA 29237  
Db 12271 GATATCCCTTACAGGCTCACTGAGTCTGCGCCGACGAGTACGGCTAGTT---GAAGCGAAT 12327  
Qy 29238 ACGTGCCTTATACCGTCACTGAGTCACTGAGTACGCTATCAGTACGCTCTATTCGCCGTAGAGAAA 29297  
Qy 12328 GAGAGCTACCGGTGTGCGCGATGGCGCGGAAAGCCGTACGTCAGTTTATGAACGG 12387  
Db 29298 GAAACGAAATTTCTGCTGGGTGACTGCCATTTGAAATCGCAGTACCACTATGAACGT 29357  
Qy 12388 TACCACAATGATCCTCAATGCCAACAGAGCGGCTACTCTCTAGTGATGAATACGGTTTC 12447  
Db 29358 ATCATCAGTGATCCACAGCTCAGCCAGAGTATCCGACTGCAACACGATATCTTTGGTCAA 29417  
Qy 12448 CCACTGGTCAAGTGTCAATTTATCCAGAGCGCTCCGTCGCGGCAATCCATAT 12507  
Db 29418 TCACGCAAAAGTGTGATATTTGCTGCGCCACGCGCGGAAACCGCGGTAAATCCCTAC 29477  
Qy 12508 CCGCGTCTTACCGCGGAGCTGTTTGGCCAAACAGTTATGACGAGCAGCAGAGATTA 12567  
Db 29478 CCACCTACCTTCCGGAAGCACTATTCGACAGTAGCTATGATGACCAAGCAACAGATTA 29537  
Qy 12568 CGCTGGGTGTCACACAGAGCAGTGCACATCACTTGTGTTTCACTGTCTGAGGGGCAATTGG 12627  
Db 29538 CGTCTGTTGAGGCAAAATAATAGCTGGCATCACTGACT-----GACGAGGAAACTGG 29591  
Qy 12628 TTGTTGGGTTTGGCGGAGCGCTCGGGAGCAGTGTATTCAGTACTCTGCGGCAACAGCTG 12687  
Db 29592 CGATTAGTTTACCAATGCAACCGCGTGTATTTATCTTATGATGATGACCGGCAACAAATTT 29651  
Qy 12688 CCGGAAAGGGTCTGACGCTGGAACACCTGTTGGCGCCGAAAGCCCTGCTCGGATAGT 12747  
Db 29652 CCAACGAAAGGATCTCTTGTGAAGTCTTGTCTGAAAGCCGATGGCTTACTAGCAGATGAA 29711  
Qy 12748 CAGGTGCTGCTGCGGCTCAGCAGCAAGTCTGTTATCTGATTTTCAAGACGTTGCTG 12807  
Db 29712 AAAGCAGCGCTTATCTGGGCAACACAGAGCTTTTACACCCCGGTCAATCGGAGTC 29771  
Qy 12808 ACGTCTGCTCCGCACTCCCGCCCAAGTGTAGCTTTTATCGAAACGCGCGCTGCTGAT 12867  
Db 29772 ACCTAGAAAAGCCCGCTTACAGGCGCTGTTAGCGTTCGAGGAAACCGCCATGATGAC 29831





Db 5689 ATGGAGGAGATCTGTCAAGTGTACACAGCGCTCATTTCTTACCAACTGGGATAA 5748  
QY 5471 TTCAACAAAGCTTTACAGCACTGGGGGGGGTCTCAGAGCTGGTTTACTATCGGAAAC 5530  
Db 5749 TACAATAAAGCTTACAGCACTTTGGCGGGTATGGCTAAACTCTCTTACTATCCAGAGAAT 5808  
QY 5531 TACCTGACCCGAGCGTCCGTATCGGCGGACCGGCATGATGGACACCCCTGCTGCACTCT 5590  
Db 5809 TACATCGATCCGACGCTACGATATGGGCAGACAAAATGATGGATACGTTGCTGCAATCC 5868  
QY 5591 GTGAGCCAGAGCAGTATCAACCGCGATACCGTGGAGGATGCCCTTTAAAACTTCTGACC 5650  
Db 5869 ATCAGCCAAAGCCAAATTAATATCGATACCGTAGAAGATGCCCTTTAAATCTTACCTAAC 5928  
QY 5651 ACCTTTGAGCAGATGCGCAATCTGAACACTGTGACGCGGATATCAGATACGCGCAGCATG 5710  
Db 5929 TCATTCGAAACAGGTGGCTAATCTGGAATCCTCAGCGCCTACCATGACAACTTAATAAT 5988  
QY 5711 ACGCAGGGACTACATGGTATGTGGTGGCGAGCATCACAGATCAGACTAAGTGGTACTGG 5770  
Db 5989 GATCAAGGATTAATCTTATCTTATCGGACCGTAGTAAACAGAAAGTGAATCAATATTATTGG 6048  
QY 5771 CGCAGCGCCAAACACAGCAAAAATCCAAGACTCAATGATGCCCGGAATGCCCTGGACCGGA 5830  
Db 6049 CGCAGTGTGGATCACAATAATCCAGCGAAGTAAATTCGCCGTAAATGCCCTGGAGTGA 6108  
QY 5831 TGACAAAAATTAATCGCGGAATGAATCCGTGGTGCAGATCTTGTGTGCTCGGTGTTTTTC 5890  
Db 6109 TGTACAAAAATGATTTGTCATTAACCCCTACAAAGACTATTCCACCGGTAAATTTTC 6168  
QY 5891 AACAGTCGGCTTATCTGCTGGGTGGAAGAAATCAGTCTGCTGATACGAGGACAGAG 5950  
Db 6169 CAACTCTGGCTGATCTTATCTGCTGGACAAAAAAGGCGACTAAACAGGAAGTGA- 6227  
QY 5951 AGCAGCAACAAACACGAGCAGAGCTACAGCTGAAACTGTGTTCCGGCGCTACGACGGT 6010  
Db 6228 --TAAACCGCTCGGGTTATTATTAATGAATGAATTAAGCGATATCCGTTATGACGGC 6285  
QY 6011 ACATGAGTTCCCGGTGCTGTCGACATTAACCGGCAACATCGC-----ATTTCCGGA 6063  
Db 6286 ACCTGAATACACAGCTACCTTTGATGTAACCAAAAAATATCCGATTTAAATCTGGGA 6345  
QY 6064 AACCGAGGCGATGATGCTGCTGATATCCCTGACTGAGCAGCTCTATTGCGGTTTTA 6123  
Db 6346 AATAAACACCTGGACTTACTGCTCAAGCTTCAAGCGAGAGATGAATGCTGGTGA 6405  
QY 6124 CTCCTGTACACGCAAGCCGGACTTTGATTAACGCTCAGCTGATTTCTGTGGATAATGATAT 6183  
Db 6406 TTTTATAAAAAACAAGATCAATTAATCAATACACAAACACAGTACCATAAAGACTA 6465  
QY 6184 GAGCTAAATGTCATCTCAGATATAGGATTTTAAAGCGGTGTCAGTACGAATTTAATAC 6243  
Db 6466 TATATCACTTCCAATATGCTCTTAAGGAAATGACAC-CTGAAAAATCACAAACCTAACGC 6524  
QY 6244 GAGCACTGAGAAATTTATTAATATGCTTTTTCAGACCCCTCCGCTAATTTATTTGTCAG 6303  
Db 6525 TTATAACAGTTTGAATTAATAGTATTAATGTTGTCATTAATTCGATGTCGATAAGTAA 6584  
QY 6304 TGCAACGAGTTTAATTTGATGATGTTATCCACAGCGATTTCTCACTCTTAAATTTCTAAAA 6363  
Db 6585 CGAAATCCCTTCATCAGTAAATAGTAAATACGGTTATGATGGGGAGATGGCTATCTGAG 6644  
QY 6364 TACAAGTACTGTTTTTACTAAGAATTCCTCTCTTTTGAAGCCGAGAGCTTCATATTAC 6423  
Db 6645 TATGGTGTATGGCGGAAATATTTTCAAGCAATCAAACTGGAGTCTCTCATCAGATAAGTTAA 6704  
QY 6424 AGCAATGTTTCGTGTTTTTGTAGTACTGCTGCACTCGCCACTCAATCTACCATAGAA-- 6481  
Db 6705 ACTCTCACCAAGTTTAAGAAATTAATCATATGAGCTTTGAGCCGCAACCGCAACCAATG 6764  
QY 6482 AAATTCGTTTACGAGGAGTAAATTTGAGGAAATTAATTTTATGAGCCGAGCGCCGCC 6541

Db 6765 CAACCTGATGAAGAAATACGCTCAGCTTGGTGATATAAATTTATTTATTTACTACTCTAGG 6824  
QY 6542 GCGGATTTGACGGAATTTGTGGAGTGGATGTTTCTAATTTCAAAAGTAT-----ACCAGG 6596  
Db 6825 TATTAACCCCAATAATTTGTGGAATAAAAAATTTCAATTTACCCTGTTTATCAGTATAGTGG 6884  
QY 6597 TCGGAAAAAGACGAGTGGTGCTCACTGTAAATCTTATTTCCGCTCACTGCGGTTAGTGTT 6656  
Db 6885 GAACACTACCAATATGAGAAAGAGCTGCTGCTGTTTTATCGAGAAAGTACTACTAATTT 6944  
QY 6657 CTGTTGAGTTATTTATGATTCATCAAAATAAATACTTTCAGCGGAAATTTTGTGAGATAAA 6716  
Db 6945 TGTAGAGCGCTGGTTCCCTTAACTTCCCTCTCGCTCTCAAGAAATGTCACACCACTCG 7004  
QY 6717 TGATTAACCGCTTTAATTTAGCGGCACTCATCAAAAGTTTAATTTACGTGCTGCTTATTTGGCT 6776  
Db 7005 CGGTGACATTTAGTGTAACTATGTTTATTAACAAACATAGTACGATGTTCCATTT 7064  
QY 6777 CTCAGATTTTGGAGTGTAAAGTGCCTCATGCTCGGCACCTTCAGATATATGATTAATACG 6836  
Db 7065 TAAACAATATTTCTATATGATGACCAAGTGTATTTGACACTGATGTTTTCAGGATATT 7124  
QY 6837 ATGATATCATACTGACATCCGCGGTAAATGGGACTGAAATTTAAATCTTGGCCTTCGCTG 6896  
Db 7125 ATCTATTAATACGAACATTAATCAATTCAAAAGTTAAAGTAAATAGTGAAGCCGAAGTAT 7184  
QY 6897 AATGTTAATGATTAAGTGTAGTCTGCAATCCGGGAAT-----AATCTTTTCAACAC 6948  
Db 7185 CACAGAGCAAACTTTTGTAGCGAGGAAACAGATAATGTCGCCCAATTCGCTCCGCTT 7244  
QY 6949 CAAATCGCTGAGTTTTACGGTTAATACCACTGATATTTGTT-----GAAGA 6993  
Db 7245 CGAAGAAATGAATATCAGTTTAAAGAGCTTGAATAGATATCTCCACACTGACATTTCA 7304  
QY 6994 TGAGTTTGAAGTGAAGTTTACGTTTACCGCTGCTCGATCAGATAAAGCTGCTGCGCCGC 7053  
Db 7305 TAAATGAAGCAAGTATTGATATCACCTTTATCGATTTGCTGAGAAATTTGACGATAA 7364  
QY 7054 CCGGAGCGGCATATTAAACCGTCAITTCGAAACATTAATTAATGACACTTCCGTTATGCAATT 7113  
Db 7365 TAGTATGATCGTAACTTAGCGGAAGAACATTTTCAGTATTCGTATTTATCAAAAAACGGA 7424  
QY 7114 ACGTAAAAATACGCTGGCGGCGAGTATTTCTGCTGCGGTAAACGATGTG---- 7168  
Db 7425 AACTGATTAATGCCCTGACCCCTGACCAATATGCAAAACGGGGCGCAATATATCGATGGGG 7484  
QY 7169 -----GCGCTTATTCGCTCAACACACCTCTTTGCGCCCAACTGGTCGACGCGCGGAATAC 7224  
Db 7485 AAACCTTTGTTATTCGCTTAAATACGCTATTTCGCCGTCAATTTAATTAGCGGACCAACGC 7544  
QY 7225 CCGGATTTGACACCATTTTTCATGAGACCCAGAGGCTTACCGAACCCGCGCTTGAAGA 7284  
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QY 7285 GGGGAGTGAATGTTT-----ATGAGCTTCTCGGAGCAATGCCCTCTATTTCG 7335  
Db 7605 AGATCTCTGATGCTATGGAACCAATGAGCTTCAACGGCGCAACAGGCTCTATTTCG 7664  
QY 7336 GGAGCTGTTTCTATTACAGCCGATGATGTTTCCAGCGGTTTGTTCAGGAAACAGACATT 7395  
Db 7665 GGAAGTCTTACTACACCCCGATGCTGATTCCTCAACGTTTGTGTCAGCAACAAACATT 7724  
QY 7396 CCGGAAAGCCACCGCTGCTGCTGATGTTGTTGAAACCCGCGCGGCGGACGCTGTTAAACGG 7455  
Db 7725 CGATGAGGCTAACCGTTGGCTGAAATATGCTCTGGAACCCCATCCGTTTATTTGTCAATGG 7784  
QY 7456 GGTGCTGAGAAATTAACCTGGAATGTCGCTCGCTGGAGGAGGACACCGCTGGAACGA 7515  
Db 7785 TCAATGCAACATTAACCGCTGGAATGTTGCGCCCATTAAGAAGACACTAGTTGGAACGA 7844  
QY 7516 CTCGCGCTGGAATCCATTTGACCCCGATGCAATAGCCCACTAGTACGCCCATCAATTTACAA 7575  
Db 7845 TGATCCGTTGGATTTCAATTTGATCCCTGATACCATAGCTCAACATGATCCAATGCACCTACAA 7904

Qy	7576	GGTGGCCACCTTTATGTCGTACCTCGACCTGCTGATTTGCCCGGGTGTATCCCGCTACCG	7635
Dd	7595	AGTCGCCACCTTTATGCGCACCTTAGATCTGTTGATCGAACGGGGAGATTACGCTATCG	7564
Qy	7636	GCTGCTCGAGCGGACACCTTTAACGAGCGCCGATGTGTAGTCGTGACGCGCTTGACCT	7695
Dd	7965	CCAAATTGGAGCGGACACCTCGCTGAAGCCAAAATGTGTATATGTCAGGCACTGCATCT	8024
Qy	7696	TCCTGGGCGAGCGCTTATATTTCTTTGACGCGGACTGTCGCGGTGACCTGGGTGA	7755
Dd	8025	ATTGGGTGATAAACCCTCATCTACACTCAGTTGAGCAATGAATGATCCAGAGCTAGAAGA	8084
Qy	7756	CGCAGCGAGGAGTGACGCGAGCGGATTAACAGGAGCGCTGTCGCGCGGT	7815
Dd	8085	GGCGCAGCTCTTGAANAACAACAGGCACATGCCAAGAAATAGCAGATTACGACAAG	8144
Qy	7816	GGTGCCCGCTCCGAGACACGAGCGGCGAATTCCTGACGGCACTGTTCTCCGCGAGCA	7875
Dd	8145	ACTTCTTACATCCACAGGGCTAAAGATGAAATCAAAACAGATCTTTTCTCGCGCAAGT	8204
Qy	7876	GAACGAGGTCTCAAAAGGCTACTGGCAACCTTTGGCACGCGGCTCCATAACCTGGCCA	7935
Dd	8205	CAACGAAGTGATGCTGAGCTACTGGCGAAGAACTAGAAACAACGGTGTATTAACCTCGGCCA	8264
Qy	7936	CAACCTCTCAATTGACCGCGCGCTTTCCCTGCTCGCTAGCGCAACGCGCTCCGAACC	7995
Dd	8265	TAACCTCTTATGATGTCACCTTTACATTTGCTATTTTTCGCAACACGAGAGATCC	8324
Qy	7996	GTCGCGCTCGAGAGTCGCTGTCACAGCGCGAGGGTGTGTCAGACACTGCGCGCGC	8055
Dd	8325	AAAAGCGCTGCTCAGCGCGCTGTCGCGAGTTCACAAAGTGAAGTAATCTTCATCAGA	8384
Qy	8056	GGTGATCCGCTTTACAGTTTCCGGTTCATGCTGGAGAACCGCGGGATGTGAGCCT	8115
Dd	8385	ATTATATCAGTGTGGCGTTTCCCTCATATGCTGGAAGAACGCCGATGATGTGCTCA	8444
Qy	8116	GCTGACCGGTTCGGCAACACACTGCTCGGTATTTACCGAGCGTCAGGATCGGAGGCGCT	8175
Dd	8445	GCTAACCCCAATTCGGCTCCACATTTGCAAAATATTTATCGAACGTCAGATCGGAGGCATT	8504
Qy	8176	GGCCAAATCTGTGACAGCCAGGCACTGATGATAGCGCAGCGCTTCGCGAGCAGGA	8235
Dd	8505	AAACACGCTGTGCAAAATCAGCGCGCAGAACTGATATTGACCAATCTCAGCATACAGA	8564
Qy	8236	TAACGCTCTCGAGAAATCGATCGGATATTCGCGCTCGAGGAGCGCGCGCGC	8295
Dd	8565	CAAAACCATCAAGAGCTGTGCTTCCGTCGTGGAAGAACTGTGCTAGAAAAAACCGCGCGAAC	8624
Qy	8296	GCAGATCGTGTGAAAGTGTGTTGATAGAGCGGAGCTCAACACCGCGCAAAA	8355
Dd	8625	CCAGTCGCTTTTGATAGCTACAGCAATTTCTACGATGAAGACATCAACGCGGTTGAAA	8684
Qy	8356	ACAGGCAATGACTGTGACTCAGTTCGTCCGTGCTGCGGCACTCAACCGCGCTCTTT	8415
Dd	8685	ACAGGCAATGGCGTGTGCTTCCGTCGTGGCATCTCTACAGCCCTTCAAGCATCACA	8744
Qy	8416	TTTGGCGAGCGCGCGCCGATATGCTGCCCAATATTTAGCGGCTGCGCGTCCGGGCTC	8475
Dd	8745	TCGTGGCGGCGCAGCATTTATCTGCGCGCCCAATCTTCGGCTTCGCTGATGTGGCAG	8804
Qy	8476	CCGCTATGGGCGACTATTAAAGCCACCGCATCGGCATCCAGGTGCTCCGATGCCAC	8535
Dd	8805	CCGTGGGGGGCGATCCGCCAGCCACAGGTAATGTCTAGGATTTCTCCGCCAGTGTAT	8864
Qy	8536	CCGCATATACGCGCAAAAATCAGCCAGTCGGAAGTGTACCGCGCTCGCGGGAGGATG	8595
Dd	8865	GAACACGAAGCGGATAAATCAGCCAACTCTGAAGCCTACCGTCGGCGTCTCAGGAATG	8924
Qy	8596	GGAAATCCAGGTCATAGTCGAGTCTGAGTGGCGCAGATTGATGCCAGCTGGCGGC	8655
Dd	8925	GGAAATTCAGCGTAAATACCGCGAGGAGGAGCTGAAACAAATCGATGCTCAACTTGGTTC	8984
Qy	8656	CATGGCAGTCGCGCGGAAGGGGCTGAGCTGCAGAAAACTTACTTTGAGACCAGCAGAC	8715
Dd	8985	GCTGGCAGTCGCGGTGAAGCGCAGCTATTTCAGAAAAACCAGCTTAAAAACCAACA	9044
Qy	8716	CNAGGCACAGGCGCAGTTGGCATTCTCGCAGAGTAAGTTCAACAATACGGCTCTGTACAG	8775
Dd	9045	GCAGACTCATGCAACAACCTTCTGCAACAATAAGTTTCAGTAATCAGCGCTGTACAA	9104
Qy	8776	CTGGCTCGCGGGCAGGTGTCGCGCAATTTATACCAAGTTCTATGACTGCGCAGTATCCCG	8835
Dd	9105	CTGGCTCGGTGTCGATTTGTCGCCAATTTACTTCCAGTTCTATGATTTACGGTAGCTCG	9164
Qy	8836	CTGCTGATGGCGCAACAGCCCTGGCAGTGGGATAAATTCGAGACTAGGTGCG---TTTAT	8892
Dd	9165	CTGTTTGTGGGGAATGGCCTATCGCTGGGAGACTAAGATACCGCATCACGCTTTAT	9224
Qy	8893	CNAGCGGGGCTTGATGGGGCAAAATGCGGTCTGTGGCGCGGGGAAACCTTGATGCT	8952
Dd	9225	CAAAACCGCGCTGCGAGGAAACCCATGCGGTGCTCGCGGGTGAACCTTAATGCT	9284
Qy	8953	GAATCTGGCGCAGATGGAGCAGCGCTGTGACGGGGGATGACGGGCAATAGAGGTGAC	9012
Dd	9285	GAATCTGGCACAGATGGAAGATGCCCACTGAAACAGGATAAACGGCTACTGGAGGTAGA	9344
Qy	9013	GGGACGCTGCTGCTCGGAGGTCTATACAGCCTCGCGGAGGATCGCGCATTTCTCTCT	9072
Dd	9345	ACGTACCGTTTCGCTGCGCGAAGTCTATGCCAAATTTACCGCAAGAT---AAATTTATCCT	9401
Qy	9073	GGCGGACAAGGTGGTGGAACTGTGTAGTAACGGTTTCGGGAGTTCGGGTACGAAAAAGCAA	9132
Dd	9402	GACTCAGGAAATAGAGAAGTTGTGTAGTAAGTTTCAGGCGAGCGCGCAAGCAATAA	9461
Qy	9133	CGGATTTACAGAT---GCATCAACAGCAA-----CTCAGGCCCACTGAAACTGGCTGA	9183
Dd	9462	TAAGCTGGCGTTAGTACCAATACCAATACCTCTCTAGAACGCTCAATTCGTTATCTAC	9521
Qy	9184	CCTCGGTATCGGCAACGATTTACCCGCTCTCCCTTGGCAACCATGAGGCGCATCAACAAT	9243
Dd	9522	CTTGAACATTTAGCAGCGATTATCCTGATTTCTATTGGTAAAAACCGCTGATTAAACAGAT	9581
Qy	9244	AGCGTACGCTCCCGCGCTGTGTCGCGCTATCAGGAGCTCGGTGCGGTTCTCAGCTA	9303
Dd	9582	CAGCGTTACCTCTGCCAGCACTGCTAGGACCTATCAGGATGTGCAAGCAATTTCTGTCTA	9641
Qy	9304	CGCGCGAA---GTATGCTCATGCCCGGGTTCAGCGCTGCGCGCTCTCACACGGAAT	9360
Dd	9642	CAGCGAAAAAGCCTCTGAATTTGGCTGAAAATTCATTAAGCGGTTCTCATGGAT	9701
Qy	9361	GAACGACAGCGGCCAATTCCAACTGGATTTCATGACCCGCGTTACTCTGCGTTTGAAGG	9420
Dd	9702	GAATGACAGCGGTTCAGTTCCAACTGGATTTCACGATGCAAAATTCCTGCGGTTCGAAGG	9761
Qy	9421	ACTTCCAGTTGATGACAGGAGCCCTGACACTGAGCTTCCCGGATGC-----	9468
Dd	9762	AATCAAAATCGATGA---AGGTACGCTGACATTTAGCTTCCCAATAGCAATTTAGTAAAGA	9818
Qy	9469	-----TGACGGCAAAACAACAGCGGATGCTCCTCAGTCTGAGCAGCATCAT	9513
Dd	9819	AGACAAAAAAGAGCAAAAAAGGCAACAACAGCCATGCTGGAGAGTCTGAACAGCATCAT	9878
Qy	9514	CCTGCATATCCGTTACACCAATTTACAGCTGATAGGTATCAACATAGCGCA---GGCCCC	9569
Dd	9879	TCGTGATATTCGCTACACCATTCGCCAATAACGATTTTAAATTAAGTCTTAAACAGCGCCC	9938
Qy	9570	CGAACGAGGCGCTCGAGGAGACTGAGCATGCAAAATCATCAAGACATGCGCCATTACTGC	9629
Dd	9939	CTAAGCGGGCGCTGCAAGGAGTCTTT-CATGCAAAATTTCAAGATTTTCAAGTATTACAGA	9997
Qy	9630	CCCCAGTTGCTTTCGCGGGCGGTGCGGTTCACCGGCTCAAGGGTGATATCGCGCGGC	9689
Dd	9998	ACTATCATTTGCCCAAGGAGGAGCGCTATTCACGGGAATGGGGGAAGCTTTTAAACCCCAAC	10057
Qy	9690	AGGGCCGATGTTGCGGCGACCCCTGATATTCTCTTCCGCTTATGAGCCCCCGGCGGTTA	9749

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 Db 15856 TCATCTCAGACCGATCGGAAAGGAAACATTCAGAGGCTAACCTATGATGGCGGGCAGC 15915  
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 Db 15916 TAAACGGAGCTGTTAACTTTAAAGAACCAACCGGAAACAGTGTATCAGATCCCTGA 15975  
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 QY 15534 TACTCAGCGTCAATTAACGATCGGAGAGACCGCTTCTGGCGTAACAGAAAGTGGTAC 15593  
 Db 16144 TCATCAGTATCCGTAAATCGCAGAAAGCACCCGCTTCTGGCAATCAAGAAAGTGGCGC 16203  
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 QY 15654 TGGCAATGCGCGCAGCAGGCAACGACTTACATTCGCTTACAGCCCCCTTCTCTACAG 15713  
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 QY 15774 CCGCAGTGGCCCACTGCTCCCTGCGCAACGAAACAATAATATATACGACAGACATCACGTTA 15833  
 Db 16378 CTAAATCCAGCACAGTTTACCGGCGACGCAAAACAATACACCAACAACATCACGTTT 16437  
 QY 15834 GTGACCGCAGCAATAGGCGGTACTGAGCACTGTCGGGAGTGGCGTCAAGTGTGATA 15893  
 Db 16438 CTAACCGGAGCAATCGCGAGTACTCAGCACTCTGACCGAAGATCCGGCGCAAGTAGATG 16497

QY 15894 TGCTGTTTCAGTGCAGGAGTACACAGAGCACCTGCGAGCGGGGCAAGCACTGCTGTGGA 15953  
DB 16498 CTTTATTTGATGCGAGCGGACATCAGAAACAGCTTGATATCAGGACAAAACCTGACTGGA 16557  
QY 15954 CGCACGTGAGAACTCAAAAGGTGACACCGGTGCTGCTGATGAGGGGGGCG---GGAACG 16010  
DB 16558 ATACACCGGTGAACTCAACATGTCATTTGTTGAAACCGGACAAAGGGCGCAATGATG 16617  
QY 16011 ACAGCGAAAGCTATCGGTATGATGCGGCGAGTCAGCGTATTATCAAAACCGGACGCGG 16070  
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QY 16071 AAATGCGCAACAACTTCAGACACAGCGGGTGTGTACTCCCGGGGCTCGAGTTACGTA 16130  
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QY 16131 TCATGGCAATGGCGTACGCGGAAAGAAAGCCTGCGAGTTATTACCGTGGGCGAGGCTG 16190  
DB 16738 TAAACAAAACAGCAGCATCACACCGAAGATTTGCAAGTTATCACAGTAGGAGAGCGG 16797  
QY 16191 GCGGGCACAGTCCGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 16250  
DB 16798 GTCGGGACAGGTACGAGTATTAATTTGGATAGCGGTCAACCGGAAGATATCGACAATA 16857  
QY 16251 ACTCGTGCCTTACAGTTACGATAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 16310  
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QY 16311 AGGTTACCTTATCAGTGAGAGAGGTTTACCCGTTATGCGGAAACCGCTGTTCTGACGG 16370  
DB 16918 AAGGAGAAATATTAGTGAGAGAGTACTATCCCTATGCGGCGACGCGATTATGGGCAA 16977  
QY 16371 CGGAGTGAGTTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 16430  
DB 16978 CAAGGAGCGGACAGAGCCAGTTATATAAACCATTCGTTATTCAGGTAAGAGCGGGATG 17037  
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QY 16491 CCAGGACCGGCGAGGACCGGTGGAACGGGTGAACCTGTTCCGATGCTGCGGAATAATC 16550  
DB 17098 GTCCGATCCGCGAGGACAGTAGATGGTTGAATTTATATCGATGGTAAGGAATAATC 17157  
QY 16551 CCGTCACGCTGTTGA 16566  
DB 17158 CGGTTACTGCTTGA 17173

## RESULT 2

US-09-817-514A-3  
; Sequence 3, Application US/09817514A  
; Patent No. 6639129  
; GENERAL INFORMATION:  
; APPLICANT: ffrench-Constant, Richard  
; APPLICANT: Bowen, David  
; APPLICANT: Rocheleau, Thomas  
; APPLICANT: Waterfield, Nicholas  
; TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS  
; FILE REFERENCE: 61645  
; CURRENT APPLICATION NUMBER: US/09/817,514A  
; CURRENT FILING DATE: 2000-03-26  
; PRIOR APPLICATION NUMBER: US 60/191806  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 4431  
; TYPE: DNA  
; ORGANISM: Photorhabdus luminescens  
; FEATURE:  
; NAME/KEY: CDS

LOCATION: (1)..(4431)  
US-09-817-514A-3

Query Match: 5.9%; Score 1108.8; DB 4; Length 4431;  
Best Local Similarity 56.8%; Pred. No. 3.6e-298;  
Matches 2493; Conservative 0; Mismatches 1732; Indels 225; Gaps 12;

QY 9598 ATCAAAATATCATCAAGACATGGCCATTACTTGCCTCCCACTGCTGCTTCCGGGGCGGTGCG 9657  
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QY 9658 GTCACCGGCTCAAGGGTGATATCGCGGGCGGAGGCGCGGATGCTGCGGACCCCTGAGT 9717  
DB 61 ATTACCGGTATGGTGAAGCATTAACACAGCGCGCGGATGCTGCTGCGGCTTATCC 120  
QY 9718 ATTCCCTTGGGTTAGCCCGCTGCGGGTTAGCCCGCCACCTGCGGACCTAATTAATCAC 9777  
DB 121 CTGCCATTACCCATTTCCCGCGGGCGTGTATACGCACTCTGCTCACTCTGAAATTAAC 180  
QY 9778 AGCGGTCGCGGAAACCGGCTTGTGGCATTTGGCTGGGCTATCGCGGCTGCTGCTGCTG 9837  
DB 181 AGTGGAAACCGGTAACAGCCCATTTGCTCGGTGGGACTGCGGCTGCTGCGCAATTCGT 240  
QY 9838 CGTGTACGCGCAACCGGAGCACCTACTACGATGATATCTGATGAATTCACCGGTCCGGAC 9897  
DB 241 CGTCCGACAGTACCGGCTGACGAAATACGATGAACCGATATCTTCTGCGGCGCGAA 300  
QY 9898 GGTGAGGTGCTGCTGCGGCACTCAGCGCTGCTGCGACCCCAAGAGCAAGGAGGCGCAC 9957  
DB 301 GGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
QY 9958 TCACTACTGGGATAAACCAGCGGAGCTTCAAGCTTCAAGCTTACCGTTCACGTAACG 10017  
DB 361 TCATTCAGGCACTCAATTTGGTGGCACTTCCCGCTTACCTGTTATCGCTCCGCTA 420  
QY 10018 GAGGGTAGTCTCAGCGCTTGGAGCTTGGCTGCTGCGCGCGAGACAGAAACCGAATTT 10077  
DB 421 GAAAGCCACTTTAAACCGGTTGGAATATGCAACCCCAACCAACCGCGCAACCGATTTC 480  
QY 10078 TGGGTTATATACCTTACCGGACAGGTGGCTGCTGCTGCGCGGAAATGCGGAGCTGCG 10137  
DB 481 TGGCTGATATACAGCCCGGACGAGGCTTCAATTTACTGGGCAAAATCTCAGGACGCT 540  
QY 10138 ATCAGCAACCCACAGCCCAACACAGAGCGGGTTTGGCTGATGAGTCTCGGTATCA 10197  
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DB 661 GACGAGCTAGCAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720  
QY 10318 GGTAAACCGTCAGCGGCTCGGAGCTACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 10374  
DB 721 GGAACCTGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780  
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QY 10495 TATGAGTTGTTTAACTGCGGACTCGCGGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCT 10554  
DB 895 TATGAGTACGGTTTGAATTTGGCTGCTGCGGCTTATGCGGCGGCGGCGGCGGCGGCGG 954  
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Db 955 CGTCTACAAACCTATCTGGTCAGGCAAAAGGGGATGATGAACCTCGCTAGTGTGCGGT 1014  
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QY 11155 GACATGCTTATCGGCGCGCAGTGTGCGCTTATTCGGCAAAACGATGGTTGG 11214  
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QY 11395 GTGAATATTTCCCGGTTTATAGCAAGTCACTACGTTTAAACCTGACCAAGATTTGCTG 11454  
Db 1795 ATCGTATTCGCGGATTCAGCAATCTGCGCCAGTTTAAATCTGATCAGTTTCACTG 1854  
QY 11455 GCGGATACCGAGGTTCGGTACCAAGACCTGATTTATGCGATGAGTACCGGTTAGTC 11514  
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QY 11515 ATTTATTTCAACAGAGTGTATATTTTCGCGAGCCGATACGTCGTTCTTGGCGAAA 11574  
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Db 1975 GGCCTGCGTTTGTATGATACCTGCCAGTTGCAAGTAGCCGATGTAACAAGGTTAGCGTT 2034  
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QY 11695 GCAGACAAACCTCTGTTGTTGATGGCATGAACAAATATGGGGCCCGGATGCACCTG 11754  
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QY 11755 CACTATCGCAGTTCGGTTCAGTTCCTGGTGTGATGAGAAAGCCGAGCACTGCGGGCAGGC 11814  
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QY 11815 AGTTCCTCTGCTCTACCTGCCATTTACATTTGCATACCTCTGTGGCTTCGGTGTGACG 11874  
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Db 2275 GATGAATCAGCGGCAATAAGTTAGTACCACTGTTATGCTCACGGCGCTTGGGAT 2334  
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Db 2335 GGACGTGAACGGGAATTTTCGTGCTTTCGTTATGTTGACACAGACAGCATCAACTC 2394  
QY 11995 GCAAGCAGGTTACCGGACGGAACGTAGTATGCTTCTGTGAGCGGAACTGTGATGCC 12054  
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QY 12115 GCTTTTTCGCAATTCGCGACCGCTTCACTGTGCGTTTCAGGAGAGGATGAGCAGATAT 12174  
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QY 12349 CCGATGGCGCGGAAGCGGTACGTGTTTATGAACGATACCAATGATCTCAATG 12408  
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QY 12469 AATTATCCACGACCGCTCCGTGCGGCAATTCATATCCGGCTTCCTTACCGGAGC 12528  
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QY 12709 GAACACCTGTTGGCGCCGAAAGCTGCTCGGATAGTACGTCGTTACGCTGGGGGT 12768  
Db 3106 GAAACCCCTGTGCTGAAATATAGCCTGATTCGCGATGATAAACCTCGCAATACCTCAAT 3165

QY	12769	CAGCAGCAAGTCTGGTATCTGATTCACAAGACGTTGGCCACGTCGCTGCTCGCCCACTC	12828
DB	3166	CAGCAACGAAAGCTTCTATACCGACGGGAATAACCAACACCGCTGAAACACCGACGGA	3225
QY	12829	CCCCCAAGGTAGCTTTTATCGAAACGGCGCTGCTGGATGAGGGTATCGTCAGTTTCACGTG	12888
DB	3226	CAAGCGTTAATCGCCTTTACCGAAGACGGCGGTATTAAACGGAATCTCTGTTATCCGCGTTT	3285
QY	12889	GCTGCCCTACATTGTGGATGA-----ACATCTCGAGCAACGCGGTTACCGGCCAA	12936
DB	3286	GATGGCGGTATTACGCCAGACGAATTAACCGGAATACTGCACACGCGCGGATACCAACA	3345
QY	12937	TCCGGATACCTTTTCCCTCGAGCGCAGGAAGACAGAACAGGCATTTGTGACCCAGTGTGAC	12996
DB	3346	GAGCCTTATCTGTTTCCACGCAACCGCGAATAA-----AGTTTGGGTAGCGCGTCAA	3399
QY	12997	GGATATGTTACCTATCCCGCGGCAGAGACATTTCTGGCTACGCTATCCTTTTCGGGACAGT	13056
DB	3400	GGCTATACCGATTACGGGACGGAAGCAATTTTGGCGTCTGTGCGACACAGCTAACACGC	3459
QY	13057	ATGTTACCGCGCCAGTTTACCCTGACCGCTGACGGGTACGACTCGGTCATCACGCACTGG	13116
DB	3460	CTGTTAAACCGGGAATGACGTTTAAATGGGATATCTCACTATTGTTGTCATCACCCAAACC	3519
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DB	3520	CAAGATGCTCCGGCCTCACCGTCTCAGCCAAATTATGACTGCGGCTTTCTCACACCAACG	3579
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DB	3580	CAACTGACTGACATCAACGATTAATGTGATCTCATCACCTTGGATGCTCTGGGACGCCCT	3639
QY	13237	ACCACCCTCGCATTTCTGGGGCACGGGAATGTTATGGCCACCGGTTTACAGT-----	13287
DB	3640	GTACCGCAACGTTTCTGGGGGATCGAAGCGGTGGCAACAGGTTACTTCTTCATCAGAA	3699
QY	13288	GATGCCACGTTGTCGTTCCGACCGCGCAGCAGCGCTCTGGCGTTGACGGCGCCCTA	13347
DB	3700	GAATAACCATTTCTCCACCAACGATATCGATACCGGTATTAAATCTAACGGGACCACTC	3759
QY	13348	CCAGTAGCACAGTGTCTGGTGTATGTCACGGACAGTTGG-----	13386
DB	3760	CCTGTGCGCAGTGTCTGTGCTATGACCCGGACAGTTGGATGCCACTATTCACTCAGTCAAGAA	3819
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QY	13387	-----GGAGATGACGCAATAGAAAA-----	13408
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DB	4000	ACCACAGACGGTTATGACCGCGACTCTGAGCAGCAAAATTCGCCCAACAAGTCGATTTAGT	4059
QY	13492	GACGGTTTTGGCGGTGAGTTGCAATCGGCAACCCGCGCAGCGCCGAGGGCAACGCCCTGGCAA	13551
DB	4060	GATGGTTTTGGCGTCTGCTACAAGCTCTGTACGACATGAGGACGAGCGAAGCCTGGCAA	4119
QY	13552	CGAGGACGGCAACGGCAAACTGGTGAACGGCCAGTGCAGGATTCGCCGCTCACTGTGAGCAACG	13611
DB	4120	CGTAACCAAGACGGTTCTCTGGTGAACAAAGTTGGA-----GAATACC	4161
QY	13612	AATTTCCGCTGGCGGTCAACGGGAGGGCGGAGTAGTATGCAATAAAGGCTCGCTGTTCCGG	13671
DB	4162	AAACCGGTTGGCGGTACGGGACGCAACCGAATATGATAATAAAGGGCAACCGATACGC	4221
QY	13672	GTTTATACGCGGTATTTTCTGGACAGTTGGCAATATGTCAGTGTGATGACAGTGCCTGCCAG	13731

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; REFERENCE/DOCKET NUMBER: 960296.93804
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4458 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..4458
; US-08-851-567B-31

Query Match          5.1%; Score 969.8; DB 4; Length 4458;
Best Local Similarity 53.8%; Pred. No. 2.5e-259;
Matches 2395; Conservative 0; Mismatches 1857; Indels 201; Gaps 11;

QY 9598 ATGCAAAATCATCAACACATGGCCATTACTGCCCCACAGTTGGCTTCGGGGCGGTGCG 9657
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QY 9658 GTCACCGGGCTCAAGGGTGATATCGCGGCGGAGGCGCGATGGTGGCGGACCCCTGAGT 9717
DB 61 ATCAATGGCATGGGAAGACGACTGAATGCTGCGGCGCCCTGATGGAATGGCTCCCTATCT 120
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DB 121 CTGCCATTACCCCTTCGACCGGCGAGAGGACGGCTCTGGATTAATCGCTGATTTACAGC 180
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DB 181 AACAGTGCAGGTAAATGGGCTTTTCGGCATCGGCTGGCAATGCGGTTATGTCCATTAGC 240
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DB 241 CGAGGACCCACATCGCATTCACATACGGTAATGATGACGACACGTTCTATCCCCACAA 300
QY 9898 GTGAGGTGTGGTCCGGCACTACCGGTGCTGGCACCCCAAGAACACGCGAGGCC--- 9954
DB 301 GCGAGGTGATGAATATCGCCCTGATGACCAAGGCAACCTGATATCCGTCAAGACGTT 360
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DB 421 CAGATCCTGGATTTCAGTAATAATCGAATATGCGCAACCTTGCCTCCGGTCAAGAGACGC 480
QY 10072 GAATTTGGGTGTTATACCCCTGACGACAGGTGGCTCTGCTGGGCCGCAATGCGCAG 10131
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QY 10132 GCTCGCATACGCAACCCACAGCCCCAACACAGACGCGGTTGGCTGATGAGTCTCG 10191
DB 541 GCTTGTCTGCAAAATCCGCAAAATGACCAACAAATCGCCCGAGTGGTGTCTGGAAGAACT 600
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DB 781 CCGGAAGAGTGGCTGTTTCATCTGGTCTTTGACCAAGTGGAGCGGATACCTCACTTCAT 840
QY 10429 GAAGCGCGCGCTGGCAAAACACAGGAAGTGGGAGTGGCTGTGCTGAGGATGTTTT 10488
DB 841 ACCGTGCCAACATGGGA---TGCAGGTACAGCGCAATGCTGTGTACGCCGATATCTTC 897
QY 10489 TCCGGGTATAGTGTGGTTTTAACTCGCGGACTCCGCGCTGTCGCGTCCAGTGTGTGATG 10548
DB 898 TCTCGCTATGAATATGGTTTTGAAGTGGCTACTCCGCGCTTATGTCACCAAGTGTGATG 957
QY 10549 TTCCATTACTAGGTGTTCTGCGGGGGAGTTTCGGGAGCGAATGATCGCGCAGCATTTGAT 10608
DB 958 TTTTACCGCACCGCGCTCATGSCCGGAGAAGCAGTACCAATGACGCCCGGAACTGGTT 1017
QY 10609 TCTCGCTGTGCTGGAATACAGGGAAGTCTTCTCAGTCTGCTCGAGAACGTGAC 10668
DB 1018 GGACGCTTAATACTGGAATATGACAAAAACGCGAGCTCACCAGTTGATTACCATCCGT 1077
QY 10669 CAGGTGGCTTATAGTTCGAGCGGAGCGTCTTGTGCTTCCGCGCACTGGCATTTGGGTG 10728
DB 1078 CAATTAAGCCATGAATCGGACGGGAGGCGAGTCACTCCAGCCACCTAGAACTAGCCTG 1137
QY 10729 CAAACCTTTACCCCGCGACATTTGCGCATCGCAGACGCGTGACGATATGGGCAAGTTG 10788
DB 1138 CAACGGTTGATCTCGAGAAATCCGACATGCGCAACGCTTTGACGCACTAGATAATTT 1197
QY 10789 AGTTGCTTAAACCTTATCAGCTTGTAGACCTTAACGGGAAAGGTGTGTTGGGTATCTCG 10848
DB 1198 AACTCGCAGCAACGTTATCACTGTTGATCTCGGGGAGAAAGGTGTGACAGTATGCTG 1257
QY 10849 TATCAGGACAGCGGTGCTGTTGTTGACCGTGAACCGTACGCGCAGTTCGCGGATGATCCG 10908
DB 1258 TATCAAGATCGAGGCGCTTGTGTTGATTAAGTCCGCAACGTCAGGAAGACGAGACAGC 1317
QY 10909 GATGCTGTGACCTGGCGGGCGCTGCGGCCCTCGCGCAATGCCCGCTTTTGATTAACAGC 10968
DB 1318 AATGCGCTCATTACGACAAATCGCCCACTGCCTACCTACCCAAATTTGACGATAAT 1377
QY 10969 GGCATCTGGCGGATCTTAATGGGATGTTGCGGTGAGTGGTGTGTTACCGCCCGCTG 11028
DB 1378 GCCTCATTTGATGATATCAACGAGACGCGCAACTGGATTGGGTGTTTACCGCCTCGGT 1437
QY 11029 GTGGCGGGATGTATGATCGCACCCCGCGCGAGTGGTTCATTTCACTTCCACCCCTGTCA 11088
DB 1438 ATTCCGGATACCATAGTCAGCAACCCGATGGAAGTGAACGCACTTTACGCAATCAAT 1497
QY 11089 GCCTTGGCGGTAGAATATGCGCATCCAAAGCAGTGTCTCGCCGATATCTCGGGGCTGGG 11148
DB 1498 GCCTTGGCGGTGAATATTTTTCATCAAGCATCCAGTTTCGCTGACCTTACCGGGCAGGC 1557
QY 11149 TTAACGACATGTTGCTTATCGGGCGCGCAGTGTTCGCTCTATTCGGGCAAAACGAT 11208
DB 1558 TTATCTGATTTAGTTGATTCGCGCGCGGAAACGCTGCTATATGCGCAACGAGCAAC 1617
QY 11209 GGTTCGAATAAAGGGAGACCGTGCAGCAAAACGGAAGACTCACTCTCGCGTCCCGGG 11268
DB 1618 GGTTCGCGTAAAGGAGAGATGTCCCAATCCACAGGTATCACCTGCTGTCAAGGG 1677
QY 11269 GTTGACCCACGTPACCTCTGTCGCTTCACTGATATGGCTGGCAGTGGACGAGCATTTG 11328
DB 1678 ACCGATGCCCGAAACTGGTGGCTTTCAGTGATATGCTCGGTTCCGGTCAACAACATCTG 1737
QY 11329 ACGGAGGTGCTGCTAATGAGTACGTTACTCGGCAAAACCTGGGCAACGCTGTTTCGGT 11388
DB 1738 GTGGAATCAAGGTAATCGCGTCACTGTTGGCGGAATCTAGGGCATGCGCGTTTCGGT 1797
QY 11389 CAGCGGTGAATATTTCCGGTTTTAGCCAGTCACTGACTACGTTTAAACCTGACCAAGATA 11448
DB 1798 CAACCACTAATCTGTGAGATTTAGCCAGCCCGAAATAGCTTCAATCCGCAACGCGCTG 1857
QY 11449 TTGCTGGCGGATACCGACGGTTCCGGTACCGAGCCTGATTTATGCGATGATGACCGG 11508

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Db	1858	TTTTCTGGCGGATATCGACGGCTCGGACACACCGACCTTATCTATGCGCAATCCGGCTCT	1917
Qy	11509	TTAGTCAATTTATTTCAACAGAGTGGTAATATTTTCGCCGAGCGCATACGCTGCTCTTG	11568
Db	1918	TTGCTCATTTATCTCAACCAAGTGGTAATCAGTTTGTATGATGCCCGTTTGACATTTAGCGTTG	1977
Qy	11569	CCGAAAGGTGTGGCTATGATCGCACTGCGAGTCTGCAAGTGGCGGATATCCAGGGGCTG	11628
Db	1978	CCGAAGCGGTACAATTTGAACAACATCTGCGCAATTCAGTTCGCCGATATTCAGGGATTA	2037
Qy	11629	GGGTGCTAGCTGTACTAGCGTCCCGCATGTGCGCGCTCATCACTGGGTGTCAT	11688
Db	2038	GGGATCCAGCTTGATCTGACTGTGCCACATATCGCGCCACATCACTGGGCTGTGAC	2097
Qy	11689	TTATFCGCGACAGAAACCTGGTTGTTGAATGGCATGAACAAATATGGGGGCCCGCAT	11748
Db	2098	CTGTCACTGACCAACCTCGTTGTTGAAATGTAATGAACAATACCGGGCGCACATCAC	2157
Qy	11749	GCATGCACTATCGCAGTTCGGTGCAGTCTTGCTGCTGATGAGAAACCGGACATCGGG	11808
Db	2158	ACGCTACATTTATCGTAGTTCCGGCGCAATTCGGTGGATGAAATAATACAGCTCACAAA	2217
Qy	11809	GCAGGCAAGTTCCCTGCTCTACCTGCGCAATTTACATTCGATACCCCTGTGGCGTTCGGTG	11868
Db	2218	GCAGGCAAAATCTCCGGCTGTGATCTGCGCTGTTCCAAATGATTTGCTATGGTATACGAA	2277
Qy	11869	GTGCGAGATGAGATCACCGTAAACCGTCTGGTCAGCGACGTGTTTATCGCCACGGCGTC	11928
Db	2278	ATTGAGATGAATACGCGCAACCGGCTCACAGTGAAGTCACTTACAGCCACGGGCTC	2337
Qy	11929	TGGACGGGACAGAAACCGAGATTTCCGGGGTTTGGTTTGTGAGATCAGGATACCGAT	11988
Db	2338	TGGGATGGTAAAGACGGGAATTCAGAGGATTTGGCTGCTCAAAACAGACAGATACCACA	2397
Qy	11989	ACCTTGGCAAGCAGGTTACGGCACGGAAGTACGTTGCTGTGAGCCGGAAGTGG	12048
Db	2398	ACGTTTTC----TACGGGCAACCGCCCGAAGACGGCGGACCGTCGCTGAGTATTAGCTGG	2454
Qy	12049	TATGCCACCGGGGTACCGGACGTAGACGAGCGTCTGCGGAGACGTATTGGCAAAACGAT	12108
Db	2455	TTTGGCCACCGGCATGGATGAAGTAGACAGCCATTTAGCTACGGAATATTGGCAGGACAG	2514
Qy	12109	CGCGCCGCTTTTGGCCGATTTGCGACCGGTTTCACTGTGCG-----TTTCAAGAGAGGAT	12162
Db	2515	ACGCAAGCTTTATAGCGGATTTGAAACCGGTTATACCGTTCTGGGATCACACCAACAGACA	2574
Qy	12163	GAGCAGACATATACTCCGACGACAGCAGACATTTCTGGTTGACGAGCCCTTGAAGGC	12222
Db	2575	GACCAAGCATTTACCCCAATGAGACACACGTPAATCTGGCTGACGCGAGCGCTTAAAGGC	2634
Qy	12223	ATCTGTGCGCAGTAGATTATACGGTGCAGTGGCAGCAGCCAGGCGCATATCCCTTAC	12282
Db	2635	CAACTGCTACGCACTGAGCTCTACGGTCTGGACGGAACAGATGAAGCAACAGTGCCTTAT	2694
Qy	12283	AGCGTCACTGAGTCTCGCCCGCAGGTAACGCTAGTTTGAAGCGAATGGAGA----CTACCCG	12339
Db	2695	ACCGTCAAGTGAATCGCGCTATCAGGTACGCTCTATTTCCCGTAAATAAAGAAACTGAATTA	2754
Qy	12340	GTGGTGTGGCCGATGGCGCGGAACCGCTACGTAGTTTATGAACGGTACCAATGAT	12399
Db	2755	TCTGCTGGGTGACTGCTATTGTAATAATCGCAGCTACCACTATGAACGTATCATCTGAC	2814
Qy	12400	CCTCAATGCCAACAGACGGCGGTACTCCTCAGTGAATGAATACGGTTTCCCACTGGCTCAG	12459
Db	2815	CCACAGTTTCAGCCAGAGTATCAAGTTTGCAACAGATATCTTTGGTCAATCATCTGCAAGT	2874
Qy	12460	GTCAAGTGTCAATTTATCCAGACCCCTTCGTCGGCGGACAAATCCATATCCGGCGTCCCTTA	12519
Db	2875	GTGATATTCCTGGCGCGCCGCGAATAACAGCAGTGAATCCCTACCGGCTACCCCTG	2934
Qy	12520	CCGCGCAGCTGTTTCGCAACAGTTATGACGACGACGACAGATATTTAGCCTGGGGTTG	12579
Db	2935	CCGGAACCGTATTTGACAGCAGCTATGATGATCAACAACACTATTAAGTCTGCTGGTGA	2994





Qy	8069	TACAGTTTCCGGTCATGCTGGAGAACGCCCGGGGATGTGTGACCTGCTGACCGGGTTC	8128	Db	3273	-----GCAACACATGGATTTGAGTCAGCTAGGTTGGTATAACTCT	3311
Db	2193	TGGCGCTATCCGTTATTGGTAGAACGGCCGCTCTGCCGTGAGTTTGGTGACTCAGTTC	2252	Qy	9203	TACCCGCTCCTTGGCACCATTAGCGGCATCAAAACAAATAAGCTGACGCTCCCGCG	9262
Qy	8129	GGCAACACACTGCTCGGTATTACCGAGGCTCAGGATGGGAGGCGCTGGCCAAACTGCTG	8188	Db	3312	TACAACCTGGGTAAACGAGAAAGAACGTCGTATTAAACGATTCGCCGTCACCTGCGCAACA	3371
Db	2253	GGCAACAGCTTACAAACACGTTTAGAACATCAGGATTAATGAAATAATGACGATACTGTTG	2312	Qy	9263	CTGCTCGGCCCTTATCAGGACGTCGCTGCGGTTCTCAGCTACGCGGAAAGTATGGTCATG	9322
Qy	8189	CAGACCCAGGGCAGTGAACCTGATACGCCAGGGCCCTTCGCCAGCAGGATAACGTCCTCGAG	8248	Db	3372	CTTCTGGGCGCATATCAAGATCTTGAAGCCACACTGGTAAATGGTGGGAATCGCC---	3428
Db	2313	CAGACTCAACAGGAAGCCATCTGNAACATCAGCACGATATACAAACAAATAATCTAAAA	2372	Qy	9323	CCCCGGGGTTGACGCGCTGCGGCTCTCACACGGAATGAACGACGCGCCAAATTCCAA	9382
Qy	8249	GAATTCGATGCGGATATTGCGGCCCTGGAGAGAGCGCCGCGCGCGAGATGCGTTTT	8308	Db	3429	-----GCCATTATCACACGCTGTGAATGACGAGGCGCGTGTGTT	3467
Db	2373	GGATTACAAACACAGCCTGACCGCATTAACGCTAGCGCTGATGCGGACACATTCGCGCAA	2432	Qy	9383	CTGGATTTCATGACCCGCTTACCTGCGCTTTGAGGACT---TCCAGTTGATGACACA	9439
Qy	8309	GAACGTTACAAAGTTGTACGAGCGGACGTCACACCGCGGAAACAGGCCATGAC	8368	Db	3468	ACCGACTTTAAACACAGACCGCTTTCTGCTTTTGAAGGTGAGATGCAACACCGGACACA	3527
Db	2433	AAACATTACCGGACCTGATTAAACGGTGTCTATCTGCGGAGAAATCGCGGTCTGACA	2492	Qy	9440	GGGACCTGACACTGAGCTTCCCGGATGCTGACGGCAAAACAAAGGCGATGCTCCTCAGT	9499
Qy	8369	TTGTACCTCAGTTCCGTCGCTGTCGGCATCAACCGCGCGCTCTTTTGGCCGAGGCC	8428	Db	3528	CTGGAGCTCAATATTTTCCATGCGGGTAAAGAGGGAACGCAACAGAGTTGGTCCGCAAT	3587
Db	2493	CTACGACGACCGGCATGATTACCAATGGCGTTGCAACGGGATTTGCTGATTTGCCGCGGA	2552	Qy	9500	CTGAGGACATCATCTGTCATATCCGTTACACCAATTATCAGCTGATAGGTATCAACATAG	9559
Qy	8429	GCGCGCGATATGCTGCCCAATATTATACGGCTGCGCGCTGCGGGGCTCCCGCTATGGGCA	8488	Db	3588	CTGAGTGACATCATTTGTGCTATCTGAATTAATCATTCGAGACGCGTAAATTTCTTTCTT	3647
Db	2553	ATCGCAACCGGTAACCTTAACGCTCTTCGGGTGCTTAACGCTGATCGGAATGGGAGCG	2612	Qy	9560	CGCAG-----GCCCGCAACGAGGGCTCGGAGGAGACTGAGC---ATGCAAAATCATC	9610
Qy	8489	CTATTTAAAGCCAGCCATCGGCATCGAGTGTCTCCGATGCCATCCCGCATATCAGCG	8548	Db	3648	TGTCGATTACAGGTCCTTATCAGGGGCTGTTATTAAGGAGTACTTTATGACGAGATTAC	3707
Db	2613	CCATTAAATGGCTCCGGCAAGCAACCAAGTTGGCGCCGCGCATCCAGGATCAGAGCGCG	2672	Qy	9611	AAGACATGGGCATTTACTGCCCCCAGCTTGCTTTCCGGGGCGGTGCGGTACACCGGGTCA	9670
Qy	8549	GACAAATCAGCCAGTCGGAAGTGTACCGCGCTGCGGGAGGAGTGGGAAATCCAGCGT	8608	Db	3708	CAGAAGTATCGATTACACGCTGTCACTTCCAAAGGTGCGGTGCTATCAATGGCATGG	3767
Db	2673	GGCATTTCAGNAGTGAACAGGCTATCAGGCTGTCAGNAGATGGGCATTTGCCAAGCG	2732	Qy	9671	AGGGTGAATTCGCGCGGACAGGCCCGGATGGTCCGCGACCTTGAAGTATTTCCCTTGCCGG	9730
Qy	8609	GATAGTGGCAGTCTGAGTGGCGCAGATTGATGCCAGTCCAGCTGGCGGCCATGGCAGTCCG	8668	Db	3768	GAGAAGCACTGAATGCTCGCGGCCCTGATGGAATGGCTCCCTATCTCTGCCATTACCCC	3827
Db	2733	GATATTGTGATAACGAAATAACCAACTGGATGCCAGATACAAAGCCTGCAAGAGCAA	2792	Qy	9731	TTAGCCCGGTCGGGTTAGCCCCCAGCTGGGCACTTAATATACAGCGCGGTGCGGGA	9790
Qy	8669	CGGGAAGGCTGAGCTGACAGAAACTTACTTTAGACCCAGCAGACCCAGGCACAGCGC	8728	Db	3828	TTTCGACCGGACAGAGGACGGCTCTCGGATTAATCGCTGATTTACAGCAACAGTGCAGTA	3887
Db	2793	ATCAGATGGCAGCAAAACAGATCACGCTCTCTGAAACCGCAACAGCGAATGCCCAAGCG	2852	Qy	9791	ACGGCCCTTTGGCATTTGGCTGGGTATCGCGCGTGTGCTGTCCAGCGTCGTACGCGCA	9850
Qy	8729	CAGTTGGCATTCCTGCAGAGTAAGTTCAAACAATACGCTCTGTACAGCTGCTGCGGGC	8788	Db	3888	ATGGGCTTTTCGCAATCGGCTGCAATGCGGTGTATGTCCATTAGCCGACGACCCCAAC	3947
Db	2853	ATTTATGACCTGCAAAACCATCTGTTTACCGGCGAGGACACTGTATTAATGATGGCCCGT	2912	Qy	9851	ACGGACACCTACTACGATGATACCTGATGAATTCACCGGTCCGCGAGGTGAGGTGCTGG	9910
Qy	8789	AGTTGTCCGCAATTTATTACAGTCTTATGACCTGGCAGTATCCCGCTGCTGATGGCG	8848	Db	3948	ATGGCATTTCCACAATACGGTAAATGACGACAGCTTCTATCCCCCAAGGCGAGGTCTGA	4007
Db	2913	CGTCTCTCGCGCTCTATTACCAAAATGTATGATTCCACTCTGCCAAATCTGTCTCCAGCCA	2972	Qy	9911	TGCGGCACTACCGGCTGTGGCACCCCAAGAACACGCGCAGGCC---ACCTCACTACTGG	9967
Qy	8849	CAACAGGCTGGCAGTGGGATAAATTCGAGACTAGTTCG-----TTATCCAGCCGGGG	8902	Db	4008	ATATCGCCCTGGAATGCAAGGGCAACCTGATATCCGTCAAGACGTTAAACCGTCAAG	4067
Db	2973	AAAGCCGATTAGTACAGGAATTAGGCGGAGAAAGAGAGCGACAGTCTTTTCCAGGTTCCG	3032	Qy	9968	GGATAAACCCAGCGGAGCTTCAACGTTTCAGGTTTACCGTTACGTTACGAGGAGGTAGTC	10027
Qy	8903	GCCTGGATGGGGCAATGCGCGTCTGTGTCGCGGGAAACCTCGATGCTGATCTGGCG	8962	Db	4068	GGCTTACCTTGGCCAAATTTCTATACCGTGNCCGCTATCAAGCCCGCAGATCTCTGANT	4127
Db	3033	GTGTGGATGATCTGTGCGAAGGCTGTGTAGCAGAGAAGGTTTAAAGTTAGAGCTACAG	3092	Qy	10028	TCAGCCGCTTGGAGCTTGGCTGCCCGCGCGACG---AGACAGAAAAAGGAAATTTTGGGTGT	10084
Qy	8963	CAGATGAGCAGGCTGCTGTCAGCGGGGATGAGCGGCAATPAGAGGTGACGCGGACGCTC	9022	Db	4128	TCAGTAAATTCGAATACTTGCACACCTCGCTCCCGTCAAGAAGGACGCGCTTCTGGCTGA	4187
Db	3093	AAACTGGATGCCATCTGGCTTGACGCTGGTGTATTGGGTAGAGCCATCCGACCGCTG	3152	Qy	10085	TATATACCCCTGACGACAGGTGGCTCTGCTGGGCGGAAATGCGAGGCTCGCATCAGCA	10144
Qy	9023	TGCTGTGCGAGGCTTATACAGGCTCGCGAGAGATGGGCAATTTCTCTTGGCGGCAAG	9082	Db	4188	TATCGACACGGACGCGGCATCTACATCTTAGGGAAAAACCGCGCAGGCTTGTCTGGCAA	4247
Db	3153	TCGCTGGATACCTCTTGTGGCAGAGGACGTTAAGTGAATAATCAATAAAGTGTCTTAAC	3212	Qy	10145	ACCCCAACAGCCCAACACAGACGCGGTTTGGCTGATGAGTCTCGGTATCACTTACCG	10204
Qy	9083	GTGTGGAACTGGTCAGTAAACGTTTCGGGAGTGGGTACGAAAGCAACGAGTTACAG	9142	Db	4248	ATCCGAAATGACCAACAAATCGCCAGTGGTTGCTGGAGAAACTGTGACCGCAGCCG	4307
Db	3213	GGGAAACGGTATCTCCATCCGTTGGGTCTACTCTGGCGTGAAGGGGATATCTTCAA	3272	Qy	10205	CGCAACAGATGTATTACCAATACCGTCGGAAGATGATGACGGTTGTGACAGCGCGAGC	10264
Qy	9143	ATGGATCAACAGCAACTCGAGGCCACCTTGAAACTGGCTGACCTCGGTATCGGCAACGAT	9202				





Qy	4001	CTGTTCAACACCCACCGCTGAAACGGCCAGCTGTTTTCTGCAGATGATACCCCTCGAC	4060
Db	1552	CTGTTTAATACGCCATTACTGAAACGCAATATTTTCTACCGGATGAGGAGATTGAT	1611
Qy	4061	TTACGCTCTGAAGCAGCGAGGATGCTTTCCGCTCTCAGGCTACTGAAACGGCAATTAAC	4120
Db	1612	TTAAATTCAGGTAGCACCGCGCA---TTGCGAAAAACCATACTTAAAGCTGCATTTAAT	1668
Qy	4121	ATCAGCGCTCGGGGCTTTCCAGCTCTGGCATTTGGCAGGTTGGCCAGGTTGACAGCAGCGCTGGG	4180
Db	1669	ATTGATGATGCTCGCTCTTCCTCGCCCTGCTTAAATTTACCGACCATGATAAAGATGGA	1728
Qy	4181	T---TTAGCTGCTCTGCTGACAAATATCGCGCACTCTACCGAGTGAAACTCTCGCTGAC	4237
Db	1729	AAAATTTAAATAATACCTAAGAACTTTTCCAATTTATATATTTGGAATAATTACTGGCAGAT	1788
Qy	4238	ATCCAGACCTATCCGCTGGTGAAGTGTCAATTTGTTGCTGTCCGTTCTCCCTTTTTCAGCGGG	4297
Db	1789	ATTTCATCAATTAACCATTTGATGAACCTGGATTTATTACTGATTGCGCTAGGTGAAGAAAA	1848
Qy	4298	GTGCGCGCGCTGCTGCTCCGATAA-----TGAGCTGACGACGATTTCTGTACCAG	4348
Db	1849	ACTAATTTATCCGCTATCAGTGATAGCAATTTGGCTACCGTGATCAGAAAACTCAATACT	1908
Qy	4349	ACCACCACTGGCTCAGGAGCAGGCTCGACGGTGCAGCGATGTGTTCTCATGTCTGACG	4408
Db	1909	ATTACCACTGGCTCATACACAGAGTGGAGTGATTTCCAGCTATTATCATGACCTCC	1968
Qy	4409	ACGAGTACGCTACCTGCTGACCCCGCATTTGAGAACCTGCTCGCTTCCTTCGCGAAC	4468
Db	1969	ACCAGCTATAACAAAACGCTTAACGCTGAAATTAAGAAATTTCTGGATACCGTCTACCAC	2028
Qy	4469	GGACTGTGCGGCGTGAGCTGTTCCCGGAAAAGCTCCCGGCGATGGCGCTCCCTTTATT	4528
Db	2029	GGTTTACAAGGTTTTGATAAAGCAAAAGCAGATTTTGCTACATGTCTATGGCGCCCTATATT	2088
Qy	4529	GCCGCCCATGAGCTGGACGCCACCGATAGCGGAGGCGCATGCTGACTTGGCGGAC	4588
Db	2089	CGCGCCACTTGCAATATCATCGGAAATGTGCGCCACTCGTACTCCTTTGGCGAGAT	2148
Qy	4589	CAGTTGAAGCAGAGGGGTGACGCTGACGGAAATTTATTTTGGT-----	4635
Db	2149	AAGTTACAGCCCGCGACGCGCAATGACAGCAGAAAAATTTGCGACTGGTTGAATACT	2208
Qy	4636	-----GATGAATGCCGCCCAATATGACGACGAGCGGGCCAGATGGCAGGTTCTGC	4687
Db	2209	AAGTATACGCGGGTTTCATCGGAAGCCGTAGAAACGAGGAACATATCGTTCAGTATTGT	2268
Qy	4688	CAAGCCCTGTGGCAACTGGCACTGATCATCCGACGACCGGCTCAGACGCGCGAGCTG	4747
Db	2269	CAGGCTCTGGCAATTTGGAATTTGTTTACATTCACCGGCATCAAGAAAACGCTTC	2328
Qy	4748	ACGCTGCTGTGACGACGCGGACGCTTCCGACAGGATGGCAACCATCTGCCC---CAT	4804
Db	2329	CGTCTATTTGTGAAAAACAGAGATGTTTGGCGCTGCAACTGGAGCAGCGCCGCGCAT	2388
Qy	4805	GACCTGCGGGGCTTCGCGCATTTAGCGTTTTTCATGCGCTGTTAACCGCAGCGGACG	4864
Db	2389	GATGCCCTTTCAGTGAATTTGCTGACACGCTTTTGGCGATTGGGTGAACGCACTAGGCGAA	2448
Qy	4865	CATCGCGGGAGTCTGACCGCACTTTGAGACGGAGAACTGCTGCTAGCCCTGCTGGCC	4924
Db	2449	AAAGCTCTCGGTCTAGCGGCAATTTGAAGCTAACTCGTTAAACGGCAGAACACTGGCT	2508
Qy	4925	CGGCGCTGTACAGAAATG-----AGCAGGATGTGACCGCGGCTTTGGCGCAG	4972
Db	2509	GATGCCATGAATCTTTGATGTAAATTTGCTGTTGCAAGCCAGTATTCAAAGCAAAAAATCAT	2568
Qy	4973	GTGAGGGGGCGGTGAAACAGGCAACAGCGTGTTCACCTCTCTGGGAAGAGGTGGAACAG	5032
Db	2569	CAACATCTTCCCCAGTAACTCCAGAAAAATGGCGTTCTCTGTTGGACATCTTATCAATACT	2628
Qy	5033	GCTGACGAGTGGCTGGACATGAGTGTGAGACCTGTCTCCATTACGCCCATCCGCTCTGGCTAGC	5093
Db	2629	ATCCTGCAATGGGTTAATGTGCGCAACAATTTGAATGTGCGCCCAACAGGCGGCTTCCGCT	2688
Qy	5093	CTGATTGCCCTGAAGTACATCAATGTGTCCGATGCAGATGCACGGTTGTACACGCCAGTGG	5152
Db	2689	TTGGTCCGGCTGGATTATTTCAATCAATGAAAGAGA---CACCGACCTATATCCCAAGTGG	2745
Qy	5153	CAGGTGGTATCCGGTCTGCTCAGCGCGGGCTGAAAAGCAGCGCAGAGCTCGGCGCTGCAC	5212
Db	2746	GAAAACGGCAGCGGTATTTAAACCGCGGGTTGAAATTCACAAACAGGCTAATACATTACAC	2805
Qy	5213	GATTATCTGGAGGGGACACGACGCGCCCTTTGTGCTATTATCTGCGTAATCT-----	5268
Db	2806	GCTTTTCTGGATGAATCTCGCAGTGCAGTAAAGCACCTACTATATCCGTCAAGTCGCC	2865
Qy	5269	---GGCACCGAATCATGTATCCGGCGCGATGACCTCTTCGGGTATCTGCTGCTGGATAAT	5326
Db	2866	AAGGCAGCGCGGCTTATTTAAAGCGGTGATGACTTTGTATCAATCTTACTTGATGATAAT	2925
Qy	5327	CAGGTGTGAGCAAGGTAAAAACCAACCGCATTTGCGGAGGCCATCGCCGCGCATACCGCTG	5386
Db	2926	CAGGTTCTGCGGCATTAATAAACCAACCGCATCGCCGAGCCATTCGCCAGTATTTCAACTG	2985
Qy	5387	TATATCAACCGCGCCCTTAAACGGAATAGAACTCAGCGCCATGCGAGGTGAGGGGGCGT	5446
Db	2986	TACGTCAACCGGCAATTTGAAAAATGTGGAAGAAATGCCAATTCGGGGTTATCAGCGCG	3045
Qy	5447	CAGTTTTTCACTGACTGGGATACGTTTCAAAACAGTTTACAGCATCTGGGCGGCGTCTCA	5506
Db	3046	CAATTTCTTTATCGACTGGGCAAAATCAATAAACGCTACAGCATTTGGGCGGGTGTCTT	3105
Qy	5507	GAGCTGTTTTACTATCCGAAAACTTACTCGACCCGACGGTTCGATTCGCGGAGACCGCG	5566
Db	3106	CAATTAGTTTTACTCCCGAAAACTATATTGATCCGACCATGCGTATCGGACAAACCAA	3165
Qy	5567	ATGATGGACACCGCTGCTCAGTCTGTGAGCCAGACAGTATCAACCCGATACCGTGGAG	5626
Db	3166	ATGATGGACGCAATTACTGCAATCCGTGAGCCAAAGCCAAATTAACGCGGATACCGTCGA	3225
Qy	5627	GATGCTTTAAAACTTATCTGACCAAGTTTGAGCAGATTGGCAATCTGAACACTGTGACG	5686
Db	3226	GATGCTTTATGTCTTATCTGACATCGTTTGAACAGTGGCTAATCTTAAAGTTATTAGC	3285
Qy	5687	GGATATACGATAACCGCAGCATGACGCGGGGACTACATGTTATGTTGGGTCCGACATC	5746
Db	3286	GCATATACGATAATTAATTAACGATCAAGGCTGACCTATTTTATCGACCTCAGTGAA	3345
Qy	5747	ACAGATCAGACTAACTGGTACTGGCGAGCGCCAAACACAGCAAAATCCAAAGACTCAATG	5806
Db	3346	ACTGATCCGGTGAATATTTTGGCGCAGTGTGATCACAGTAAATTCACACGCGTAAA	3405
Qy	5807	ATGCCCGGAATGCTCGAACCGGATGACAAAAATTAATCTGCGGAATGAATTCGTTGGTCA	5866
Db	3406	TTCCGGGCTTAATGCTCGAGTGAATGGCATAAAAATGATTGTCCCAATTAACCCCTTAAA	3465

Db 3706 TGTCCGGTTATCAAGGTGAAGATACGTTGCTGGTGATGTTTATATACCAACAGACACA 3765  
Qy 6145 CTTTGATAACGCTCAGCTGATTTCTGTGGATAATGATATGACGCT----- 6189  
Db 3766 CTAGATAGTTATATAAAGCGTTCAATGCAAGGACTATATATCTTTGCTGATATGGCATCC 3825  
Qy 6190 --AAATGTCATCTCAGATATAGGGATTTTAAAGCG-----TCACTCAGCAATTTAAT 6241  
Db 3826 AAGATATAGCCCCAGAACAGAGCAATGTTTATCGGGATAATAGCTATCAACAATTTGAT 3885  
Qy 6242 ACGAGCACTGAGAAATTTATTAATATGTTTTCAGACCTTCGCGTAAATAT- 6295  
Db 3886 ACCAATATGTCAAGAGTGAATAACCGCTATGCAAGGATATGAGATTCCTTCCTCG 3945  
Qy 6296 -TTTGTCAAGTCAACGAGTTTAAATTTGATGTTTAT-----CCACAGC 6337  
Db 3946 GTAAGTAGCGTAAGACTATGTTTGGGAGATTTATACCTCAGCATGGTATATAACGGA 4005  
Qy 6338 GATTTCTCACTCTTAATTTCTAAACTACAAGTACTGTTTTTAC----- 6381  
Db 4006 GATATTCCAACTATCAATTAACAAGCCGATCAAGTGAATTTAAAAATCTATATCTCACCA 4065  
Qy 6382 TAATGAAGATTCCTCTCTTTTGAGCCGAGAGCTTCATATTACAGCAATGTTTCGTGTTT 6441  
Db 4066 AAATTAAGAATTTATTCATAATGGATATGAAGGACAGAGGCGCAATCAATGCAATCTGATG 4125  
Qy 6442 TGTTAGTACTGCTGGCATCGCACTCAATCTACCATAGAAAATTCGTTCAAGCAGGGAT 6501  
Db 4126 AATAAATATGCAAACTAGGTGATAAATTTATGTTTATATAGCTTGGGGGTCATPCCA 4185  
Qy 6502 AGAATTTGAGAAATTAATTTTATGAGCGCCAGCGCGCGGATTTTGACGGATTTGT 6561  
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Qy 6593 CAGTCGGAAAGAGAGTGGTGTCATCTGTAAATCTTATTCGTCACCTGGGTTAGT 6652  
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Qy 6758 -----TACGTGTCGTCTATTGGCTCTCAA 6781  
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Qy 7835 -----CGGACGCGGAATTCCTGAGCGCACTGTTCTCCGCGCAGAGAGAGGTTG 7885  
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Db 5866 ATGATGAAATTTACTGGCAGACATTTAGTCTCAGAGAGTATACAATCTGCGTATAACCTCTCT 5925

Qy	7946	ATTGACGGCCAGCGCTTTCCCTGTCCGTTCTTAGCCACGCGCTCGAAACCGTCCGCCCTG	8005
Db	5926	ATCAGCGCCAGCGCTTATATCTGCCAATCTATGCCACACCGGCCGATCGAAAGCGTTA	5985
Qy	8006	CAGAGTGCCTGTCAACAGCGGCCAGGCTGCTCAGACATGCGCGCGCGGTGATGCGG	8065
Db	5986	CTCAGCGCGCGCTTGCACCTCTCAAGTGGAGGCAAGCTACCGGAATCAITTTATGTCC	6045
Qy	8066	CTTTACAGTTTCCCGGTCATGCTGGAGAACGCCCGGGGGATGTTGAGCTGCTGACCGGG	8125
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Qy	8126	TTCCGCAACACACTGCTCGGTATTACCGAGCGTCAAGATCGGAGGCGCTGGGCCAAACTG	8185
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Qy	8186	CTGCAGACCCAGGCACTGAACATGATACGCCAGGCGCTTCCGACAGAGATATAGCTCTC	8245
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Db	6226	GAAGATTTGATGCCGAGAAACCGGTGTTGGAAAAATCCAAAGCGGAGGACCAATCGCGC	6285
Qy	8306	TTTGAACGTTTACAAAGTGTGTACGAGCGGAGCGTCAACACCGCGCAAAAAACAGGCCATG	8365
Db	6286	TTTGTAGCTAGGCAAACTGTACGATGAGATATCAACGCGGTGAAACCAAGCCATG	6345
Qy	8366	GACTTGTACTCAGTTGCTCGTGTCTGTGGCATCAACCGCGCGCTCTTTTGGCGGAG	8425
Db	6346	ACGCTACGAGCGTCCGCGCGCGGCTTTACCACGGCACTTCAGGCGATCCCTCTCGGCGGT	6405
Qy	8426	GCCCGGCCGATGCTGCCCAATATTACGGCTGCGCGCTCGGGGCTCCCGCTATGGG	8485
Db	6406	GCGCGCGCTGATCTGGTGCCCTTAACATCTTCGGCTTTGCGGCTGGCGCAGCCGTGGGG	6465
Qy	8486	GCACATTTTAAAGCCACCGCCATCGGCATCCAGGTGTCCTCCGATGCCACCCGCATATCA	8545
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Qy	8546	GCGGACAAATACGCCAGTCGGAAGTGTACGCGCTGCGCGGAGGAGTGGGAAATCCAG	8605
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Qy	8606	CGTGATAGTCGCAGTCTGACGTGGCGCAGATTGATGCCAGCTGGCGGCCATGGCAGTG	8665
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Db	6766	GGTCGACTGGCGGGAATTTACTTCAGTTTCTAGCATTTGCGCGCTGCGCGCTGCCCTGATG	6825
Qy	8846	GCGCAACAGGCGCTGGCAGTGGGA---TAAATTCGAGACTAGTGGTTTATCCAGCGCGGG	8902
Db	6826	GCAGAACAGGCTTACGTTGGGAACCTCAATGATGACTCTGCCGCTTCATTAACCGGGC	6885
Qy	8903	GCCTGGATGGGGCAATGCGGCTCTCTGGCGGGGAAACCTCTGATGCTGAAATCTGGCG	8962
Db	6886	GCCTGGCAGGGAACCTATGCGGCTCTCTTGCAAGTGAACCTTTGATGCTGAGTCTGGCA	6945
Qy	8963	CAGATGAGCAGGCGCTGAGCGGGGATGAGCGGCAATAGAGGTGACGCGGACGGTCT	9022
Db	6946	CAATGGAAAGCGCTCATCTCTGAAACGCGCAATAAACCGCGCATTTAGAGGTTGAACCCACAGTA	7005

Qy	9023	TGCTGTGCGAGGTCTATATACGACCTGCGGAGGAT---GCGGCATCTCTCTGGCGCAG	9079
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Qy	9080	AAGTGTGTGAACTGGTTCAGTAAACGGTTCCGGCAGTCCGGGTACGAAACGACACGGATTA	9139
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Qy	9140	CAGATGG-----ATCAACAGCAACTCGAGGCCACCTGAAACTGGGCTGC	9184
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Qy	9245	AGGTCACGCTCCGGGCGTGGTTCGGCCCTATCAGGACGTCCGTGGGTTCTCAGCTAC	9304
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Db	7426	GCCATTGATCA---AGGCACGCTGACACTGAGCTTCCCAAAATGCATCTATGCGCGAGAAA	7482
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Db	7483	GGTAAACAAGCCACTATGTTAAAAACCTTGAAAGATATCATTTTGGCATATTCGCTACACC	7542
Qy	9533	ATTA	9536
Db	7543	ATTA	7546

## RESULT 6

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US-09-637-048C-1
; Sequence 1, Application US/09637048C
; Patent No. 6590142
; GENERAL INFORMATION:
; APPLICANT: Patell, Jim
; APPLICANT: Merlo, Donald
; APPLICANT: Herman, Rod
; APPLICANT: Roberts, Jean
; APPLICANT: Guo, Lining
; APPLICANT: Schafer, Barry
; APPLICANT: Sukhapinda, Kitisri
; APPLICANT: Owens Merlo, Ann
; TITLE OF INVENTION: Transgenic Plants Expressing Photorhabdus Toxin
; FILE REFERENCE: 50698
; CURRENT APPLICATION NUMBER: US/09/637,048C
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/148,356
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 7551
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(7548)
US-09-637-048C-1
Query Match 4.5%; Score 848.8; DB 4; Length 7551;
Best Local Similarity 48.8%; Pred. No. 2.6e-225;

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Matches 3662; Conservative 0; Mismatches 3347; Indels 495; Gaps 31;

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QY 5269 --GGACCGCAACATGATATCGGGCGGATGACCTCTTCGGGTATCTGCTGCTGATAT 5326  
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QY 5327 CAGGTGTCAGCCAAAGGTAAAAACCCCGCATTTGCGAGGCCATCGCCGGCATAGCGGTG 5386  
DB 2926 CAGGTTCCTGCGGCAATTAACCCACCCCGATCGCGAGGCCATTTGCCAGTATTCACCTG 2985  
QY 5387 TATATCAACCGGCGCCTTAACGGGAATAGAACTCAGCGCCATGGCAGAGGTGAGGGGGGT 5446  
DB 2986 TACGTCAACCGGCGCATFTGAAATAATGGAAGAAAAATGCCAAATTCGGGGGTATTACGCCGC 3045  
QY 5447 CAGTTTTTCACTGACTGGGATAGTTCAACAAACGTTTACAGCACCTTGGCGGGCGCTCA 5506  
DB 3046 CAATTCCTTTATCGACTGGGACAAATACAAATAACGCTACAGCACTTGGCGGGGTGTTCT 3105  
QY 5507 GAGCTGGTTTACTATCCGGAAAACTACCTCGACCCCGCGGTCCGTATCGGGCAGACCGGC 5566  
DB 3106 CAATTAGTTTACTACCCGGAAACTATATTGATCCGACCATCGGTATCGGACAAACCAA 3165  
QY 5567 ATGATGGAACCCCTGCTGAGTCTGTGACGAGCAGATATCAACCGCGAATACCGTGGAG 5626  
DB 3166 ATGATGAGCGCATTAAGTCAATCCCGTCAGCCAAAGCCAAATTAAGCGCCGATACCGTCGAA 3225  
QY 5627 GATGCCCTTAAACCTTATCTGACCAAGTTTGGAGGATGCGCAATCTGAACCTGCTCAGC 5686  
DB 3226 GATGCCCTTATGCTTATCTGACATCGTTTGAACAGTGGCTTAATCTTAAAGTTATTAGC 3285  
QY 5687 GGATATCACGATAACCCAGCATGACGCGGGGACTTACATGTTGATGTGCGGAGCATC 5746

DB 3286 GCGTATCAGATATATTAATTAACGATCAAGGCTGACCTATTTATCGACTCAGTGAA 3345  
QY 5747 ACAGATCAGACTAACTGGTACTTGGCGCAGCGCAACACAGCAAAATCCAAAGCTCAATG 5806  
DB 3346 ACTGATCGCGTGAATATTTATTTGGCGCAGTGTGATCAAGTAAATTCACACGCGTAA 3405  
QY 5807 ATGCCCGCGAATGCTGACCGGATGGACAAAATTAATCTGCGGAATGATCGTGGTCA 5866  
DB 3406 TTCCGCGGTAAATGCGCTGAGTGAATGGCATAAAAATTTGATTTGCCAATTAACCTTTATA 3465  
QY 5867 GATCTTGTGCTCGGTGTTTCAACAGTCCGCTTTATGCTGCTGGGTCAAGA--- 5922  
DB 3466 AGCATATCCGTCAGTGATATATAATCCCGCTGTATCTGCTCTGGTGGAAACAAAG 3525  
QY 5923 -----GAATCAGTCTGCTGATACGGAGGAGAGACGACAAACACGACGAGAGC 5974  
DB 3526 GAGATCACCAACACAGACAGGAAATAGTAAAGATGCTATCAAACTGAAACGGAATATCGT 3585  
QY 5975 TACAGCTGAACTGCTGTTCCGGCGCTACGACGCTACATGAGTTCGCCGCTGCTGTC 6034  
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DB 3766 CTAGATAGTTATAAAAAACGCTTCAATGCAAGGACTATATATCTTTGCTGATATGGCATCC 3825  
QY 6190 --AAATGTCATCTCAGATATAGGGAATTTTAAAGCG---TCAGTCAACGAATTTAAT 6241  
DB 3826 AAGATATGACCCCAAGACAGAGCAATGTTATCGGTAATAGTATCAACAATTTGAT 3885  
QY 6242 ACGAGCAGTGAAGAAATTTATTAATAATGTTTTTTCAGACCTTCGCGTAAATTTAT----- 6295  
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QY 6296 -TTTCTCAGTCAACGAGTAAATTTGATGATGTTAT-----CCACAGC 6337  
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QY 6338 GATTTCTCACTCTTTAATTTCTAAAACTACAAGTACTGTTTTTAC----- 6381  
DB 4006 GATATTCCAACTATCAATTAACAAAGCCGATCAAGTGATTTTAAAAATCTATATCTCACCA 4065  
QY 6382 TAATGAAGATTCCTCTCTTTTGACCGCAGAGCTTCATATTACAGCAATGTTTCGTGTTT 6441  
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QY 6502 AGAATTTGAGGAAAAATTAATTTTATGACGGCCAGCGCCGCGGATTTGACGGATTTGT 6561  
DB 4186 AATAACTCGTCAATAAAGCTCATGTTTACCCCGTCTATCAATATAGCGGAAACACCACT 4245  
QY 6562 GG-----GAGTGGATGTTTCTTAATTCAAAAGTATAC 6592  
DB 4246 GGACTCAATCAAGGGAGACTACTATTCACCGGTGACCACTTATCCATCTAAAGTAGAA 4305  
QY 6593 CAGGTCGGAAGAAAGACGAGTGGTCACTGTAATAATCTTATTCGTCACCTGCGCTAGT 6652  
DB 4306 GCTTGGATTCCTGGAGCAAAACGTTCTCTAACCAACCAAAATGCGCCCATTTGGTATGAT 4365  
QY 6653 GGTCTGTTGAGTTATTTATTGATTCATCAATAAATATCTTCAGCGGAATTTTGTGAGAT 6712

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Qy 6713 AATATGATAACCGCTTTAAATAGCGGAGTACATCAAAAGTTAA- 6757  
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Qy 6758 -----TACGTGTCGTCTAATTTGGCTCTCAA 6781  
Db 4486 GCAAAAGTTCAGATAATAGTCAAAAGCGGTGGCAAGGCAAACTTTTACCGCAGATAAA 4545  
Qy 6782 GATTTTGGAGTGTAAAGTCTGCTCATGCGGCACTTCAGATAATGAATTAATGATGAT 6841  
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Qy 6887 CTTTCCGCTGAATGATATGATAAGTCTGCAATCCGGGAATAATCTTTTCAAC 6946  
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Qy 6947 ACBAATCGTGAGTTTACCGTTAATACAGTGAATATGTTGAAGATGAGTTGAGGTG 7006  
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Qy 7007 ACGTTTACGTTACCGGCTGCGATCAGAAATACGTCGTGTCGCGCGCCGACGGCCATA 7066  
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Qy 7148 TTCCTCGGGTAACGATGTGGCGCTTATTCGCTCAACACCTCTTTGCGCCGCAACTG 7207  
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Qy 7244 ----- 7243  
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Qy 7244 -----TCCATGGAGACCCAGAGCTTACCGAACCCGCTTGAAGAGGGAGTATG 7294  
Db 5206 AACCTTAATCCATTTTGACCCATTTTGAGAGCTCAATGCTCTGAATATATATAGTAGC 5265  
Qy 7295 GTGTTTATGAGCTTCTCCGAGGCAATGCCCTCTATTCTTGGGAGCTGTTCTATTACAG 7354  
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Qy 7355 CCGATGATGTTGTCAGCGGTTGTTGACGGAACAGCACTTCCGGGAAGCAACCGCTGG 7414  
Db 5326 CCGATGCTGTTGCTCAACGTTTCTGCATGAAACAGAACTTCGATGAAGCAACCGTTGG 5385  
Qy 7415 CTGCAGTATGCTGGAACCCGCGCGGCACTGTGTAAACGGGTGCTGCAGAAATTAACCC 7474  
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Qy 7475 TGGAAATGCTCGCTCGGAGGAGGACACCGGCTGGAAACGACTCGCGCTGGACTCCATT 7534  
Db 5446 TGGAACTGCGCGCTTACTTGGGAAGACACCAAGTTTGGAAACAGTATCTTTGGATTCGCTC 5505

Qy 7535 GACCCGATGCAATAGCCAGTAGTACGCCCATGCAATTACAAAGTCCGCCACTTTATGTCG 7594  
Db 5506 GATCCTGACGCGTAGCAGACAGCATCCAAATGCACTTCAAAAGTTTCAACTTTTATCGGT 5565  
Qy 7595 TACCTCGACTGCTGATTGCCCGCGGTGATGCCGCTTACCGGCTGCTCGAGCGGACACC 7654  
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Qy 7655 CTTAAACGAGCCCGGATGTTGTTACGTCAGGCGCTTGAACCTTCTGGCGGACGAGCCCTAT 7714  
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Qy 7715 ATTTCTTTGACCGCGACTGTTGCGGCTTGACCTGGTGCACGACCGACCGAGGTGACG 7774  
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Qy 7775 CGACGCGATTACACGAGGCGCTTGTGGCGTGGCGGTTGTGGCGCTCCCGAGACA 7834  
Db 5746 CAAATGCTCACGACAGCGCAATAGTCGCTCTGCGGAGAAATATACCTACACCGCACCT 5805  
Qy 7835 -----CGHACGGGAATTCCTGACGGCACTGTTCTCTCCGACGAGAAAGAGGTG 7885  
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Qy 7886 CTCAAAGGCTACTGCGCAAACTTGGCACAGCGGCTCCATAACCTGCGCCACACCTCTCC 7945  
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Qy 8006 CAGAGTGGCGTCTCAACAGCGCGAGGTGCTGACGACTGCGCGCGCGGTGATGTCG 8065  
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Qy 8306 TTTGAAACGTTTACAAAGTTGTACGAGGCGGAGCTCAACACCGCGCAAAACAGGCCATG 8365  
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Qy 8366 GACTTGTAACCTCAGTTGCTCGGTGCTGGCATCAACCGCGCGGTCTTTTGGCGGAG 8425  
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Db 6406 GCGCGCGGATGCTGGTGCTTAACATCTTCGGCTTTGCGGCTGGCGGAGCCGCTGGGG 6465  
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Qy 8546 GCGGACAAATACGCGAGTGGGAAGTGTACCGCGCTGCGCGGAGGAGTGGGAAATCCAG 8605  
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Qy 3344 CTGGACTTTTCAATCCAAACAAATGAATACATTAATTAAGTAAAGTGTGTAAC 3403  
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Qy 3404 CTGAATGAAGCACTGTTTAAATACATATACATCAATTAATTAAGAACGCTAGCGGAGAC 3463  
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Qy 3464 TCACAGCAGATTAACCCCTGAGCTTATACCTTATGGGATGGAACATATCTTTTATAATTTC 3523  
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Qy 3584 AGCAATCTTTACTCGGGATTAACAGCTTCAAAAAGGGTTCGCTATAGCATTCCTGTT 3643  
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Db 1252 TCTTGGGCATATGCCCGCAAAATTTACCGTTGAAGAGTATACCAATACTCTTTCTG 1311  
Qy 3761 CTTAAATTAATAAGTTNTCCGCTATACAGGCCACGGGATGACCAACGGCGGAAATA 3820  
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Qy 3821 TATCAAAATACCAATATTTCTAATAACGGTCTACACATTCACCATGGGTCTGAGTAAA 3880  
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Qy 3881 ATCTTCTGTCGTGTTACCTGATGCGTCACTATCACTGATGCTTGAATGGCCCGTCACTGATA 3940  
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Qy 4636 -----GATGAATGCGGCCCAAAATGACGACGAGCGGGCCAGATGGCAGGTTCTGC 4697  
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Qy 4805 GACCTCGCGCGCTTCGCGACATTAACGCTTTTTCATGCGCTTCGCTTAAACCGACGCGGAGC 4864  
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Qy 4865 CATGCCGGGAGTCTGACCGCACTTGAGACCGGAGAACTGTCGTGACGCTCTGCTGGCC 4924  
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Qy 4925 CGGGCCCTGTACAGAAATG-----AGCAGGATGTGACCGCGCTTTGGGCGAG 4972  
Db 2509 GATGCCATGAATCTTGATGCTTAATTTGCTTTGCAAGCCAGTATTCAAGCACAATAATCAT 2568  
Qy 4973 GTGAGGGGGCGGTGAACAGGACAAACAGGTTTTCACCTCTGCGGAAGAGGTGAGCAG 5032  
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Qy 5093 CTGAATGCCCTGAAGTACATCAATGTGTCGATGACAGTGCACGCTTTGTACAGCCAGTGG 5152  
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QY 9365 GACAGCGGCAATTCCTCAATGATGACCCGCGTTTACCTGCGGTTTGAAGGACTT 9424  
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Db 7543 ATTA 7546  
|||||

RESULT 8  
US-10-435-835-1  
; Sequence 1, Application US/10435835  
; Patent No. 6717035  
; GENERAL INFORMATION:  
; APPLICANT: Patelli, Jim  
; APPLICANT: Merlo, Donald  
; APPLICANT: Herman, Rod  
; APPLICANT: Roberts, Jean  
; APPLICANT: Guo, Lining  
; APPLICANT: Schafer, Barry  
; APPLICANT: Sukhapinda, Kitisri  
; APPLICANT: Owens Merlo, Ann  
; TITLE OF INVENTION: Transgenic Plants Expressing Photorhabdus Toxin  
; FILE REFERENCE: 50698  
; CURRENT APPLICATION NUMBER: US/10/435,835  
; CURRENT FILING DATE: 2003-05-12  
; PRIOR APPLICATION NUMBER: US 60/148,356  
; PRIOR FILING DATE: 1999-08-11  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 7551  
; TYPE: DNA  
; ORGANISM: Photorhabdus luminescens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(7548)  
US-10-435-835-1

Query Match 4.5%; Score 848.8; DB 4; Length 7551;  
Best Local Similarity 48.8%; Pred. No. 2.6e-225;  
Matches 3662; Conservative 0; Mismatches 3347; Indels 495; Gaps 31;  
QY 2510 CTGACGGATTATTCTCGCGTTCGTTTCCCGAGGTCAAAAAATCACTGGCGACACCTG 2569  
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Db 61 CTGACAGATTATGACACAGCTTATATCATGATGACACAGGCAAAAAGGATATCGC 120  
|||||  
QY 2570 TCATGGGAGAGTCTGCTATCTGTACAGTCAGCGCAGCACGAAACAGAAAGAAACCGG 2629  
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Db 121 TCCTGTCCGAACACAGCTTATATCATGATGACACAGGCAAAAAGGATATCGC 180  
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Db 181 CTGTATGAACGCGTATTCTCAACGCGGCAATCCCAATACAAATGCGGTGCACTTT 240  
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QY 2690 GGAATACGCGAGCAGCCGCGAGTCGCA---GCTATGATGACTGTTTGGCTCCCGCA 2746  
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Db 241 GCATTTCTGCTCCCAATGCTGAACGATGAGGTATTAACAATCAATTTAGCGGTAGACC 300  
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QY 2747 GACCGTTTCGCCGCCCGGCTCGGTGGCTCCATGTTCTTCACCGCGGCGTATCTGACC 2806  
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Db 301 AGTCAATATGTTGCGCGGGTACCGTTTCTTCCATGTTCTCCCGCGCTTATTTGACT 360  
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QY 2807 GAGCTGTACGTTAGGGGAAGGACCTGCACTCCGGACACCTCGCTGTTCCGGCTGGACATC 2866  
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Db 361 GAACTTTATCGTGAAGCAGCAATTTACACGCAAGTGAATCCGTTTATTTATCTGGATACC 420  
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QY 2867 CGCGCTCCGACCTCGCGCGCTGGCCCTTAGCCAGAATAATATGAGACGAGCTCTCC 2926  
|||||  
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QY 2927 ACCCTGAGCTCTCCAATGAGC---TACTGTATCGCGGTATCGGGCAGCGGAAGGGCTT 2983  
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Db 481 ACACCTCTCTTCTCAATGAGCTGTTATTTGGAAGACATTTAAACATGAATCTTAACTGAA 540  
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QY 3044 CACTGGGCTAGAGCGCGCCGCAAGCAATTTCTGGTSCAGGACCCGACGCTGATGGGG 3103  
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Db 601 CATGATGCTTATGAAAATGCTGCTGAAGTTATCCAGCTACAAGATCTCTGGACTTGAGCAA 660  
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QY 3104 TTCAGCCGTAATCCGGATGTGGCGAGCTTATGACCCCTGCTCCATGCTGCCCATTTGAA 3163  
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Db 661 CTCAATGCAATCACCGGCAATTCGCGGTTGATGATCAAGCCTCCCTATTTGGTATTAAC 720  
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QY 3164 GCCGATATTTCAACCGAGCTGTATCAGATCTGCGCGGAAGAAATACGACACAGCTTAC 3223  
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QY 3224 GAAGCACTCTGGAGTAAGAAATTTGCTGATATGCTCCCTCTCTACTGTTATCTTATGAT 3283  
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QY 3404 CTGAATGAAAGCACTGGTTTAAATACTATACATCATTTATTTAAGAACGCTAGCGGAGAC 3463  
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Db 952 GTCAACAGCAGTGATGGCAGGTTAAGGTATATCGGATCACCGCGAATATACACCAAT 1011  
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QY 3464 TCACAGCAGATTAACCTGAGCTTATACCTTATGGGATGGAACATATCTTTATATATTC 3523  
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QY 3524 ACGTGTGTCAACGATATCAGAGATAGTTTCAAACTAGGCTCGTTAGGTTCTACAGT 3583  
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QY 3584 AGCAATCTTTACTCTGGGATTTATCAGCTTCAAAAAGGGTTTCGGTATATAGCATTCCTGTT 3643  
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Db 1132 CTGTTCGAACTGAAGGCGCTCTCAAGTCATATAGATATCTCCGCAATATCACTTA 1191  
|||||  
QY 3644 GAAATAGATGAAGGAAGTTAAATGATGGAT---CACAAATAGGATGATGAGGAAGGG 3700  
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QY 3701 GGGGATATTTACTCAACAGTAACTTCACTGATTTGATATATGATCTCCGATATTCATT 3760  
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Db 1432 GTTTTCTGACTAAATATTTATATGACGCTTATGCTTATTCATGCTGAAACTGCCCTGATA 1491  
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QY 3941 TTGTGCAACGAAACCATCAGTGACACAGCGGTTCAGCGCGGAAACCGGCTCTTCCACACG 4000  
DB |||||  
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DB |||||  
DB 1552 CTGTTTAATACGCCATTACTGAACGGCAATATTTTCTACCGCGGATGAGGAGATTGAT 1611  
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DB 1669 ATTGATGATGTCGCTCTCCGCTCTGCTTAAATTTACCGACCATGATAATAAAGATGGA 1728  
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DB 1729 AAAATTAATAAATAACCTAAAGAAATCTTTCCAAATTTATATATTGAAATTTACTGGCAGAT 1788  
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QY 4589 CAGTTGAAGCCAGAGGGCTGACCTGACGGAATTTATTTCTTTGGT----- 4635  
DB |||||  
DB 2149 AAGTTACGCGCGGAGGCGCAATGACAGCAGAAATTTCTGGACTGGTTGAATACT 2208  
QY 4636 -----GATGAATGCCGCCCAATGACGAGCAGCGCGGCCAGATGGCAGGGTTCTGC 4687  
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QY 4805 GACCTGCGGCGCTTCGCGACATTTACCGGTTTTTCATGCCGCTCGTTAAACCGCAGCGCAGC 4864  
DB |||||  
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DB |||||  
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DB |||||  
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DB |||||  
DB 3526 GAGATCACCACAAACAGACAGGAAATAGTAAAGATGGCTATCAAACTGAAACGGATTATCGT 3585  
QY 5975 TACACGCTGAACCTGCTGTTCCCGCGCTAGCAGGTACATGAGATTGCTCCCGGTGCTGCTTC 6034  
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 7089 ----- 7088  
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 5086 GATGTCCTCATTTGAATCAAGATTATCAGCCCAAGGTTTATATGACCTTCAAGAAATCACCA 5145  
 7244 ----- 7243  
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 7655 CTTAACGAGCCCGGATGTTGCTGAGGCTCGAACCTTCTGGCGGACGAGCCCTAT 7714  
 5626 CTCACGAAAGCAAGATGTTGATATGCAAGCGCTGCACTATTAGTGACAAACCTTAT 5685  
 7715 ATTTCCTTTGACCGCCGACTGTTGACCCCTGGGTGACCGCTGGGTGACGACGCGAGGTGACG 7774  
 5686 CTACCGCTGAGTACGATGAGTATCCAGGACTAGACAGAGCCCGGATATCACTACC 5745  
 7775 CGACGGGATTAACAGAGGCGCTGCTGCGCGTGGCGGTTGGTGGCTCCCGTCCCGAGACA 7834  
 5746 CAAAATGCTCACGACAGCGCAATAGTCGCTCTCGCGGAGAAATATACCTACCGCGCACCT 5805  
 7835 -----CGGACGCGGAATTCCTGAGCGCACTGTTCTCTCCGCGACGAGAACGAGGTG 7885  
 5806 TTATCATTTGCGCAGCGCTAATACCTTGACTGATCTCTTCTCTGCGCAATCAATGAAGTG 5865



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; OTHER INFORMATION: Description of Artificial Sequence:hemicot tcda
; US-09-637-048C-3

Query Match 4.3%; Score 815.2; DB 4; Length 7577;
Best Local Similarity 48.5%; Pred. No. 6.4e-216;
Matches 3641; Conservative 0; Mismatches 3368; Indels 495; Gaps 31;

Qy 2510 CTGACGAAATTAATCTCGCGTTTCGTTCCGAGGTCAAAAATCACTGCGGACACGCTG 2569
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
66 CTCACTGACATCTCCCAACAGCTCTCTTCAACGAGTTCAGACAACAAGTCTCTGAGCACCTC 125
Qy 2570 TCATGGGGAGAGTCTGCTATCTGTACAGTCAGCGCAGCACGACAAAGAAAACCCGG 2629
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
126 TCCTGGTCCGACACCAATGACCTTCACTACATGACGCTCAGCAAGCTCAGAAGGACAACAG 185
Qy 2630 CTCACGAATCCCGTATTTCTGGCCGGCGGAATCCCTACTGTGTGAATCCGTTCCGCTG 2689
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
186 CTCTACGAGGTAGGATCCTCAAGAGGGCTAAACCAACTCCAGAAGCTGTGTCACCTC 245
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Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
246 GCCATCTTGGTCCAAACGCTGAGTTGATTTGTGTACAAACCAAGTTCTCTGGCAGAGCT 305
Qy 2747 GACCGTTTCGCCCGCCCGGCTCGGTGGCTCTCATGTTCTCACGGCGGGGTATCTGACC 2806
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
306 AGCCAGTACGTGGCTCTCTGGTACAGTCTCTCCATGTTTCAGCCAGCGCTTACCTCACT 365
Qy 2807 GAGCTGTACCGTGAAGGCAAGGACCTGCATCCGACACCTCGCTGTTCGGCTGGGACATC 2866
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
366 GAGTTGTACCGCGAGGCTAGGAACCTTCATGCTTCTGACTCCGTTACTACTTGGACACA 425
Qy 2867 CGGCGTCCGACCTGGCGGCTCGGCCCTTAGCCAGATAATATGGACGACGAGCTCTCC 2926
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
426 CGCAGACGACCTCAAGAGCATGGCCCTCAGCCAAACAGAACATGGACATTTGAGTTGTC 485
Qy 2927 ACCCTGAGCCTGTCCAATGAGCTACTGTATCGGGTATCGGGGACGCGGAAGGCTTGAC 2986
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
486 ACCCTCTCTTTAGCAACAGAGCTTCTCTTGGAGTCCATCAAGACTGAGACCAAGTTGGAG 545
Qy 2987 GACCACAGC---GTCAGGGAGCTCTCGCGGGTATCGCTGACCGGCGCTGACCCCTAT 3043
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546 AACTACACCAAGGTCATGGAGATGCTCTCACCTTCAGACCAAGCGGTGCAATCCATAC 605
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786 GAGGAGTTGTACAAGAGAACTCTCGCAACATTCAGCGAGCCCTCTCTTGCAATGCCTGAG 845
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Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
846 TACCTCAAGAGGTACTCAACTTGTCTGATGAGGAGCTTTCT-----CAATTCATT 896
Qy 3344 CTGGACTTTTCAAATCCAAAACAATGAATACATGATTAATAGTCAATTAAGTGTGCTAACT 3403
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
897 GCGAAGGCTTCCAACCTTCGGTCAACAGGAGTACAGCAACAACCAAGCTCATCACTCCAGTT 956
Qy 3404 CTGAATGAAGACACTGGTTTTAATACATATACATATTATTTAAGAACGCTAGGCGGAGAC 3463
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
957 GTGAATCTCTGTATGGCACTGTGAGGTCTACCGCATCAACAGCTGAGTACACCACAAC 1016
Qy 3464 TCACAGCAGATTAACCCCTGAGCTTATACCTTTATGGGATGAAACATATCTTTATAATTC 3523

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Db 2094 GCAGCCACCCCTCCAACTCTCTCTGAGAAAGTGGCTCACTCTGTCTTGGCTCGGCTGAC 2153  
Qy 4589 CAGTTGAAGCCAGAGGGGCTGACGCTGACGAAATTTATCTTTTGGTGATGAATCCGCC 4648  
Db 2154 AAGCTCCAACTGGTGATGGTGCCATGACTGCTGAGAAGTTCTGGGACTGGCTCAACACC 2213  
Qy 4649 CCAA-----TGACGAGCAGCGCGGCCAGATGGCAGGGTTCTGC 4687  
Db 2214 AAGTACACACCCAGGCTCTCTGAGGCTGTTGAGACTCAAGAGCACATTTGTGCAATACTGC 2273  
Qy 4688 CAAGCCCTGTGGCACTGGCACTGATCATCCGACAGCACCGGCTCAGCAGCGGAGTG 4747  
Db 2274 CAGGCTCTGTGCACAGTTGGAGATGGTTACCACTCCACTGGCATCAACGAGAAGCGTTTC 2333  
Qy 4748 ACGCTGTCTGTGACGACCGCGGAGCTTCCGACAGG---ATGGCACCATCTGCCCAT 4804  
Db 2334 AGACTCTTCGTACCAAGCCCTGAGATGTTCCGTGCTGCCACAGGTGCTGCACCTGCTCAT 2393  
Qy 4805 GACCTGCCCGGCTTTCGCGACATTAACGCGTTTTCATGCCGTCGTTAAACCGCAGCGGACG 4864  
Db 2394 GATGCTCTCTCCCTCATCATGTTGACCAAGTTTCGCTGACTGGGTCAAGCTCTTGGTGAG 2453  
Qy 4865 CATGCCGGGAGGTCTGACCGCACTTGAGACCGGAGAACTGTGTCAGCCCTGCTGGCC 4924  
Db 2454 AAGGCTTCTCTGCTTGGCTGCTTCGAGGCCAACTCCCTCACTGCTGAGCAACTTGCT 2513  
Qy 4925 CGGCGCTGTCAAGAAATGACAGGATGTGACCGCGCTTGGCGCAGGTGAGGGGGCC 4984  
Db 2514 GATGCCATGAACCTTGATGCCAACCTTTGCTCCAGCTTCCATTCAGCTCAGAACCAAC 2573  
Qy 4985 GGTGAACAGGACA-----ACAGCGTGTTCACCTCTCGGGAAGAGGTGGACGAG 5032  
Db 2574 CAACACCTCCACCTGTCACTCCAGAGAACCTTCTCTGCTGACCTCCATCAACACC 2633  
Qy 5033 GCTGAGCAGTGGCTGGACATGAGTGAGACCTGTGTCATTAAGCAATCGGCTGGCTAGC 5092  
Db 2634 ATCCCTCAATGGGTCAACGTGGCTCAGCAACTCAACGTGGCTCCACAAAGGTGCTCTGCT 2693  
Qy 5093 CTGATTGCCCTGAAGTACATCAATGTGTCGATGACAGTGCACCGTTGTACAGCCAGTGG 5152  
Db 2694 TTGGTGGTCTTGACTACTCA-----GTCCATGAAGGAGACCAACCTACGCTCAATGG 2750  
Qy 5153 CAGGTGGTATCCGCTCTGCTGAGCGGGGTGAAAAGCAGCCAGAGCTCGCGCTGCAC 5212  
Db 2751 GAGAACGACGTGGTGTCTGACTGCTGTCTCACTCCCAACAGGCCAACACCTCCAT 2810  
Qy 5213 GATTATCTGAGGAGGGGACAGCAGCGCCCTTTGTGGTATATATCTGGCA 5272  
Db 2811 GCTTTCTTGATGAGTCTGCTCTGCTGCTCCCTCTCCACTACTACATCAGGCAAGTCGCC 2870  
Qy 5273 CCGAACATGGTATCCGG-----CGCGATGACCTCTTCGGGTATCTGCTGGATAT 5326  
Db 2871 AAGGACGTGTGGCATCAAGTCTCGGATACCTCTACCAATACCTCTCTCATTTGACAAAC 2930  
Qy 5327 CAGGTGTGAGCAAGTAAAAACCAACCGCATTCGGAGGGCATCGCGGCATACGGCTG 5386  
Db 2931 CAGGTCTGTGTCATCAAGACCAACAGGATCGCTGAGGCCATCGCTTCAATCCAACTC 2990  
Qy 5387 TATATCAACCGGGCCCTTAAACGGAATAGAACTCAGCGCCATGGCAGAGGTGAGGGGCGT 5446  
Db 2991 TACGTCAACCGCGCTCTTGAAACGTTGAGGAGAACGCCAACTCTGGTGTCTATCTCTCGC 3050  
Qy 5447 CAGTTTTTCACTGATGGATACGTTCAAAAGTTTACGACCTCGGGGGGCTCTCA 5506  
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Qy 5507 GAGCTGGTTTACTATCCGGAATACTACCTCGACCGGCTCGGTATCGGGCAGACCGGC 5566  
Db 3111 CAACCTGTCTACTACCCAGAGAACTACATTCAGCCCAACCATGAGGATTTGTCAGAACCAAG 3170  
Qy 5567 ATGATGACACCCCTGCTGCTGTGTCAGCGCAGAGCAGTATCAACCGGATACCGTGGAG 5626  
Db 3171 ATGATGATGCTCTCTTGGCAATCTGTCTCCCAAAGGCCAACTCAACGCTGACACTGTGGAG 3230

Qy 5627 GATGCCCTTTAAACCTTATCTGACCAACGTTTGAGCAGATTTGCCAATCTGAACACTGTGACG 5686  
Db 3231 GATGCCCTTATGAGTACTACTCACTCTCTCGAGCAGAGTTGGCAACCTCAGGTCACTCTCT 3290  
Qy 5687 GGATATCACGATAAACGCGCAGCATGACGAGGGGACTACATGGTATGTGGGTGCGAGCATC 5746  
Db 3291 GCTTACCATGACAAACATCAACACGACCAAGGTCTCACTACTTCACTTGGTCTCTCTGAG 3350  
Qy 5747 ACAGATCAGACTAACTGGTACTGGCGCAGCGCCAAACACAGCAAAATCCCAAGACTCAATG 5806  
Db 3351 ACTGATCTGGTGAAGTACTACTGGAGATCCGTGGACCAAGCAAGTTCAACGATGGCAAG 3410  
Qy 5807 ATGCCCGCGAATGCTCGACCGGATGACAAATAATTAACCTGCGGAATGAATCCGTGGTCA 5866  
Db 3411 TTGCTGCAAAACGCTTGGTCTGAGTGGCAAGATGACTGCTCCCTATCAACCCATACAG 3470  
Qy 5867 GATCTTGTGCTCGTGGTGTCTTCAACAGTCCGCTTTATGCTGCTGGGTGCAAGAGAAAT 5926  
Db 3471 TCCACCATCAGACCTGTCTATCAACAGAGCGCTCTACTTGTCTGGCTTGAGCAGAG 3530  
Qy 5927 CAGT-----CTGCTGATACGGAGCAGAGCAGCAACCAACGACAGAGC 5974  
Db 3531 GAGATCAACCAAGCAAACTGGCAACTCCAAGGATGGTTACCAAACTGAGACTGACTACCGC 3590  
Qy 5975 TACACGCTGAAAATGCTGCTCCGCGCTACGACGGTACATGGAGTTCCTCCGGTGTCTGTT 6034  
Db 3591 TACGAGTTGAAGTTGGTCTCATCCGCTACATGGTACTGATGGTACCTGGAAACACTCCAACTCACCTTC 3650  
Qy 6035 GACATTAACCGGCAACATCGCATTTTCCGGAACCGAGGGCATGATGACCTGTAATCC 6094  
Db 3651 GATGTCAACAAAGATCAGCGAGTTGAAGTTGGAGAAGAACGCTGCTCCTGGTCTCTAC 3710  
Qy 6095 CTGACTGAGAGCTCTATTGGCC-----GTTTTACTCCGCTACCGCAAGCCGGA 6144  
Db 3711 TGGCGTGGTTACCAAGGTGAGGACACCTCTTGGTCTATGTTCTACAACACGACAGACACC 3770  
Qy 6145 CTTTGTAT-----AACGCTCAGCTCATTTCT 6169  
Db 3771 CTTGACTCTTACAAGAACGCTTCCATGCAAGGTCTCTACATCTTCGCTGACATGGCTTC 3830  
Qy 6170 GTGGATAATGATATGACGCTAA-----ATGCTCATCTCAGATATAGGATTTTT 6217  
Db 3831 AAGGACATGACTCCAGAGCAAGCAACGCTCTACCGTGACAACCTCTACCAACAGTTCCAG 3890  
Qy 6218 AAGAGCCTGACTCAGAAATTTAATACGACACTGAGAAATTTAATAATATGTTTTTCA 6277  
Db 3891 ACCAAACAACTCAGGCGGTGTCAACCAACAGATACGCTGAGGACTACGAGATCCCAAGCTCT 3950  
Qy 6278 GACCCCTCCGCTAATTTATTTGTCAGTGCAACGAGTTTAAATGATGATGTTATCCACAGC 6337  
Db 3951 GTGAGCTCTCGAAGGACTACGGTGGGTGACTACTACCTCAGCATGGTGTACAACGGT 4010  
Qy 6338 GATTTCTCACTCTTAAATCTTAAACCTACAAAGTACTGTTTTTACTAATGA----- 6387  
Db 4011 GACATCCCAACCATCAACTACAGGCTGCTCTTCGACCTCAAAATCTACATCAGCCCA 4070  
Qy 6388 -----AGATTCTCTCTTTTGAACGCGCAGAGCTTCATATTACAGCAAAATGTTTGGTGT 6441  
Db 4071 AAGCTCAGGATCATCCAAACGCTACGAGGCTCAGAAAGAGGACCAAGTGCACCTGATG 4130  
Qy 6442 TGTAGTACTGCTGGCATCCCACTCAATCTACATAGAAAATTCGTTCAGGCGAGGAT 6501  
Db 4131 AACAGTACGGCAAGTTGGGTGACAGTTCAATGTTGTACACCTCTCTTGGTGTCAACCCCA 4190  
Qy 6502 AGAATTTGAGGAATAATTTTTATGAGCGCCAGGCGCGCGGATTTGACGAGTTGT 6561  
Db 4191 AACAAAGCTCCAAACAGCTCATGTTCTACCCAGTCTACCAATACTCTGGCAACACCTCT 4250  
Qy 6562 GG-----GAGTGGATGTTTCTTAATTTCAAAAGTATACAGGTTCGGAAGAAAGACAGTTG 6614  
Db 4251 GGTCTCAACCGGGTAGACTCTTGTTCACAGGGACACCACTACCCCAAGCAAGGTGGAG 4310

QY 6615 G-----TGTCAGTGAATACT 6631  
Db 4311 GCTTGGATTCTGGTGCAAGAGGTCCCTCACCACCAACAGAACGCTGCCATTGGTGATGAC 4370  
QY 6632 TATTCCGTCTACTGGCGTTAGTGGTTCTGGTTGAGTTATTATTGATTAATCAATAAATAC 6691  
Db 4371 TAGGCCACAGACTCCCTCAACAAGCCTGATGACCTCAAGCAGTACATCTTCATGACTGAC 4430  
QY 6692 TTCAAGCGGA----- 6701  
Db 4431 TCCAAGGGCACAGCCACTGATGTCCTGGTCCAGTGGAGATCAACACTGCAATCAGCCCA 4490  
QY 6702 --TTTTGTCCAGATAAATAGATAACCGCTTTAAATTAGCGGCAGTACATCAAAAGTTAATTA 6759  
Db 4491 GCCAAGGTCCAAATCATTTGTCAGAGGTGGTGGCAAGGAGCAACCTTTCAGCTGACAAG 4550  
QY 6760 CGTGTGCTCATTTGGCTCTCAAGATTTTGGAA--GTGTAAAGTGGCTCATGCGCGCACTT 6817  
Db 4551 GATGTCTCCATCCAGCCCAAGCCCATCTTCGATGAGATGAATCAACAAATTCACAGCTCTT 4610  
QY 6818 CAGATATGAATTAATCGATGATATACATGACTGACATCCGCGGTAAATGGGACTGAAAT 6877  
Db 4611 GAGATTGATGGTTCTGGCCCTCAACTTCATCAACAACCTCTGCTTCCATTGATGTCACCTTC 4670  
QY 6878 AAATCTCTGGCCTTCCGCTGAATGATTAATGATAAGCTGAGTCTGCAATCCGGGAATAAT 6937  
Db 4671 ACTGGCTTCTGCTGAGGATGGCCGAAGTTGGGTTACGAGAGCTTCTCCATCCAGTCAAC 4730  
QY 6938 CTTTTCAACACCAATCGCTGAGTTTACCGTTTAATACCAAGTGAATTTGGAAGATGAG 6997  
Db 4731 CTTAAGGTTTCCACTGACACAGCACTCACCCCTTCATCAACAAGAGACGGTGTCTGATAC 4790  
QY 6998 TT-----TGAGGTGACGTTT 7012  
Db 4791 ATGCAATGGCAAGACTACCGCAACAGGTTGAACACCCCTCTTCGAAGGCAACTTGTGGCC 4850  
QY 7013 ACGTTACCCCTGTGATCAGATAAAGCTGCTGGCGCCCGGAGCGGCATATTAACC 7072  
Db 4851 CGTGCCACCAAGCATTGACACCATCTCAGCATGGAGACCAGAACATCCAAAGGCCA 4910  
QY 7073 GTCAATTGAAACATTAATATGACATTCGGTTATCGCAFTACGTAAAAATACGGGTGGC 7132  
Db 4911 CAGTTGGGCAAGGTTTCTACGCCACCTCTGTCATCCACCTTACAACTCAGCACTCAT 4970  
QY 7133 GCGCAGTATATTGTTTCACTGGCGGTAAACGATGTGGCGTT----- 7174  
Db 4971 GGTGATGAGAGGTGGTTCAAGCTTACATCAAGCAGTGGTTGACAACTCCCACTCCCAATC 5030  
QY 7175 -----ATTGCGCTCAACACCCCTCTTTGGCC----- 7199  
Db 5031 ATCTACTCTGGTCAACTCACTGACACCAACATCAACATCACCTCTTCTCACCACCTTGAC 5090  
QY 7200 ----- 7199  
Db 5091 GATGTCCCACTCAACAGGACTACCATGCCAAGTCTACATGACCTTCAAGAAGTCTCCA 5150  
QY 7200 -----CCCAACTGTCGACGGGCGAATACCGGGATTGACCACT- 7239  
Db 5151 TCTGATGGCACCTGGTGGGTCCACACTTCGTCGATGACAAAGGGCATCGTCAACCATC 5210  
QY 7240 -----TCTTTCCATGGAGACCCAGAGGCTTACCGAACCCCGCTTGAAGAGGGGAGTGAT 7294  
Db 5211 AACCCAAAGTCCATCTCACCCTCTCGAGTCTGTCAACGTTCTCAACAACATCTCCTCT 5270  
QY 7295 GTGTTTATGACTTCTCCGAGCAATGCGCTCTATTTCTGGAGCTGTTTCTATTACAG 7354  
Db 5271 GAGCCAAATGACTTCTCTGTGGCCAACTCCCTCTACTTCTGGAGTGTGTTCTACTACACA 5330  
QY 7355 CCGATGATGGTGTTCAGCGGTTGTTGACAGAACAGCACTTCCGGAGACCAACCGCTGG 7414  
Db 5331 CCAATGCTTGGCTCAAGGTTGCTCCATGAGCAGAACTTCGATGAGGCCAACAGGTGG 5390  
QY 7415 CTGACGATATGCTGGAAACCGCGGGCAGGTGGTAAACGGGGTGTGTCAGAAATTACACC 7474

Db 5391 CTCAAGTACGTCTGGAGCCCATCTGGTTACATTGTGTCATGGTCAAAATCCAGAACTACCAA 5450  
QY 7475 TGGAAATGTCCGTCCGTGGAGGAGACACGGCTGGAAACGACTCGCGCGTGGACTCAAT 7534  
Db 5451 TGGAACTCTCAGGCAATGCTTGGAGACACCTCTGGAACCTCTGACCACTCTGACTCTGTG 5510  
QY 7535 GACCCGATGCAATAGCCAGTACGACCCCATCATTAAGGTCCGCACTTTATGTGCG 7594  
Db 5511 GACCCGTGATGCTGTGGCTCAACATGACCAATGCACTACAAGGTCTCCACCTTTCATGAGG 5570  
QY 7595 TACTCTGACCTGCTGATTCGCGCGGTGATGCGCGCTACCGGTGCTCGAGCGGAGCAC 7654  
Db 5571 ACCTTGGACCTCTTGTATGCCAGAGGTGACCATGCTTACCGCCAAATGGAGAGGAGCAC 5630  
QY 7655 CTTAACGAGCCCGGATGTGTTACGTCCAGGCCCTGAACTTCTGGGGACGAGCCCTAT 7714  
Db 5631 CTCAACGAGGCAAGATGTGTACATGCAAGCTCTCCACCTCTTGGGTGACAAAGCCATAC 5690  
QY 7715 ATTTCCTTTGACGCGGACTGGTGGCGTTGACCTCTGGGTGACGACGACGAGGTGACG 7774  
Db 5691 CTCCCACTCAGCACCACTTGGTCCGACCCCAAGGTTGGAACGCTGCTGTGACATCACT 5750  
QY 7775 CGACGCGATTACCCAGAGGCGCTGCTGGCGGTGGCGGTTGGTGGCCGCTCCCGAGACA 7834  
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QY 7835 C-----GACGCGGAAATTCCTGACGGCACTGTTCTCCCGACGAGAAACGAGGTG 7885  
Db 5811 CTCTCCCTCAGATCTCTAACACCCCTCACTGACTTGTCTCTCCACAGATCAACGAGGT 5870  
QY 7886 CTCAAAGGCTACTGGCAACCTTGGCACAGCGCTCCATAACCTGCGCCACACACCTCTCC 7945  
Db 5871 ATGATGAATCTATGGCAAACTTGGCTCAAAGGTTCTACAACCTCAGACACAACCTCTCC 5930  
QY 7946 ATTGACGGCAGCGCTTTCCCTGTCCGTCTACGCCACGCGCTCCGAACCGTCCGCGCTG 8005  
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QY 8006 CAGAGTGGCGTGTCAACAGCGGCGAGGTGTGTGACGACTGCGCGCGCGGTGTGTCGG 8065  
Db 5991 CTCTCTGCTGTGTGTCTACCAAGCAAGGTGGTGGCAAGCTCCAGAGTCTTTCATGTCC 6050  
QY 8066 CTTTACAGTTTCCGCTCATGTGGAGAACGCCGCGGGGATGTGAGCTGTGTCAGCGGG 8125  
Db 6051 CTCTGAGGTTCCCAACATGTTGGAGAACGCCGCTGGCATGTTCTCCCACTCAACCCAG 6110  
QY 8126 TTCCGCAACACACTGCTCGGTATTACCGAGCGTCAAGATCGGAGCGCTGGGCCAAACTG 8185  
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QY 8186 GTGCAAGCCAGGCAAGTGAATGATACGCGAGGGCTTCGCCAGCAGGATACGTCCTC 8245  
Db 6171 CTCCAGAACCGGCACTGAGTTGATCTCACAACTTGTTCATCAAGAACAAGACCAAT 6230  
QY 8246 GAGGAATCGATCGGATATTGCGCGCTGGAGGAGCGCGCGCGCGGAGATGCGT 8305  
Db 6231 GAGGAGCTTGATGCTGAGAGACAGTCTTTGAGAGAGCAAGGCTGGTGGCCCAATCTCGC 6290  
QY 8306 TTTGAAACGTTTACAAAGTGTGTACGAGGGGAGCGTCAACACCGCGGCAAAAGGCGCATG 8365  
Db 6291 TTGACTCTTACGGCAAGCTTACGATGAGAACATCAACGCTGTGTGAGAACCAAGGCGCATG 6350  
QY 8366 GACTTGATCTCATGTTGCTCGGTGTGTGGCATCAACCGCGCGCTCTTTTGGCGGAG 8425  
Db 6351 ACCCTCAGGGCTTCCGAGCTGGTCTCAGCACTGTGTCCAAGCCTCTCGCTTGGTGTG 6410  
QY 8426 GCGCGCGCGGATGTCGCCAATATTTACGGGCTGCGCGTGGGGGCTCCCGCTATGGG 8485  
Db 6411 GCGCTGTGACCTCGTCCAAACATCTTCGGTTTCGCTGGTGGTGGCTCCAGATGGGT 6470  
QY 8486 GCATATTTAAAGCCACCGCCATCCGCGATCCAGGTGTCTCCGATGCCACCGCCATATCA 8545

Db 6471 GCCATTGCTGAGGCTACCGGTTACGTCATGAGTCTCTGCCAACGTCATGAACACTGAG 6530  
Qy 8546 CGGACAAAATCAGCCAGTCGGAAGTGTACCGCGCTCCCGGGAGGAGTGGAAATCCAG 8605  
Db 6531 GCTGACAGATCAGCAATCTGAGACCTACAGAAGGCGCCCTCAAGAGTGGAGATCCAA 6590  
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Db 6591 AGGAACACGCTGAGGAGAGTGAAGCAAAATCGATGCTCAACTCAAGTCTCTGGCTGTC 6650  
Qy 8666 CGCCGGGAAGGCTGAGCTGCAGAAACTTACCTTGAGACCCAGCAGACCCAGCAG 8725  
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Qy 8726 CGCAGTTGGCATCTCTGCAGAGTAAGTTCAACAATACGGCTCTGTACAGCTGGCTGGG 8785  
Db 6711 TCCAGTTGGCTTCTCCCAAGGAGTTCTCCAAACAGGCTCTCTACAACTGGCTCAGA 6770  
Qy 8786 GGCAGTTGTCGGCAATTTATACAGTTCTATGACCTGGCAGTATCCCGTGGCTGATG 8845  
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Qy 8846 GCGCAACAGGCTGGCAGTGGGA---TAAATTCAGACTAGGTGCTTTATCCAGCCGGG 8902  
Db 6831 GCTGAGCAAGCTTACCGCTGGAGTTGAACGATGACTCCGCCAGGTTCAATCAAGCCAGGT 6890  
Qy 8903 GCCTGGATGGGGCAATGCCGCTCTGCTGGCGGGAAACCTGTGATGCTGAATCTGGCG 8962  
Db 6891 GCTTGGCAAGCCTACGCTGGTCTCTCTGCTGGTGGACCCCTCATGCTCTCTGGCT 6950  
Qy 8963 CAGATGAGCAGGCTGGCTGACGGGGAGTGAAGGAGTGAAGGCTTGGAGGTGGAGGACATG 9022  
Db 6951 CAAATGGAGTGTCTCACTCAAGAGGCAAGAGGCTTGGAGGTGGAGGACATG 7010  
Qy 9023 TGCCTGTGGAGTCTATACAGGCTGCG---GAGAGTGGGCAATCTCTTGGCGGAC 9079  
Db 7011 TCCCTTGTGAGGTCTACGCTGGTCTCCCAAGGACCAAGGCTTCTCCCTTGTCTCAA 7070  
Qy 9080 AAGCTGTGGAACTGTGTCAGTAAGCTTGGCGGAGTGGGTGAGAAAGCAAGCAAGTGA 9139  
Db 7071 GAGATTCAAGTGGTCAAGCAAGTGTCTGGTCTGCTGTTCTGGTAAACAACAATTG 7130  
Qy 9140 CAGATGG-----ATCAACAGCAACTCGAGGCGCACCTTGAAACTGGCTGAC 9184  
Db 7131 GCTTTCGGCGCTGTGACTGACCAAGACCTCCCTCAAGCTCTGTCTCTCTGCTGAC 7190  
Qy 9185 CTCGGTATCGCAAGATTACCGGCTCTCCCTTGGACCATGAGGCGCATCAAAACAATA 9244  
Db 7191 CTTAAGATCAGGGAGGACTACCCAGCTTCCCTTGGCAAGATCAGGCGCATCAAGCAAAATC 7250  
Qy 9245 AGCCTCAGCTCCCGGCGTGGTCCGCCCTTATCAGGACGTCGCTGGGTTCTCAGCTAC 9304  
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Qy 9305 GCGGGAAGTATGCTATGCCCGGGTTGACGCGCTGGCGGTCTCACAGGGAATGAAC 9364  
Db 7311 GGTGACAAGGCTGTTTGGGAAACGTTGGAGGCTCTTGTGTCTCTCATGGCATGAAC 7370  
Qy 9365 GACAGCGGCATTTCCAACTGGATTCAATGACCCCGGTTTACCTGCGGTTTGAAGACTT 9424  
Db 7371 GACTCTGTCAATTTCAACTTGACTTCAACGATGGCAAGTTCTCTCCATTCGAGGGCAT 7430  
Qy 9425 CCAGTTGATGACACAGGACCTCAGACTGAGCTTCCGGATGCT-----GAC 9472  
Db 7431 GCCAT---TGACCAAGGACCCCTCACCTCTCTTCTCCCAACAGCTTCCATGCCAGAGAG 7487  
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Qy 9533 ATTA 9536  
Db 7548 ATCA 7551

## RESULT 10

US-10-435-835-3  
; Sequence 3, Application US/10435835

; Patent No. 6717035

; GENERAL INFORMATION:

; APPLICANT: Patell, Jim

; APPLICANT: Merlo, Donald

; APPLICANT: Herman, Rod

; APPLICANT: Roberts, Jean

; APPLICANT: Guo, Lining

; APPLICANT: Schaffer, Barry

; APPLICANT: Sukhapingda, Kitiwari

; APPLICANT: Owens Merlo, Ann

; TITLE OF INVENTION: Transgenic Plants Expressing Photorhabdus Toxin

; FILE REFERENCE: 50698

; CURRENT APPLICATION NUMBER: US/10/435,835

; CURRENT FILING DATE: 2003-05-12

; PRIOR APPLICATION NUMBER: US 60/148,356

; PRIOR FILING DATE: 1999-08-11

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn ver. 2.0

; SEQ ID NO 3

; LENGTH: 7577

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (3)..(7553)

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:hemicot tcda

US-10-435-835-3

## Query Match

Best Local Similarity 4.3%; Score 815.2; DB 4; Length 7577;

Matches 3641; Conservative 0; Mismatches 3368; Indels 495; Gaps 31;

Qy	2510	CTCAGCGATTATCTCGCGTTCTCCCGAGGTCAAAAAATCACTGGCGCAGCTG 2569
Db	66	CTCACTGACATCTCCACAGCTCTTCAACGAGTTTCAGACAACAGTCTCTGAGCACCTC 125
Qy	2570	TCATGGGGAGAGTCTGCTATCTGTACAGTCAGCGCAGCAGCAACAAGAAACCGG 2629
Db	126	TCCTGGTCCAGACCCATGACCTTACCATGACGCTCAGCAGCTCAGAGGACAAAGG 185
Qy	2630	CTCACCGAATCCCGTATTTCTGGCCCGGGCGAATCCCTCTACTGTGTAATCCGTTGCGCTG 2689
Db	186	CTCTACGAGCTAGGATCTCTCAAGAGGGCTAAACCAACTCCAGAACGCTGTCCACCTC 245
Qy	2690	GGATACGGCAGGCA---GCCGGCAGTCGCGAGCTATGATGATGTTGGTCTCCGCGCA 2746
Db	246	GCCATCTGGCTCCAAACGCTGAGTTGATTTACAAACCAACAGTTCTCTGGCAGAGCT 305
Qy	2747	GACCGTTTCGCCCGCCCGCTCGGTGGCTCATGTTCTCACCGGGCGGTATCTGACC 2806
Db	306	AGCAGTACGTGGCTCTCTGTACAGTCTCTCTCATGTTTACGCCAGCGGTTACTCACT 365
Qy	2807	GAGCTGTACCGTGAAGGAGGACCTGCAATCCCGACACCTCGCTGTTTCCGGCTGGACATC 2866
Db	366	GAGTTGTACCGCGAGGCTAGGAACCTTCATGCTTCTGACTCCGTCTACTACTTGGACACA 425
Qy	2867	CGCGTTCGCGACCTTGGCGGCTGGCCCTTAGCCAGNATATATGACGAGAGCTCTCC 2926
Db	426	CGCAGACCAACCTCAAGAGCATGGCCCTCAGCAACAGAACATGGACATTTGAGTTGTC 485
Qy	2927	ACCTGAGCTGTCCCAATGAGTACTGTATCGGGGTATCGGGCAGCGGAAGGCTTGGAC 2986
Db	486	ACCTCTCTCTTGAAGCAAGAGCTTCTCTTGGAGTCCATCAAGACTGAGACAAAGTTGGAG 545
Qy	2987	GACGACAGC---GTCAGGGAGCTGCTCGCGGGTATCGCGCTGACCCGCTGACCCCTTAT 3043
Db	546	AACTACACCAAGGTCATGGAGATGCTCTCCACCTTCAGACCAAGCGGTGCAACTCCATAC 605



Qy	3044	CAC	TGGGCGGTACGAGCGGCCGCCCAAGCCATTCTTGTTGCAGACCGCAGCGCTGATGGGG	3103
Dd	606	CAT	GATGCCCTACGAGAAGCGTCAGGGAGGTCAATCCAACCTTCAAGACCCTGGCTTGAGCAA	665
Qy	3104	TT	CAGCCGTAATCCGGATGTGGCGCAGCTTATGGACCCCTCGCTCCACTGCTGGCCATTGA	3163
Dd	666	CT	CAACGCTCTCTCAGCCATTGCTGGTTTTGATGCACGAGCATCTCTTGCTCGGTATCAAC	725
Qy	3164	GCC	GATATTTTCA	3223
Dd	726	GC	CTCATCTCTCTGAGTTGTTCAACATCTTGACTGAGGAGATCACTGAGGCGAACGCT	785
Qy	3224	GA	AGCCTCTGGAGTAAGAATTTTGGTGATATGCTCCCTCCTCACCTGTTTATCTTATGAT	3283
Dd	786	GAG	GAGTTGTACAGAAAGAACTTCGGCAACATTTGAGCCAGCCTCTCTTGCAATGCCTGAG	845
Qy	3284	GC	ACTTGCACATTTTATGATCTGTATTACGATGAGCTAATCTTCGTTATTTGTTATTAAAGG	3343
Dd	846	TAC	CTCAAGAGGTACTACAACCTTGCTGTGATGAGGAGCTTTCT-----CAATTCATT	896
Qy	3344	CT	GACTTTTTCAAAATCCAAAACAATGAATATCTACATTAATAGTCAAATTAAGTGTGTAAC	3403
Dd	897	GG	CAAGGCTTCCAACITTCGGTCAACAGGAGTACAGCAACAACNGCTCATCACTCCAGTT	956
Qy	3404	CT	GAATGAAAGCACCTGCTTTAAATAACATPATACATCATTTATTAGAACGCTTAGCGGGAGAC	3463
Dd	957	GT	GAACTCCTCTGATGGCACTGTGAAGGCTCTACCGCATCACAGTGAGTACACCAAAAC	1016
Qy	3464	TC	CAGCAGATTAACCTGAGCTTATACCTTATGCGGATGGACATATCTTTATATTTTC	3523
Dd	1017	GC	TACCAAAATGGATGTGTAGTTGTTCCCATTGCGTGGTGAGAACTACAGACTTGACTAC	1076
Qy	3524	AG	CGTGTGTCAACGATATCAGAGGATAGTTTTCAAACCTAGGGTGGTTAGGTTCTTAACAGT	3583
Dd	1077	AAG	TTCAAGAACTTCTCAACGCGCTCCTACTCTCCATCAAGTTGTAACGACAAGGGAG	1136
Qy	3584	AG	CAATCTTTACTCTGGGATATTACAGTTTCAAAAGGGGTTGCTATAGCATTCCTGTT	3643
Dd	1137	CT	TGTCAAGCACTGAGGGTGTCTCTCAAGTGAACATTTAGTACTCTGCAACATCAACCTC	1196
Qy	3644	GAA	ATAGATGAAGGAAAGTTAAATGATGGGAT---CACAAATAGGATTGAGTAGGMAAGGG	3700
Dd	1197	AAC	CAGCTGACATCTCTCAACCATTCGAGATTGGTTTGGACGAGTCTTTCCTCTGGC	1256
Qy	3701	GG	GGGATATTACTCAACAGTAAACTTCACTCTGATGAATATGATCTCGCATATTCAATT	3760
Dd	1257	TC	TGGCGCTACGCTGACGCAAGTTCACTGTTGAGGAGTACAAACAGTACTCTTTCCCTC	1316
Qy	3761	CT	TAAATTAATAAGTTATCCGCTATACAGGCHACGGGCATGACACGGCGGAATA	3820
Dd	1317	TT	GAAGCTCAACAAGGCNAATTCGCTTCAGCAGAGCCACTGAGTTGTCTCCCAACCATCTTG	1376
Qy	3821	TAT	CAAAATCAACAATTTCTTAATAACGGTCTCACCATTCACCAATGGGTCTTGAGTAAA	3880
Dd	1377	GAG	GCAATTGAGGTTCTGTCAACTTCAACTTGACATCAACACTGATGTGCTTGGCAG	1436
Qy	3881	AT	CTCTGCTGGTTCGTTACTTGATCGGTCACATATCAGCTTTGATGTGGCCCCGCTCACTGATA	3940
Dd	1437	GT	CTTCTCACCAGTACTACATGCAACGCTTACGCCATTCATGCTGAGACTGCACTCATC	1496
Qy	3941	TT	TGCAACGGAACCATCAGTGACCGGCGTTTCAGCGCGGAAACCGGCCCTGTTTCAACACG	4000
Dd	1497	CT	CTGCAACGCAACCCATCTCTCAACGCTCTCAACAGCTCTCAACAAACGAGCTTCCCAAGTTGCAAGG	1556
Qy	4001	CT	GTTTCAACACCCACCGCTGAACGGCGCAGCTGTTTTCTGCAGATGATACCCCCCTCGAC	4060
Dd	1557	CT	CTTCAACACTCTCTTGAACGGCCAGTACTTCTCCACTGGTGATGAGGAGTTGAC	1616
Qy	4061	TT	ACGCTCTGAAGCACCGGAGGATGCTTTTCGCTCTCAGGCTACTGAACACGGCATTTTAAAC	4120
Dd	1617	CT	CAACTCTGGCTCCAC---AGGTGACTGGGAAGAAGACCATCTTTGAAGAGGGCCCTTCAAC	1673

Qy	4121	ATCAGCGCCTCGGGGCTTTCACGCTCTGGCAGTGGCCAGCGGTGACACGACGCGTGG- 4179
Db	1674	ATTGATGATGTCCTCTCTCTTCCGCTCTCTTGAAGATCACAGATCACGACAACAGGATGGC 1733
Qy	4180	--GTTTAGCTGCTCTGCTGACAAATATCGCGCACTCTACCGAGTGAACCTCTCTGGCTGAC 4237
Db	1734	AAGATCAAGAACAACTTGAAGAACCTTTCAACCTCTACATTGGCAAGTTGCTTGAGAC 1793
Qy	4238	ATCCAGCACTATCCGCTGGTGAAGCTGTCAATGTTGCTGTCCGCTCTCCCTTTTCAGCGGG 4297
Db	1794	ATCCACCACTCACCATTGATGAGTTGGACCTCTTGCTCATTTGCAGTCTGGTAGGCAAG 1853
Qy	4298	GTGGCCGCGGCTGCTGTCGCGAATAATGAG-----CTGACGCAAGTTTCTGTACCAG 4348
Db	1854	ACCAACTCTCTGCAATCTCTGACAAGCAGTTGGCAACCTCATCAGGAAGTTGAAACACC 1913
Qy	4349	ACCACCACTGGCTCAGGAGCAGGGCTGAGCGGTGACGATGTGTTCTCTGATGCTGACG 4408
Db	1914	ATCACCTCTCGGCTTCACACCCAGAAGTGGTGTCTTCCAACTCTTTCATCATGACCAAGC 1973
Qy	4409	ACGCAGTACGGTACCCTGTGACCCCGCAATTGAGAACTGTCTCGCTTCCCTGGCGCAAC 4468
Db	1974	ACCTCTACAAAGACCCCTCACTCTGTGATCAAGAACTCTTGGACACAGTCTACCAC 2033
Qy	4469	GGACTGCGGGCGGTGAGCTGTTTCCCGGAAAACGCTCCCGGCGATGGCGCTCCCTTTATT 4528
Db	2034	GGTCTCCAAAGCTTCGACAAGGACAAGGCTGACTTGTCTCATGTCATGGCTCCCTACATT 2093
Qy	4529	GCCGCGCCATGCACTGAGCGCAACGGATACGGCGAAGCGGATGTCTGACTTGGGCGGAC 4588
Db	2094	GCAGCACCCCTCAACTCTCTCTGAGAACGTGGCTCACTGTCTTGTCTCTGGGCTGAC 2153
Qy	4589	CAGTTGAAGCGCAGGGGCTGACGCTGACGGAAATTTATTCTTTTGGTGTATGAATGCGGCC 4648
Db	2154	AAGCTCAACCTGGTGATGGTGCATGACTGTGTGAGAGATTCTTGGGACTGGCTCAACACC 2213
Qy	4649	CCAAA-----TGACGACGACGGCGGGCCAGATFPGCAGGGTTCTGTC 4687
Db	2214	AAGTACACACCGGCTCCTCTGAGGCTGTTTGAGACTCAAGAGCACATTTGTCAATACTGTC 2273
Qy	4688	CAAGCCCTGTGGCAACTGGCACTGATCATTCCGACGACACCGGCCCTCAGCAGCGCGAGCTG 4747
Db	2274	CAGGCTCTTGCAAGTTGGAGATGGTCTACCACTCCACTGGCATCAACGAGAACGCTTTC 2333
Qy	4748	ACGCTGTGCTGACGACCGCGGACGCTTCCGCACAGG---ATGEGCACCATCTGCCCCAT 4804
Db	2334	AGACTCTTGTACCAAGCTGAGATGTTCCGTTGCTGCCACAGGTGCTGCACCTGCTCAT 2393
Qy	4805	GACCTGCGGCGCTTCCGCAATTACGCGTTTTTCATCGCGTTTATCGCGTAAACGACGCGGACG 4864
Db	2394	GATGCTCTCTCCTCATCATGTTTGACCAAGTTTCGCTGACTGGGTCAACGCTCTTGGTGAG 2453
Qy	4865	CATGCCGGGAGGTCTCTGACCGCACTTGAGACCGGAGAACTGTCTGTCAGCCCTGCTGGCC 4924
Db	2454	AAGGCTTCTCTGTCTTGGCTGCTCTCGAGGCGCAACTCCCTCACTGCTGAGCAACTTGCT 2513
Qy	4925	CGGSCCTGTCAAGAAATGACGAGGATGTGACCGGCGCTTTGGCGCAGGTGAGGGGGGCC 4984
Db	2514	GATGCCAATGAACCTTGATGCCAACCTCTTGTCTCAAGCTTCCATTCAAGCTCAGAACCA 2573
Qy	4985	GGTGAAACAGGACA-----ACAGCGTGTTCACCTCTGGGAAGAGGTGGACCAAG 5032
Db	2574	CAACACCTCCCACTGTCACTCCAGAGAACGCTTTTCTCTGTGGACCTCCATCAACACC 2633
Qy	5033	GCTGAGCAGTGGCTGGACATGATGAGACCTGTCCATTACGCCATCCGGTCTGGGCTAGC 5092
Db	2634	ATCCTCAATATGGGTCAACGTTGGCTGACGAACTCAACGTGGCTCCCAAGGTGTCTCTGCT 2693
Qy	5093	CTGATTGCCCTGAAGTACATCAATGTCTCCGATGACAGTGCACCGTTGTACAGCCAGCTGG 5152
Db	2694	TTGGTGGCTTGTGACTACATCCA---GTCCATGAAGGAGACACCAACTACGCTCAATGG 2750
Qy	5153	CAGTGGTATTCGGCTGTGCTGACGGCGGGCTGAAAAGCAGCCAGAGCTCGGCGCTGCAC 5212

Db 2751 GAGAACGAGCTGGTGTCTTGAATGCTGGTCTCAACTCCCAACAGGCCAACACCTCCAT 2810  
Qy 5213 GATTATCTGAGAGGGGACACGAGCGCCTTTGTGGTATTATCTGCGTAAATCTGGCA 5272  
Db 2811 GCTTTCTTGATGAGTCTCGCTCTGCTGCGCCTCTCCACCTACTACATCAGGCAAGTCGCC 2870  
Qy 5273 CCGAACATGATATCCCG- - - - -GCGGATGACCTCTTCGGGTATCTGCTGCTGGATAAT 5326  
Db 2871 AAGCAGCTGCTGCCATCAAGTCTCGGATGACCTCTACCAATACCTCTCATTTGACAAC 2930  
Qy 5327 CAGGTGTCAGCAAGGTAATAAACAACCCGCAATTTGCGAGGCCATTCGCCGCATACCGCTG 5386  
Db 2931 CAGGTCTCTGCTGCAATCAAGACACCCAGGATCGCTGAGGCCATCGCTTCCATCCAACTC 2990  
Qy 5387 TATATCAACCGGCCCTTAAAGGAATAGAACTCAGCGCCATGCGAGAGGTGAGGGGCGT 5446  
Db 2991 TAGCTCAACCGCGCTTTGAGAACGTTGAGGAGAACGCCAACTCTGGTGTCTCTCTCGC 3050  
Qy 5447 CAGTTTTTCACTGACTGGGATACGTTCAACAAAGCTTACAGCACCTGGGGGGCGTCTCA 5506  
Db 3051 CAATTCTTCATCGACTGGGACAGTACAAAGAGGTACTTCCACCTGGGCTGGTGTCTCT 3110  
Qy 5507 GAGCTGGTTATATCCGGAATACTACTCGAACCAGCGTCCGTATTCGGGCGAGACCGGC 5566  
Db 3111 CAACTTGTCTACTACCCAGAGAACTACATTTGACCCAACTAGAGATTGGTCAAGCCAAAG 3170  
Qy 5567 ATGATGACACCTGCTGAGTCTGTCAGCCAGCAGAGTATCAACCGCATACCGGTGAG 5626  
Db 3171 ATGATGATGCTCTCTTGGCAATCTGCTCCAAAGCCAACTCAACCGCTGACACTGTGGAG 3230  
Qy 5627 GATGCTTTTAAACCTATCTGACCAACGTTTGGAGCAGATTGCCAATCTGAACTGTCTCAGC 5686  
Db 3231 GATGCTTCTATGACTTACTCACTCTCTTCGAGCAAGTTGCCAACTCAAGGTCACTCT 3290  
Qy 5687 GGNATACCAATAAACGACATAGACGAGGGACTACATGGTATGTTGGTCCAGCATC 5746  
Db 3291 GCTTACCATTGACAACTCAACACGACCAAGGCTCACCTACTTCTGCTCTCTGAG 3350  
Qy 5747 ACAGATCAGACTACTGTTGCTGCGCGAGCGCCAAACACAGCAAAATCCAAAGTCAATG 5806  
Db 3351 ACTGATGCTGGTGAATCTGAGTGACCAAGATTGACTTGCCCTATCAACCATACAAAG 3410  
Qy 5807 ATGCCCGGAATGCTGGAACGATGGACAAAATAAATCTGCGGAATGAACTCGTGTCTCA 5866  
Db 3411 TTGCTGCAACGCTTGGTCTGAGTGACCAAGATTGACTTGCCCTATCAACCATACAAAG 3470  
Qy 5867 GATCTTGTGTGCTCGGTGTTTTTCAACAGTCGCTTTATGCTGCTGGTTCGAGAGAAT 5926  
Db 3471 TCCACCATCAGACCTGTCACTACAGAGCGGCTCTACTTGTCTTGGCTTGAGCAGAAAG 3530  
Qy 5927 CAGT- - - - -CTGCTGATACGGAGCGAGAGCAGCAACACCGCAGCAGAGC 5974  
Db 3531 GAGATCAACAGCAAACTGGCACTCCAGGATGGTTACCAAACTGAGACTGACTACCCG 3590  
Qy 5975 TACACGCTGAACTGTCTTCCGCGCTACGACGTTACATGGAGTTCCCGGTGTGCTTC 6034  
Db 3591 TAGAGTTGAAGTTGGTCTACATCCGCTACATGTTGTTACCTTGGAACTCCAACTACCTTC 3650  
Qy 6035 GACATTAACGGCAACATCGCATTTCCGAAACCGAGGCCATGATGATGACCTGTAAATCCC 6094  
Db 3651 GATGTCAACAAGAGATCAGCGAGTTGAAAGTTGGAGAAGAACCGTCTCTGCTCTCTAC 3710  
Qy 6095 CTGACTGAGCAGCTCTATTGGC- - - - -GTTTTACTCGTACAGCAGACCGGA 6144  
Db 3711 TGGCGTGGTACCAAGGTGAGGACACCTCTTGGTCACTGTTCTTACACACAGCAGACAC 3770  
Qy 6145 CTTTGAT- - - - -AACGCTCAGCTGATTTCT 6169  
Db 3771 CTTGACTCTTACAAGACGCTTCCATGCAAGGTCTTACATCTTGGTGTGATGGCTTCC 3830  
Qy 6170 GTGGATTAATGATGACGCTAA- - - - -ATGTCATCTCAGATATAGGATTTTT 6217

Db 3831 AAGGACATGACTCCAGAGCAAAAGCAAGCTCTACCGTGACAACTCTACCAACAGTTTCGAC 3890  
Qy 6218 AAGAGCGTCACTCAGCAATTTTAATACGACACTGAGAAATTTATTAATATGTTTTTCA 6277  
Db 3891 ACCAACAACTGAGCGGTGTCAACACAGATACGCTGAGACTACGAGATCCCAAGCTCT 3950  
Qy 6278 GACCTTCCGCTAAATTTATTTGTGAGTCAACAGTTTAAATGATGATTTATCCACAGC 6337  
Db 3951 GTCAGCTCTCGAAGGACTACGGCTGGGTGACTACTACCTCAGCATGGTGTACAAAGGT 4010  
Qy 6338 GATTTCTACTCTCTTAAATTTCTAAATCTAAGTACTGTTTTTAACTAATGA- - - - - 6387  
Db 4011 GATATCCCAACCATCACTACAGGTGCTCTTCGAGACCTCAAAATCTACATCAGCCCA 4070  
Qy 6388 - - - - -AGATTCCTCTCTTTGACGCCAGAGCTTCATATTACAGCAAAATGTTTCGTGTTT 6441  
Db 4071 AAGCTCAGGATCAATCAACCGCTACGAGGTGAGAGAGAACCAAGTGCACCTTGTATG 4130  
Qy 6442 TGTTAGTACTGCTGGCATCGCCACTCAATCTACATAGAAAAATTCGTTCAGGCAGGGAT 6501  
Db 4131 AACAACTACGGCAAGTTGGTGACAAGTTTCAATGCTCTACACCTCTCTTGGTGTCAACCCA 4190  
Qy 6502 AGAATTTGAGGAAATTAATTTTATGAGCCAGCGCGCGGAGTTTGAACGGATTTGT 6561  
Db 4191 AACACAGCTCCAAACAAAGCTCATGTTCTACCCAGTCTACCAATACTCTGCGCAACACCTCT 4250  
Qy 6562 GG- - - - -GAGTGGATGTTTCTAAATTCAAAAGTATACAGGTCCGGAAGAGACAGTTG 6614  
Db 4251 GGTCTCAACAGGGTAGACTCTTTGTTCCAGGGACACCACTACCCAAAGCAAGGTGGAG 4310  
Qy 6615 G- - - - -TGTCACCTGTAAAAATCT 6631  
Db 4311 GCTTGGATTCTGGTGCCAAAGAGTCCCTCACCAACCAAGACGCTGCCATTTGGTGATGAC 4370  
Qy 6632 TATTCGCTCACTGGCGTTAGTGGTTCTGTTGAGTTATTTATGATTCATCAATAAATAC 6691  
Db 4371 TAGCCACAGACTCCCTCAACAGCGCTGATGACTCAAGCAGTACATCTTTCATGACTGAC 4430  
Qy 6692 TTCAGCGGA- - - - - 6701  
Db 4431 TCCAAAGGCACAGCCACTGATGTCTCTGTCAGTGGAGATCAACACTGCAATCAGGCCCA 4490  
Qy 6702 - - - - -TTTTTTCAGATAAATGATTAACCGCTTTAAATAGCGCAGTACATCAAAAGTTAATTA 6759  
Db 4491 GCCAAGTCCAATCATTTGCAAGCTGTGGCAAGGAGCAACCTTTCAGCTGACAAG 4550  
Qy 6760 CGTGTGCTCTATTTGGCTCTCAAGATTTTGGGA- - - - -GTGTAAGTCGCTCATGCCGCACTT 6817  
Db 4551 GATGTCTCCATCCAGCAAGCCCATCTTCGATGAGATGAATCACTACCAATTCACAGCTCTT 4610  
Qy 6818 CAGATATCAATTAATCGATGATATCATCTGACATCCGCGCTAAATGGGACTGAAATTT 6877  
Db 4611 GAGATTGATGGTTCTGGCTCAACTTCATCAACAACTCTGCTTCATTTGATGTCACCTTC 4670  
Qy 6878 AAATCTGCGCTTCCGCTGAATGGTATTAATGATTAAGCTGAGTCTGCAATCCGGAATAAT 6937  
Db 4671 ACTGCTTCTGCTGAGATGCGCCAAAGTTGGGTTACGAGAGCTTCTCCATCCAGTCAAC 4730  
Qy 6938 CTTTTCAACACCAAAATCGGTGAGTTTACCGTTTAAATCCAGTGAATTTGTTGAAGATGAG 6997  
Db 4731 CTTAAGGTTTCCACTGACAAACGCACTCACCTTTCATCAACACGAGAACGGTGTCTAGTAC 4790  
Qy 6998 TT- - - - -TGACGTGACCTTT 7012  
Db 4791 ATGCAATGGCAAGCTACCGCACCAAGTTGAACACCTCTTTCGAAAGGCAACTTGTGGCC 4850  
Qy 7013 ACCTTCACCGCTGCTCCATCAGATAAAGCTGCTGCGCCCGCGGAGCGGCATATTTAAACC 7072  
Db 4851 CGTGCCACCAAGGCTTGCACCATCTCAGCATGGAGACCCAGAGACATCCAGAGACCA 4910  
Qy 7073 GTCATTCGAAACATTAATATGACATTCGTTTATTCGATTAATGTAATAAATACGCGTGGC 7132  
Db 4911 CAGTTGGGCAAGGGTTTTCAGCGCACCTTCGTCATCCCACTTACAACTTACAGCTCAT 4970

QY	7133	GCCAGTATATTCGTTTCACTCGGGGTAAAGATGTGGCGCTT-----	7174	CTTTACAGTTTCCCGTTCATGCTGGAGAACGCCCGGGGATGGTGAGCCTGCTGACCGGG	8125
Db	4971	GGTGATGAGAGTGGTTTCAAGCTCTATCAAGACACGTGGTGACAACAACCTCCACATC	5030	CTCTGGAGGTTCCCAACATGTTGGAGAACGCCCGTGGCATGCTCTCCCAACTCACCCAG	6110
QY	7175	-----ATTGCGCTCAAAACACCCCTCTTTGGCC-----	7199	TTTCGGCAACACACTGCTCGGTATTACCGAGCGTCAAGGATGCGGAGCGCTGGGCCAAACTG	8185
Db	5031	ATCTACTCTGGTCAACTCACTGACACCAACATCAACATCACCCCTCTTCATCCCACTTGAC	5090	6111 TTTCGGTTCCACCTCCAGAACATATTGAGAGGCAAGATGCTGAGGCTCTCAACGCTTG	6170
QY	7200	-----	7199	8186 GTGCGAACCCAGGGCAGTGAACTGATACGCCAGAGGCTTCGCCAGCAGAGATTAACGTCCTC	8245
Db	5091	GATGTCCCACTCAACAGGACTACCATGCGCAAGGTCTACATGACCTTCAAGAAGTCTCCA	5150	6171 CTCGAAACAGGACAGCTGAGTTGATCTCTCAACAACTTGCTCCATCCAGACAAGACATT	6230
QY	7200	-----GCCAACTGGTTCGACCGCGGCAATACCGGATTGACACCAT-	7239	8246 GAGGAAATCGATCGCGATATTGCCGCTCTGGAGGAGAGCCGCCGCGCGCAGATGCGT	8305
Db	5151	TCTGATGGCACCTGGTGGGGTCCACACTTGTCCGTTGATGACAAGGGCATCGTCAACATC	5210	6231 GAGGAGCTTGATGCTGAGAAGACAGTCTTTGAGAAGACAGGCTGGTCCCAATCTCGC	6290
QY	7240	-----TCTTTTCCATGGAGACCCAGAGGCTTACCGAACCCGCGCTGGAAGAGGGGAGTGAT	7294	8306 TTGTGAACGTTTACAAAGTGTGTACAGAGCGGACGTCAACACCGCGGCAAAACAGGCCATG	8365
Db	5211	NAACCAAAGTCCATCTCACCCACTTCGAGTCTGTCAAAGTCTCAACAACATCTCCTCT	5270	6291 TTTCGACTCTACGGCAAGCTCTACGATGAGAACATCAACGCTGGTGAGAACACGAGCCATG	6350
QY	7295	GTGTTTATGAGACTTCCGGAGCAATGCGCTCTATTTCTGGAGCTGTCTTATTACAG	7354	8366 GACTGTGACTCAGTTTCGTGCTGCGGATCAACCGCCGCGCTCTTTTGGCCGAG	8425
Db	5271	GAGCCAATGGACTTCTGTGTGCAACTCCTCTACTTCTGGAGTGTCTTACTACACA	5330	6351 ACCCTCAGGCTTCCGACGCTGCTCACCACTGTGTCCAAGCCTCTCGCTTGGCTGGT	6410
QY	7355	CCGATGATGGTTCAGCGGTTGTCAGGAAACAGCACTTCCCGAAGCCACCCCTGG	7414	8426 GCGCGGCGGATATGCTGCCCAATATTTACGGGCTCGGCGGCTCCGCGCTATGGG	8485
Db	5331	CCAACTCTGTGGCTCAAGGTTGTCTCCATGAGCAGAACTTCGATGAGGCCAACAGGTGG	5390	6411 GCACTGTCTGACCTGTCTCCAAACATCTTCGGTTTCGCTGGTGGTGGCTCCAGATGGGT	6470
QY	7415	CTGCACTATGCTCGGAACCCGCGGCGACGTGGTAAACGGGGTGTGCAAGATTAACAC	7474	8486 GCACATTTTAAAGCCACCCCATCGGCATCGCAGTGTCTCCGATGCCACCCGCAATATCA	8545
Db	5391	CTCAAGTACGTCTGGAGCCCATCTGGTTACATTGTGCTAGGTCAAAATCCAGAACTACCA	5450	6471 GCCATTGTGAGGCTACCGGTTACGTTATGGAGTTCCTGTGCCAAACGCTCATGAACCTGAG	6530
QY	7475	TGAATGTCCGTCGTCGAGAGGAGACACCGGTGGAACGACTCGCGCTGGACTCCATT	7534	8546 GCGGCAAAATCAGCCAGTTCGGAAGTACCGCGTCCGCGGAGAGAGTGGGAAATCCAG	8605
Db	5451	TGGAACGTCAAGGCAATTGCTTGAGGACACCTCTCTGGAACCTCTGACCACTTGACTCTGTG	5510	6531 GCTGAAGATCAGCCCAATCTGAGACCTTACAGAACGCGCGTCAAGAGTGGGAGATCCAA	6590
QY	7535	GACCCGATGCANTGCCAGTACGACCCCATGCAATTAAGGTCCGCACTTATGTGCG	7594	8606 CGTGATGTCGCGAGTCTGACGCTGGCGCAGATTGATGCGCAGCTGCGCGCCTATGGCAGTG	8665
Db	5511	GACCCGTGCTGTGGCTCAACATGACCCCAATGACTACTAAGGTCTCCACCTTCATGAGG	5570	6591 AGGAACAAGCTGAGGACAGATTGAAGCAAAATCGATGCTCAACTCAAGTCTCTTGGCTGTC	6650
QY	7595	TACTCGACCTGTGATTCGCCGCTGATGCGCGCTACCGCTGCTCGAGCGGAGACAC	7654	8666 CCGCGGAAAGGGCTGAGCTGCAGAAACCTTACTTTAGACCCAGCAGACCCAGGCACAG	8725
Db	5571	ACCTTGACCTCTTGATTGCCAGAGTGACCATGCTTACCGCAATTGGAGAGGAGACAC	5630	6651 AGAAGGAGGCTGTGTCTCTCCAGAAAGACTCTCCCTCAAGACCCAAACAGGACAAACCCAG	6710
QY	7655	CTTAAAGAGCCCGGATGTGTTAGTTCAGGCCCTGAACTTCTGGGCGAGAGCCCTAT	7714	8726 GCGAGTTGGCACTTCTGCAGAGTAAGTTCAACAATACCGCTCTGTACAGCTGGCTGCGG	8785
Db	5631	CTCAAGAGGCAAGATGTGTACATGCAAGCTCTCCACCTCTTGGGTGACAAGCCATAC	5690	6711 TCCCAAGTTGGCTTTCTCCAAAGGAAGTTCTCCAAACAGGCTCTCTACAACTGGCTCAGA	6770
QY	7715	ATTTCTTTGACCGGACTGGTTCGGGTTGACCCCTGGGTGACGACCGAGGAGTGACG	7774	8786 GCAGGTTCTCGCCCAATTTATTACAGTTCTATGACTGGCAGTATCCCGCTGCCCTGATG	8845
Db	5691	CTCCCACTCAGCACCACTTGGTCCGACCCAGGTTGGACCGTCTGCTGACATCACCACT	5750	6771 GCGCGTTGGCTGGCCATCTACTTCCNAITCTAGACCTTGTGTGGCAGAGTGGCTCATG	6830
QY	7775	CGACGGGATTACAGGAGGCCCTGTGGCGGTGCGCGGTTGGTGGCCGCTCCCGAGACA	7834	8846 GCGCAACAGCCCTGGCAGTGGGA---TAAATTCGAGACTAGGTCGTTTATCCAGCGGGG	8902
Db	5751	CAGAACGCTCATGACTCTGCCATTGTGTCTTCAGGCAAGACATCCCAACTCTCTGCCA	5810	6831 GCTGAGCAAGCCTACCGCTGGGAGTTGAACGATGACTCCGCGCAGGTTCTCATGAAGCAGGT	6890
QY	7835	C-----GGACGGGAATTCCTTGACGGCACTGTTCTCCCGCAGCAGAAACAGGAGT	7885	8903 GCTTGGATGGGGCAAAATGCCGCTGTGTCGCGGGGAAACCTGTATGCTGATCTGGCG	8962
Db	5811	CTCTCCCTCAGATCTGCTAAACCCCTCACTGACTTGTTCCTCCACAGATCAACGAGGTC	5870	6891 GCTTGGCAAGGACCTTACGCTGGTCTCTCTTGTGTGAGACCCCTCATGCTCTCTTGGCT	6950
QY	7886	CTCAAGGCTACTTGGCAAACTTGGCACAGCGGCTCCATAACCTTCGCGCAACACCTCTCC	7945	8963 CAGATGAGCAGCGCTGGCTGACGGGGATGACGGGGCAATAGAGGTGACGCGGACGCTC	9022
Db	5871	ATGATGAATCTATGGCAAACTTGGCTCAAGGGTCTAAGGCTCAACCTCAGACAAACCTCTCC	5930	6951 CAAATGGAGGATGCTCACCTCAAGAGGACAGAGGGCTTTGGAGTGGAGAGGACAGTCT	7010
QY	7946	ATTGACGGCCAGCGCTTTTCCCTGTCGCTTACGCCACGCGCTCGAAACCGTCCGCCCTG	8005	9023 TGCCTGTCCGAGGTCTATACAGCCTTCG---GGAGGATGGCGCATTTCTCTGTGGCCGAC	9079
Db	5931	ATTGATGGTCAACCACTCTACCTCCCAATCTACGCCACACCACTGACCCCAAGGCTCTT	5990	7011 TCCCTGTGTGAGTCTACGCTGTCTCTCCAAAGGACAAACGCTCCATTTCTCCCTTGTCTCA	7070
QY	8006	CAGAGTCCCGTCTCAACAGCGCGCAGGGTGTCTGAGCACTGCGCGCGCGGTTGATGCGG	8065	9080 AAGGTGGTGGAACTGGTTCAGTAACGTTTCGGCAGTTCGGGTACGAAACAGGATTA	9139
Db	5991	CTCTCTGCTGCTGTGGCTACCAAGCAAGGTGGTGGCAAGCTCCAGAGTCTCTCATGTCC	6050	7071 GAGATTGACAAGTTGGTCAGCAAGGTTCTGTGTTCTGTGTTCTGGTAACAAACATTTG	7130
				9140 CAGATGG-----ATCAACAGCAACTCGAGGCCACCCCTGAAACTGGCTGAC	9184

Db 7131 GCTTTGGCGCTGGTACTGACACCAAGACCTCCCTCCAAAGCCTCTGTCTCCTTGGCTGAC 7190  
Qy 9185 CTCGGTATCGCAACGATTACCCGGTCTCCCTTGGCAACCATGAGCGCATCAACAATA 9244  
Db 7191 CTCAGATCAGGAGGACTCCCAAGCTTCCCTTGGCAAGATCAGCGCATCAAGCAATC 7250  
Qy 9245 AGCGTCAGCTCCCGCGCTGGTGGGCCCTTATCAGGACGTCCTGGGGTCTCAGGTAC 9304  
Db 7251 TCTGTACCCCTCCAGCTCTCTTGGTCCATACCAAGATGTCGAAGCAATCTCTCCTAC 7310  
Qy 9305 GCGGAAGTATGGTCATGCCCGGGGTTGAGCGCGCTGGCGGTCTCACAGGAATGAAC 9364  
Db 7311 GGTGACAAAGCTGGTTTGGCGAAGCGTTGCGAGGCTCTTGTGTCTCTCATGGCATGAAC 7370  
Qy 9365 GACAGCGSCAAATTCGAATTCGAATCAACCGCGTTACCTGCCGTTTGAAGGACTT 9424  
Db 7371 GACTCTGTCAATTCGAATTCGAATTCGAATTCGAATTCGAATTCGAATTCGAATTC 7430  
Qy 9425 CCAGTTGATGACACAGGACCTGACACTGAGCTTCCCGGATGCT-----GAC 9472  
Db 7431 GCCAT---TGACCAAGGACCTCAGCCTCTCTCTTCCCAACGCTTCCATGCCAGAGAG 7487  
Qy 9473 GCGAAACACAGGCGATCTCCTCAGTCTGAGCGACATCATCTGCGATATCCGTTACAC 9532  
Db 7488 GGAAGCAAGCCATGCTCAAGACCTCAAGCATATCATCTCTCCATCAGGTACACC 7547  
Qy 9533 ATTA 9536  
Db 7548 ATCA 7551

RESULT 11

US-09-637-048C-6  
; Sequence 6, Application US/09637048C  
; Patent No. 6590142  
; GENERAL INFORMATION:  
; APPLICANT: Patel, Jim  
; APPLICANT: Merlo, Donald  
; APPLICANT: Herman, Rod  
; APPLICANT: Roberts, Jean  
; APPLICANT: Guo, Lining  
; APPLICANT: Schafer, Barry  
; APPLICANT: Sukhinda, Kitisri  
; APPLICANT: Owens Merlo, Ann  
; TITLE OF INVENTION: Transgenic Plants Expressing Photorhabdus Toxin  
; FILE REFERENCE: 50698  
; CURRENT APPLICATION NUMBER: US/09/637,048C  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/148,356  
; PRIOR FILING DATE: 1999-08-11  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 7621  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:hemicot tcdA  
; OTHER INFORMATION: fused to the modified 15 kDa zein endoplasmic  
; OTHER INFORMATION: reticulum signal peptide  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (4)..(7614)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)  
; OTHER INFORMATION: n can be a, t, g, or c  
US-09-637-048C-6  
Query Match 4.3%; Score 815.2; DB 4; Length 7621;  
Best Local Similarity 48.5%; Pred. No. 6.5e-216;  
Matches 3641; Conservative 0; Mismatches 3368; Indels 495; Gaps 31;

Qy 2510 CTGACGATTTATTTCTCGCGTTGTTTCCGAGGTCAAAAAATCACTGGCGACAGCCTG 2569  
Db 127 CTGCTGACATCTCCACAGCTCTTTCAACGAGTTGACACAAAGTCTCTGAGCACCTC 186  
Qy 2570 TCATGGGAGAGGTCTCTATCTGTACAGTCAGGCGCAGCAGCAAGAAAGAAACCGG 2629  
Db 187 TCTGGTCCGAGACCCATGACCTCTACATGACGCTCAGCAAGCTCAGAGGACAAACAGG 246  
Qy 2630 CTCACCAATCCCGTATTTCTGGCCCGGGGAGATCCCTACTGGTGAATCCGCTTGGCCTG 2689  
Db 247 CTCCTACAGAGCTAGGATCTCAAGAGGGCTAAACCACTCCAGAAACGCTGTCCACCTC 306  
Qy 2690 GGAATACGCGAGGCA---GCCGGCAGTCGCGAGCTATGATGACTGGTTGGCTCCCGGCA 2746  
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Qy 2747 GACCGTTTCCCGCCCGCTCGGTGGCTTCAATGTTCTCACCGGCGGCTATCTGACC 2806  
Db 367 AGCCAGTACGTGGCTCTCTGCTACAGTCTCTTCCATGTTTCAGCCCGAGCTTACTCACT 426  
Qy 2807 GAGCTGTACGTCAGGCGAAGGACCTGCATCCGACACCTCGCTGTTCCGCTCGACATC 2866  
Db 427 GAGTTGTACCGCGAGGCTAGGAACTTCATGCTTCTGACTCCGCTACTACTTGGACACA 486  
Qy 2867 CGGCGTCCCGACCTGGCGGCGCTGGCCCTTAGCCAGAAATAATATGGACGAGCTCTCC 2926  
Db 487 GCGNAGCACACCTCAAGAGCATGGCCCTCAGCCNACAGAAATGAGATTTGAGTTGCTC 546  
Qy 2927 ACCCTGAGCCTGTCATATGAGCTACTGTATCGCGGTATCGGGGCGAGCGGCTTGTGAC 2986  
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Qy 2987 GACGACG---GTCAGGAGCTGCTCGCGGGTATCGCTGACCGCGCTGACCCCTTAT 3043  
Db 607 AACTACACCAAGGTCATGSGAGTCTCTCCACCTTCAGACCAACGCGGTGCAACTCCATAC 666  
Qy 3044 CACTGGCGGTACGAGGCGGCGCCCAAGCATTCTGCTGAGGACCGCGAGCTGATGGG 3103  
Db 667 CATGATGCTTACGAGAACGTCAGGAGGTATCCAACTTCAGAACCTTGGTCTTGAGCA 726  
Qy 3104 TTCAGCGTAAATCCGATGTGGCGCAGCTTATGACCCCTCGCTCCATCTGCTGGCCATTGAA 3163  
Db 727 CTCAAAGCTTCTCCAGCATTGCTGTTGATGACCAAGGATCTCTTGGCTGCTGATCAAC 786  
Qy 3164 GCCGATTTTACCGGAGCTGTATCAGATACTGCGCGAAGAAATTCAGACAGAGTTAC 3223  
Db 787 GCCTCCATCTCTCTGAGTTGTTTCAACATCTTGACTGAGGAGTCACTGAGGCGAACGCT 846  
Qy 3224 GAAGCACTCTGGAGTAAAGAAATTTGGTGATATGCTCCCTCCCTGCTGTTATCTTATGAT 3283  
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Qy 3284 GCATTTGCAACATTTTATGATCTTGTATGATGAGCTAACTTCTGTTATTTGTCTAATGAG 3343  
Db 907 TACCTCAAGAGGTACTACAACTTGTCTGATGAGGAGCTTTCT-----CAATTCAAT 957  
Qy 3344 CTGGACTTTTCAATCCAAATGAATGATATCTATTAATGATTAATGATGCTGTAAT 3403  
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Qy 3404 CTGAATGAAAGCACTGGTTTAAATAACTATATCATCATTTATTAAAGAACGCTAGGCGGAGAC 3463  
Db 1018 GTGAATCTCTGATGGCACTGTGAAGGTCTACCGCATCAACGCTGAGTACACCAAC 1077  
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Db 1078 GCCTTACCAATGAGTGTGTGAGTTGTTCCCATTCGGTGTGAGAACTACAGACTTGTGACTAC 1137  
Qy 3524 AGCGTGTGTCAACGATATCAGAGGATGATTTTCAAAGTGGTCTGTTAGGTTCTTAACAGT 3583  
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3584 AGCAATCTTTACTCTCGGGAATATCAGCTTCAAAAAGGGTTCCGTATATAGCATTCCTGTT 3643  
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1258 AACACAGCTGACATCTCTCAACCATTTGAGATTTGACACAGAGTCTCTCCCTCTGGC 1317  
QY  
3701 GGGGGATATTTACTCAACAGTAATCTCACTCTGATTTGAATATGATCCTGGATATTCATT 3760  
Db  
1318 TCCCTGGCCCTACGCTCGACCAAGTTCACTTTGAGGAGTACAAACAGTACTCTTTTCCTC 1377  
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3761 CTTAAATTAATAAGATTTACCCCTATACAAAGCCACCGGCATGACCAAGCGGGAATA 3820  
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Db  
1498 GTCTTCTCACCAGTACTACATGCAACGCTACGCCATCATCTGAGACTGCACTCATC 1557  
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3941 TTGTGCAACGGAACCACTCAGTGACCAAGGGGTTTCAGCGGGGAACCGGCCCTGTTTCAACAG 4000  
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1558 CTCTGCAACGACCCCATCTCTCAACGCTCTTACGACAAACGAGCTTCCCAAGTTGACAGG 1617  
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Db  
1678 CTCAACTCTGGCTCCAC---AGGTGACTGGAGAAAGACCATCTTGAAGAGGGCCCTTCAAC 1734  
QY  
4121 ATCAGCGCCCTCGGGGCTTTCCACGCTCTGGCAGTTGGCCAGCGGTGACACAGCGCTGG- 4179  
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1735 ATTGATGATGCTCTCTCTCTCCGCTCTTGAAGATCACAGATCACGACAAACAGGATGGC 1794  
QY  
4180 --GTTAGTGTCTGTGTAATATCGCCGACCTCTACGAGTGAAATCTCTGGCTGAC 4237  
Db  
1795 AAGATCAAGAAACAACTTGAAGAACCTTCCAACTCTACATTTGGCAAGTTGCTTGCAGAC 1854  
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4238 ATCCAGACCTATCCGCTGGTGAAGTCTCAATGTGCTGCTCCCTCTCCCTTTTCAGCGG 4297  
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QY  
4298 GTGGCCGCGGCTCGTGTCCGATAATGAG-----CTGACGCGAGTTTCTGTACCAG 4348  
Db  
1915 ACCAACTCTCTGCAATCTCTGACAAAGCAGTTGGCAACCTCTATCAGGAAGTTGAACACC 1974  
QY  
4349 ACCACACCTGGCTACGGAGCAGGGCTGGAACGGTCAGCGATGTGTTCTGTGATGCTGACG 4408  
Db  
1975 ATCACTCTCTGGGTTTCAACCCAGAGTGTGTCTTCCAACTCTTTCATCATGACGACGC 2034  
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2095 GGTCTCAAGGCTTCGACAAAGGCAAGGCTGACTTGTCTCATGTCTATGGCTCCCTACATT 2154  
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QY  
4589 CAGTTGAAGCCAGAGGGGCTGAGCTGACGGAAATTTATTCTTTTGGTGTGATGAATCGCC 4648  
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2215 AAGCTCCAACTGGTGTGATGTCATGACTGTGAGAGAGTTCTGGGACTGGCTCAACACC 2274  
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4649 CCAAA-----TGACGACGAGCGGGCCAGATGGCAGGGTTTCTGCG 4687

2275 AAGTACACACACAGGCTCTCTGAGGCTGTTGAGACTCAAGAGACATTTGCAATACTGC 2334  
QY  
4688 CAAAGCCCTGTGCAACTGGCACTGATCATCCGAGCACGGGCTCAGCAGCGCGAGCTG 4747  
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2335 CAGGCTCTTGCACAGTTGGAGATGGTTACCACTCCACTGGGATCAACAGAGAACGCTTTC 2394  
QY  
4748 ACGCTGTGCTCAGCAGCGCGGACGCTTCCGACAGG---ATGGCACCATTCTGCCCAT 4804  
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2395 AGACTCTTCTGTCACAAAGCTGAGATGTTGCTGTGCGCACAGGTGCTGCACTGCTCAT 2454  
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2575 GATGCCATGAACCTTGATGCCAACCTTCTGCTTCCAGCTTCCATTCAAGCTCAGAACCAC 2634  
QY  
4985 GGTGAACAGGACA-----ACAGCGTTCACCTCTCTGGGAAGAGTGGACAG 5032  
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QY  
5033 GCTGAGCAGTGGCTGACATGATGAGACCTGCTCCATTACGCCATCCGCTGCGGTAGC 5092  
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2695 ATCTCCAAATGGGTCAACGTGGCTCAGCAACTCAAGTGGCTCCCAAGAGTGTCTCTGCT 2754  
QY  
5093 CTGATTGCGCTCAAGTACATCAATGTCTCCGATGACAGTGCACCGTGTGTACAGCCAGTGG 5152  
Db  
2755 TTGTCGCTTTCGACTACATCCA---GTCCATGAAGGAGACACCACTTACGCTCATGG 2811  
QY  
5153 CAGGTGTTATCCGCTGTCTGACGCGCGGCTGAAAGCAGCAGAGTCTGGCGCTGACAC 5212  
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2812 GAGAACGACGTGGTGTCTGACTGTGCTCTCAACTCCCAACAGGCCAACACCTCCAT 2871  
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5213 GATTATCTGAGAGGGGACAGCAGCGCTTGTGCTGCTATTATCTGCGTATCTGGCA 5272  
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2872 GCTTTCTTGGATGAGTCTCGCTCTGCTGCCCTCTCCACTACTCATACAGGCAAGTGGCC 2931  
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5273 CCGAACATGTTATCCCG-----GCGCGATGACCTCTTCGGGTATCTGCTGTGGATAAT 5326  
Db  
2932 AAGGCACTGCTGCCATCAAGTCTCGGATGACCTCTACCAATACCTCTCTCATTTGACAAC 2991  
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5327 CAGGTGTACGCAAGGTAATAAACCCCGCATTTGGAGGCGCATCCCGCGCATACGGCTG 5386  
Db  
2992 CAGGTCTCTGCTGCCATCAAGACCAACAGGATCGCTGAGGCCATCGCTTCCATCCAATC 3051  
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3112 CAATTCTTCACTGACTGGGCAAGTACAAACAGAGTACTCCACCTTGGGCTGGTGTCTCT 3171  
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5507 GAGCTGTTTATATCCGGAATAACTACTCTCGACCCGACCGGTCCGTTTCGGGAGACGGCG 5566  
Db  
3172 CAATTGTCTACTACCCAGAACTACTATTGACCCCAACCATGAGGATTTGCTCAGACCAAG 3231  
QY  
5567 ATGATGGACACCTGCTGCTGCTGTCAGCGAGCAGTATCAACCGCATACCGTGGAG 5626  
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3232 ATGATGGATGCTCTTGTGCAATCTGTCTCCAAAGCAACTCAACGCTGACATGTTGGAG 3291  
QY  
5627 GATGCTTTTAAACCTTATCTGACCACTGTTGAGCAGATTGCCAATCTGAACACTGTGACG 5686  
Db  
3292 GATGCTTTCATGAGCTTACCTTCACTCTTCGAGCAAGTTGGCAACCTCAAGGTCACTCT 3351  
QY  
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Db 3352 GCTTACCATGACAAATCAACGACCAAGGCTCTCACTTCTCTGAG 3411  
Qy 5747 ACAGATCAGACTAACTGGTACTGGCGAGCCCAACACAGCAAAATCCAGACTCAATG 5806  
Db 3412 ACTGATGCTGGTGAATGACTGAGATCCGTGACCAACGAAGTTCAACGATGGCAAG 3471  
Qy 5807 ATGCCCGGAATGCTGGACCGGATGACAAATAAATTAACCTGCGGAATGAATCCGTGGTCA 5866  
Db 3472 TTCCTGCAAAACGCTTGGTGTGAGTGGCAAGATTCGCTGCCCTCAACCCATCAAG 3531  
Qy 5867 GATCTTGTGCTGGTGTCTTCAACAGTGGCTTTATGCTGCTGGTGGTGAAGAAAT 5926  
Db 3532 TCCACCATCAGACCTGTCACTCAAGAGCGGCTCTACTGCTGCTGGTGGTGAAGAA 3591  
Qy 5927 CAGT-----CTGCTGATACGAGGAGCAGAGCAGCAACACAGCAGCAGAGC 5974  
Db 3592 GAGATCACCAGCAAACTGGCAACTCCAGGATGGTTACCAAACTGAGACTGACTACCGC 3651  
Qy 5975 TACAGCTGAACACTGTCTCGGCGGCTACGACGGTACATGAGTTCCCGGTTGCTGTT 6034  
Db 3652 TACGAGTTGAAGTTGGCTCACTCCGCTACGATGGTACCTGGAAACACTCCAATCACCTTC 3711  
Qy 6035 GACATTACCGCACATCGATTTCCGGAACGAGGCGATGATGACCTGTAATCCC 6094  
Db 3712 GATGTCAACAGAAAGATCAGCGAGTTGAAGTTGAGAGAACCGGTGCTCTGGTCTCTAC 3771  
Qy 6095 CTGACTGAGCAGCTCTATTGGC-----GTTTTACTCTCCACAGCAGCAGCGGA 6144  
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Qy 6145 CTTTGAT-----AACGCTCAGCTGATTTCT 6169  
Db 3832 CTTGACTCTTACAAGAACGCTTCATGCAAGGCTCTTACATCTTTCGCTGACATGGCTTC 3891  
Qy 6170 GTGGATTAATGATGACCTAA-----ATGTCATCTCAGATATAGGATTTTT 6217  
Db 3892 AAGCAGATGACTCCAGAGCAAGCAACGCTTACCGTGCACAACTCTTACCAACAGTTCCGAC 3951  
Qy 6218 AAGAGCGTCAGTCAACGAATTAATACGAGCACTCAGAAATTAATTAATAATGTTTTTCA 6277  
Db 3952 ACCAAGAGTCAGGCGTGTCAACACAGATACGCTGAGGACTAGGATCCCAAGCTCT 4011  
Qy 6278 GACCCCTCCGCTAATTTTGTGTCAGTGCAACGAGTTTAATGATGATGATATCCACAGC 6337  
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Qy 6338 GATTTCTCACTCTTAATCTAAACTACAGTACTGTTTTTACTAATGA----- 6387  
Db 4072 GACATCCCAACCATCAACTACAGGCTGCTCTTCCGACCTCAAAATCTACATCAGCCCA 4131  
Qy 6388 -----AGATTCTCTCTTTGAGCCGAGAGCTTCAATATACAGCAAAATGTTTCTGTTT 6441  
Db 4132 AAGCTCAGGATCATCCACACGGCTACAGGGTCAAGAGGAAACAGTGCACCTTGAATG 4191  
Qy 6442 TGTTAGTACTGCTGGCATCGCACTCAATCTACCATAGAAAATTCGTTCAGGACGGGAT 6501  
Db 4192 AACAAAGTACGCAAGTTGGGTGACAAGTTCAATGCTGTACACCTCTCTTGGTGTCAACCCA 4251  
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Db 4252 AACAAAGTCCCAACAGCTCATGTTCTACCCAGTCTTACCAATACTCTGGCAACACCTCT 4311  
Qy 6562 GG-----GAGTGGATGTTTCTAATTAACAAAGTATACAGGTCGGAAAAGAGCAGTTG 6614  
Db 4312 GGTCTCAACCGGTGAGACTCTGTTTCCAGGGACACCACTTACCCAGCAAGGTGGAG 4371  
Qy 6615 G-----TGTCACCTGTAATAATCT 6631  
Db 4372 GCTTGGATTTCTGTGTCNAGAGGTCCCTCAACCAACGAGACGCTGCCATTTGGTATGAC 4431  
Qy 6632 TATTCGCTACTGGCGTTAGTGGTTCTGTTGAGTTATTTATGATTCATCAAAATAATATC 6691  
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Qy 6760 CGTGTGCTCTATTGGCTCTCAAGATTTTTCGA--GTGTAAGTGCCTCATGCCGCGCACTT 6817  
Db 4612 GATGTCTCCATCAGCAAGCCCATCTTCGATGAGATGAACCTACCAATTTCAACGCTCTT 4671  
Qy 6818 CAGATATATGAATTAATTCGATGATATCATACTGACATCCGCGGTAAATGGGACTGAAAT 6877  
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Qy 6998 TT-----TGAGTGCAGCTT 7012  
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Qy 7013 ACCTTACCGCTGTGATCAGAAATAACGTCGTGCTGGCCCGCGGACGGCCATATTAAC 7072  
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Qy 7175 -----ATTGCGCTCAACACCTCTTTTGCC----- 7199  
Db 5092 ATCTACTCTGGTCAACTCACTGACACCAACATCAACATCACTCTTCTTATCCCACTTGAC 5151  
Qy 7200 ----- 7199  
Db 5152 GATGTCCCACTCAACAGGACTACCATGCAAGGTCTTACATGACCTTCAAGAAAGTCTCCA 5211  
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Db 5512 TGGAAACGTGAGGCCATTTGCTTGGAGACACCTCCTGGAACTCTGACCCCACTGACTCTGTG 5571





APPLICANT: Patell, Jim  
APPLICANT: Merlo, Donald  
APPLICANT: Herman, Rod  
APPLICANT: Roberte, Jean  
APPLICANT: Guo, Lining  
APPLICANT: Schafer, Barry  
APPLICANT: Sukhapinda, Kitisiri  
APPLICANT: Owens Merlo, Ann  
TITLE OF INVENTION: Transgenic Plants Expressing Photorhabdus Toxin  
CURRENT APPLICATION NUMBER: US/10/435,835  
CURRENT FILING DATE: 2003-05-12  
PRIOR APPLICATION NUMBER: US 60/148,356  
PRIOR FILING DATE: 1999-08-11  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 7621  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence.hemicot tcda  
OTHER INFORMATION: fused to the modified 15 kDa zein endoplasmic  
OTHER INFORMATION: reticulum signal peptide  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (4)...(7614)  
FEATURE: unsure  
NAME/KEY: (1)  
OTHER INFORMATION: n can be a, t, g, or c  
us-10-435-835-6

Query Match 4.3%; Score 815.2; DB 4; Length 7621;  
Best Local Similarity 48.5%; Pred. No. 6.5e-216;  
Matches 3641; Conservative 0; Mismatches 3368; Indels 495; Gaps 31;

Qy 2510 CTGACGGATTATTCGCGTTCGTTTCCCGAGGTCAAAAATCACTGGCGACAGCGTG 2569  
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Qy 2570 TCATGGGGAGAGTCTGCTATCTGTACAGTCAGGCGGACGACGACGACGACGACGACG 2629  
Db 187 TCCTGGTCCGAGAGCCATGACCTTACCATGACGCTCAGCAAGCTCAGAGGACACAGG 246

Qy 2630 CTCACCGAATCCCGTATTCCTGGCCGCGGCGAATCCCTACTCTGTGTAATGCGTTTCGCTG 2689  
Db 247 CTCACAGGCTAGATCTCAAGAGGCTTACCCACAACTCCAGAACGCTGTCCACCTC 306

Qy 2690 GGAATACGGCAGGCA---GCCGGCAGTCGACGCTATGATGACTGTTTGGCTCCCGCGCA 2746  
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Qy 2807 GAGCTGTACCGTGTAGGCGAGGACCTGCATCCGACACACCTCGCTGTTTCCGCTGGACATC 2866  
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Qy 2927 ACCCTGAGCTGTCTCAGTACTGATGCGGATTCGGGACGCGGAGGCGCTTGAC 2986  
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Qy 3044 CACTGGGCGTACGAGGCGGCGCCGCAAGCCATCTCTGTGAGGACCGGCTGATGGG 3103

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Qy 3284 GCCTTGCACATTTTATGATCTTGTATGATGAGTAACTTCTGTTTATTTGTCATTTAAGG 3343

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Qy 3344 CTGACCTTTTCAAAATCCAAACAAATGAATACTACATTAATAGTCAATTAAGTGTCTGAAT 3403

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Qy 3404 CTGAATGAAAGCACTGGTTTAAATAACTATATCATCTATTTTAAAGAACGCTAGGCGGAGAC 3463

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Qy 3644 GAATAGATGAAGAAAGTTAAATGATGGAT---CAATATAGGTTGAGTGAAGAAAGG 3700

Db 1258 AACACAGCTGACATCTCTCAACCATTCGAGATTTGGTTTGACAGAGTCTCTTCCCTCTGGC 1317

Qy 3701 GGGGATATTTACTCAACAGTAACTTCACTCTGATGAATATGATCTGCGATATTCATT 3760

Db 1318 TCCTGGGCTTACGCTGAGGCAAGTTCACTGTTGAGGAGTACAAACAGTACTCTTTCTCTC 1377

Qy 3761 CTTAAATTAATAAAGTTATCCGCTATACAAGGCCACGGGCTATGACCGCGGAAATA 3820

Db 1378 TTGAAGCTCAACAAAGGCAATTCGTCTCAGCAGAGGCACTGAGTTGTCTCCACCATCTTG 1437

Qy 3821 TATCAATACCAATATTTCTTAATAACGCTCTCACTTACCAATGACGCGGTCTGAGTAAA 3880

Db 1438 GAGGCAATTTGTGAGGTCTGTCAACCTTTCAACTTGAACATCAACATGATGTGCTGGCAAG 1497

Qy 3881 ATCTTCTGCTGCTTACCTGATGCGGTCACTATCAGCTTGTATGCGCGCTGCTCATGATA 3940

Db 1498 GTCTTCTCACCAGTACTACATGCAACGCTAGCCATCCATGCTGAGACTGCACTCATC 1557

Qy 3941 TTGTGCAACCGAAACCAATCACTGACCGGCTTTCAGCGGCGAAACCGGCTCTGTTCCACG 4000

Db 1558 CTCTGCAACGCAACCCATCTCTCAACGCTCTCAAGCAACCAAGCTTCCAGTTTCCGACAGG 1617

Qy 4001 CTGTTCAACACCCACCGCTGAACGCGCAGCTGTTTCTGAGATGATACCCCTCTCGAC 4060

Db 1618 CTCTTCAACACTCTCTCTTTGAACGCGCAGTACTTCTCCACTGCTGATGAGGAGATTGAC 1677

Qy 4061 TTAGCTCTCAAGCACCGGAGGATGCTTTCCGCTCTCAGCGCTACTGAAACCGCATTTAAAC 4120

Db 1678 CTCACTCTGGCTCCAC---AGGTGACTGGAGAAAGCACTTTTGAAGAGGCGCTTCAAC 1734

Qy 4121 ATCAGCGCTCTGGGCTTTTCCACGCTCTGCGAGTTGGCAGCGGTGACAGCAGCGCTGG- 4179



QY 6218 AAGAGCGTCAGTCACGAATTTAATACGAGCACTGAGAAATTTATTAATATGTTTTTCA 6277  
Db 3952 ACCAAACAGTCAGCGGTGTCAACAACAGATACGCTGAGGACTACGAGATCCCAAGCTCT 4011  
QY 6278 GACCCCTCCGCTAATATTTTGTGTCAGTGCACGAGTTTAAATGATGATGTTATCCACAGC 6337  
Db 4012 GTCAGCTCTCGCAGAGGACTACGGCTGGGGTGACTACTACCTCAGCATGGTGTACACGGT 4071  
QY 6338 GATTTCTACCTCTTAATTTCTAAATCTAAGTACTGTTTTTAAATGA----- 6387  
Db 4072 GACATCCCAACCATCAACTACAAGGCTGCCTTCTCCGACCTCAAAATCTACATCAGCCCA 4131  
QY 6388 -----AGATTCCTCTCTTTTGACGCCAGAGCTTCATATTACGCAATGTTTGGTGT 6441  
Db 4132 AAGCTCAGGATCATCCACAACGGCTACGAGGTGAGAGGACCAAGTGCACCTTGATG 4191  
QY 6442 TGTGTAGTACTGCTGGCATCGCACTCAATCTACCATAGAAAATTTGTTTCAGGCGAGGAT 6501  
Db 4192 AACAGTACGGCAAGTTGGGTGACAAGTTCAATGTTCTACCTCTCTTGGTGTCAACCCA 4251  
QY 6502 AGAATTTGAGAAATTAATTTTATGAGGCCAGCGCGCGGATTTGACCGATTTGT 6561  
Db 4252 AACCAAGCTCCAAACAGCTCATGTTCTACCCAGTCTACCAATACTCTGGCAACACCTCT 4311  
QY 6562 GG-----GAGTGGATGTTTCTTAATTCAAAAGTATACAGGTGCGGAAAAGAGCAAGTTG 6614  
Db 4312 GGTCTAACAGGGTAGACTCTTGTTCACAGGGACACCACTACCCAAAGCAAGGTGGAG 4371  
QY 6615 G-----TGTCAGTGAATATCT 6631  
Db 4372 GTTTGGATTCCTGGTGCAGAGAGTCCCTCACCAACAGAACGCTGCCATTTGGTGATGAC 4431  
QY 6632 TATTCCTGCTACTGGCGTTAGTGGTTCCTGTTGAGTTAATTTATGATTCATCAAAATAAATAC 6691  
Db 4432 TAGCCACAGACTCCCTCAACAGCTGATGACCTCAAGCAGTACATCTTCATGACTGAC 4491  
QY 6692 TTACGCGGAA----- 6701  
Db 4492 TCCAAGGGCACAGCACTGATGTCTCTGTCAGTGGAGTCAACACTGCAATCAGCCCA 4551  
QY 6702 --TTTTGTCAGATAAATGATAACCGCTTTAATTTAGCGCAGTACATCAAAAGTTAATTA 6759  
Db 4552 GCCAGGTCCAAATCATTTGTCAGGCTGGTGGCAAGGAGCAAACTTCACAGCTGACAAG 4611  
QY 6760 CGTGTCTCTATTGGCTCTCAAGATTTTGGAA--GTGTAAAGTCGCTCATGCCGCGCACTT 6817  
Db 4612 GATGTCTCCATCCAGCCCAAGCCCATCTTCGATGAGATGAATACCAATTCACGCTCTT 4671  
QY 6818 CAGATATAGAAATTAATCGATGATATCATATCATCCGCGTAAATGGGACTGAAT 6877  
Db 4672 GAGATTGATGGTCTGCGCTCAACTTCATCAACAACTCTGCTTCCATTGATGTCAACCTTC 4731  
QY 6878 AATCTCGCTTCCGCTGATGATGATTAATGATAAGCTGATGTGCAATCCGGGAATAAT 6937  
Db 4732 ACTGCTCTGCTGAGGATGGCCGAAGTTGGTTACGAGAGCTTCTCCATCCAGTCAACC 4791  
QY 6938 CTTTTCACACCAAAATCGCTGAGTTTACCGTTTAATACCAAGTATGATTTGTTGAAGATGAG 6997  
Db 4792 CTTAAGGTTCCACTGACAGGCACTCACCTTCATCAACAGGAGAGGTTGCTCAGTAC 4851  
QY 6998 TT-----TGACGTGACGTTT 7012  
Db 4852 ATGCAATGGCAAGACTACCGCACAGGTTGAAACACCTCTTTCGCAAGGCAACTTGTGGCC 4911  
QY 7013 ACGTTACCGCTGTCGATCAGATAAGCTGCTGCTGCGCGCGGAGCGGCATTAATTAACC 7072  
Db 4912 CGTGCCACCAAGCATTTGACCATCTCAGCATGGAGACCCAGAACATCCAAAGAGCCA 4971  
QY 7073 GTCATTGCAAAATTAATATGACACTTTCGTTATTCGATTTAGTAAATACGCGTGGC 7132  
Db 4972 CAGTTGGCAAGGGTTCTAGCCACCTTCTGATCCCACTTACACCTCAGCACTCAT 5031  
QY 7133 GCGCAGTATATCGTTTCACTGGGGTAAACGATGTGGCGCT----- 7174

Db 5032 GGTGATGAGAGGTGGTTCAAGCTCTACATCAAGCACGTTGGTTGACAAACAATCCACATC 5091  
QY 7175 -----ATTGCGCTCAACACCTCTTTTGCC----- 7199  
Db 5092 ATCTACTCTGGTCAACTCACTGACACCAACATCAACATCAACCTCTTCTATCCCACTTGAC 5151  
QY 7200 ----- 7199  
Db 5152 GATGTCCCACTCAACAGGAGCTACCATGCGCAAGTCTACATGACCTTCAAGAAGTCTCCA 5211  
QY 7200 -----GCCAACTGGTTCGACGGGCGAATACCGGGATTTGACACCAT- 7239  
Db 5212 TCTGATGGCACTGGTGGGTCCACACTTCGTCGATGACCAAGGCACTGTCACCATC 5271  
QY 7240 -----TCTTTCCATGGAGACCCAGAGGCTTACCGAACCCCGCTTGGAAAGGGGAGTGAT 7294  
Db 5272 AACCCAAAGTCCATCTCACCCACTTCGAGTCTGTCAAGCTTCTCAACAACATCTCTCT 5331  
QY 7295 GTGTTTATGGAATTTCTCCGAGCAATGCGCTCTATTTCTGGGAGCTGTTCTATTACAG 7354  
Db 5332 GAGCCAAATGAGCTTCTCTGGTGCACCTCTCTACTTCTGGGAGTTGTTCTACTACACA 5391  
QY 7355 CCGATGATGGTTCAGCGGTTGTCAGGAAACAGCACTTCCCGGAAGCCACCCGCTGG 7414  
Db 5392 CCAATGCTTGTGGCTCAAGAGTTGCTCCATGAGCAGAACTTCGATGAGGCGCAACAGGTGG 5451  
QY 7415 CTCAGTATGTCGGAACCCGCGGCGAGCTGCTAAACCGGGTGTGAGAAATTTACAC 7474  
Db 5452 CTCAAGTACGCTGGAGCCCATCTGGTTACATTTGTCATGGTCAATTCAGAACTACCAA 5511  
QY 7475 TGAATATGTCGCTCGCTGGAGGAGGACACCGGCTGGAACGACTCGCGCTGGACTCCATT 7534  
Db 5512 TGAACGTGAGGCCATTGCTTGAAGACACCTCTCTGGAACCTCTGACCACTTGAATCTGTG 5571  
QY 7535 GACCCGATGCAATAGCCAGTACGACCCCATGATTTCAAGGTGCGCACTTTATGTGCG 7594  
Db 5572 GACCTGATGCTGTGGCTCAACATGACCCCAATGCACTCAAGGTCTCCACTTCATGAGG 5631  
QY 7595 TACTCGACCTGCTGATTCGCGGTGATGCGCTACCGGTGCTCGAGCGGACACC 7654  
Db 5632 ACCTTGACCTCTTGAATGCGAGGTTGACCATGCTTACCGCAATTTGGAGAGGAGACACC 5691  
QY 7655 CTTAAGAGCGCCGAGTGTGTACGTCAGGCGCTGAACTCTTGGGCGACGAGCCCTAT 7714  
Db 5692 CTCAAAGGCAAGATGTGTACATGCAAGCTCTCCACTCTTGGGTGACAGCCATAC 5751  
QY 7715 ATTTCTTTGACCGCCGACTGTCGCGGTTGACCTCGGTGACCGAGCCAGGAGTGACG 7774  
Db 5752 CTCCTCACTCAGCACCACTTGGTCCGACCCAAAGGTTGGACCGTGTGTGACATCACCCT 5811  
QY 7775 CGAGCGATTAACAGAGGCGCTGTCGCGGTGCGCGGTGTCGCGCTCCGAGACA 7834  
Db 5812 CAGAACGCTCATGACTCTGCCATTGTGTCTCAGGCAAGAACATCCCAACTCTCTGTCTCCA 5871  
QY 7835 C-----GGACGCGCAATTCCTGACGCGCTGTTCTCCGAGCAGAGAGAGGTG 7885  
Db 5872 CTCCTCCTCAGATCTGCTAACCCCTCACTGACTTGTCTCTCCACAGATCAACGAGGTC 5931  
QY 7886 CTCAAAAGGCTACTGGCAAACTTTGGCAGAGCGCTCCATTAACCTGCGGCCAAACCTCTCC 7945  
Db 5932 ATGATGAACTACTGGCAAACTTTGGCTCAAAAGGTTCTAACAACCTCAGACAAACCTCTCC 5991  
QY 7946 ATTTGAGCGGCGCGCTTCTTCTGCTGCTGCTGCGCTGCGCGGTCCGACCGTCCGCGCTG 8005  
Db 5992 ATTTGATGGTCAACCACTCTACCTCCCAATCTACGCCACACCACTGACCCAAAGGCTCTT 6051  
QY 8006 CAGAGTGGCGTCTGTCACAGCGCGAGGGTGTGACAGCACTGCGCGCGCGGTGATGTCGG 8065  
Db 6052 CTCCTGCTGCTGCTGCTACAGCAGGTTGTTGGCAAGTCTCCAGAGTCTTCTATGTC 6111  
QY 8066 CTTTACAGTTTCCGCTCATGCTGGAGAACCGCCCGGGGATGTTGAGCTGTGACCGGG 8125

Db 6112 CTCGGAGGTTCCACACATGTTGGAGAACGCCCGTGGCATGTCTCTCCAACTACCCAG 6171  
Qy 8126 TTGGGCAACACTGCTCGGTATTAACGAGCGTCAAGATCGGAGGCGTGGCCAACTG 8185  
Db 6172 TTGGGTTCCACCTCCAGAACATCATTTGAGAGGCAAGATGCTGAGGCTCTCAACGCTTG 6231  
Qy 8186 CTCAGACCCAGGCGAGTGAACCTGATACGCCAGCGGCTTCGCCAGCAGGATACGCTTC 8245  
Db 6232 CTCAGAACAGGAGCTGAGTTGATCTCCACAACTTGTTCATCCAAAGAACAGCAAT 6291  
Qy 8246 GAGGAATCGATCGGATATTTGCGGCTGGAGAGAGCGCGCGCGCGAGATCGCT 8305  
Db 6292 GAGGAGCTTGATCTGAGAGACAGTCTTTGAGAGCAAGGCTGGTGCCCAATCTCGC 6351  
Qy 8306 TTTGAGCTTACAAAGTTGTAGAGGCGGAGCTCAACACCGCGCAAAACAGGCGATG 8365  
Db 6352 TTGAGCTCTTACGGCAAGCTCTAGATGAGAACATCAACGCTGTGTGAGAACCAAGGCGATG 6411  
Qy 8366 GACTTGTACCTCAGTTGCTCGGTGCTGTGGCATCAACCGCGCTCTTTTGGCCGAG 8425  
Db 6412 ACCTCAGGCTTCGGAGCTGTCTACACACTGTGTCAACGCTCTCGTTGGCTGGT 6471  
Qy 8426 GCGCGGCGGATGCTGCCAATATTTACGGGCTGGCGGTGGGGGCTCCCGCTATGG 8485  
Db 6472 GCAGCTGCTGACCTCGTTCCAAACATCTTCGGTTTCGCTGGTGGTCCAGATGGGT 6531  
Qy 8486 GCACTATTTAAAGCAACCGCATCGGATCCGATCCAGTGTCTCGATGCAACCGCATATCA 8545  
Db 6532 GCCATTTGCTGAGGCTACCGGTACGTCATGGAGTTCTCTGCCAACGCTCATGAACACTGAG 6591  
Qy 8546 GCGGACAAATCAGCAGTCGGAAGTGTACCGCGTCCGCGGAGGAGTGGGAATCCAG 8605  
Db 6592 GCTGCAAGATCAGCAATCTGAGACTCAGAAAGCGCGTCAAGAGTGGGAGATCCAA 6651  
Qy 8606 CGTGATAGTGGCAGTCTGACGTGGGCGCAGATTGATGCCAGCTGGCGGCGCATGGCAGTG 8665  
Db 6652 AGGAACAAAGCTGAGCAGAGTTGAAGCAATCGATGCTCAACTCAAGTCTTGGCTGTC 6711  
Qy 8666 GCGCGGAGGAGGCTGAGCTGAGAAACTTACTTTGAGACCAGCAGACCCAGGACAG 8725  
Db 6712 AGAAGGAGGCTGCTGCTCTCCAGAGAGCTCCCTCAAGACCCCAAGCAGGAGCAACCCAG 6771  
Qy 8726 GCGCAGTTGCACTCTCGCAGAGTAAAGTTCAACAATACGCTCTGTACAGCTGGCTGCGG 8785  
Db 6772 TCCAGTTGGCTTCTCCAAAGGAATCTCCAAACAGGCTCTCTACAACTGGCTCAGA 6831  
Qy 8786 GCGAGTTGTCGCCATTTATTAACAGTTTATGACCTGGCAGTATCCCGTSCCTGATG 8845  
Db 6832 GCGCGCTTGGCTGCCATCTACTTCCAATTCACGACCTTGTGTGGCCAGGTGCTCATG 6891  
Qy 8846 GCGCAACAGGCTGGCAGTGGGA---TAAATTCGAGACTAGTTCGCTTTATCCAGCCGGG 8902  
Db 6892 GCTGACCAAGCTTACCGCTGGGAGTTGAACGATGACTCCGCGCAGGTTCAACAGCAGGT 6951  
Qy 8903 GCCTGATGGGGCAAAATGCGGTGCTGCTGGCGGGAACCTCTGATGCTGAATCTGGG 8962  
Db 6952 GCTTGGCAAGGACCTACGCTGCTCTCTTGTGTGAGACCTCTAATCTCTCTTGGCT 7011  
Qy 8963 CAGATGGAGCAGGCTTGGCTGACGCGGGATGAGCGGGCAATAGAGGTGACGCGGACGCT 9022  
Db 7012 CAAATGGAGATGCTCACTCAAGAGGGCAAGAGGGCTTTGGAGTGGAGAGGACAGTC 7071  
Qy 9023 TGCCTGTGGAGTCTTATACAGCTTCG---GGAGATGCGGCATCTCTCTGGCCGAC 9079  
Db 7072 TCCCTTGTGAGTCTACGCTGTCTCCCAAGAGCAACGCTCATCTCTCCCTTGTCTCAA 7131  
Qy 9080 AAGTGGTGAACCTGTCAGTAACGTTGGGAGTGGCGGTACGAAAGCAACGATTA 9139  
Db 7132 GAGATTGACAAAGTTGGTCAGCAAGGTTCTGGTTCTGTGGTTCTGGTAACAACACTTG 7191  
Qy 9140 CAGATGG-----ATCAACAGCAACTCAGGCGCAACCTCGAACTGGCTGAC 9184  
Db 7192 GCTTTGGGCGCTGGTACTGACACCAAGACCTCCCTCCAAAGCCTCTGCTCTCTTGGCTGAC 7251

Qy 9185 CTCGGTATCGGCAACGATTAACCGGTCTCCCTTGGCACTAGGCGGCATCAAAATA 9244  
Db 7252 CTCGAAGATCAGGAGGAGTACCCAGCTTCCCTTGGCAAGATCAGGCGCATCAAGCAATC 7311  
Qy 9245 AGCGTCAGCGCTCCCGCGCTGGTGGCGCCTATCAGGACGTCCGTGCGGTCTTCAGCTAC 9304  
Db 7312 TCTGTACCCCTCCAGCTCTCTTGGTCCATACCAAGATGTCAAGCAATCTCTCTCTAC 7371  
Qy 9305 GCGGAAGTATGTCATGCCCGGGTTGACGCGCTGGCGGTCTCACACGGAATGAAC 9364  
Db 7372 GGTGACAAGGCTGGTTTGGCGAAGCGTTGCGAGGCTCTTGTCTCTCATGGCATGAAC 7431  
Qy 9365 GACAGCGGCAATTCCAACTGGATTTCAATGACCCCGGTACTGCGGTTTGAAGACTT 9424  
Db 7432 GACTCTGGTCAATTCCAACTTGACTTCAACGATGGCAAGTTCTCTCCATTCGAGGCAAT 7491  
Qy 9425 CAGTTGATGACACAGGAGCCTGACACTGAGCTTCCCGGATGCT-----GAC 9472  
Db 7492 GCAT---TGACCAAGGACCTTCCCTCTCTTCCCAACGCTTCCATGCCAGAGAAG 7548  
Qy 9473 GCGAACAACAGCGGATGCTCTCTAGTCTGAGCGACATCATCTGCATATCCGTTACACC 9532  
Db 7549 GGAAGCAAGCCACCATGCTCAAGACCTCAACGATATCATCTCCACATCAGGTACACC 7608  
Qy 9533 ATTA 9536  
Db 7609 ATCA 7612

RESULT 13  
US-09-817-514A-7  
; Sequence 7, Application US/09817514A  
; Patent No. 6639129  
; GENERAL INFORMATION:  
; APPLICANT: ffrench-Constant, Richard  
; APPLICANT: Bowen, David  
; APPLICANT: Rocheleau, Thomas  
; APPLICANT: Waterfield, Nicholas  
; TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS  
; FILE REFERENCE: 61645  
; CURRENT APPLICATION NUMBER: US/09/817,514A  
; CURRENT FILING DATE: 2000-03-26  
; PRIOR APPLICATION NUMBER: US 60/191806  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7  
; LENGTH: 7512  
; TYPE: DNA  
; ORGANISM: Photorhabdus luminescens  
US-09-817-514A-7

Query Match 4.1%; Score 781.2; DB 4; Length 7512;  
Best Local Similarity 60.2%; Pred. No. 2e-206;  
Matches 1356; Conservative 0; Mismatches 878; Indels 18; Gaps 3;  
Qy 7301 ATGAGCTTCTCCGAGCCAAATGCCCTCTAATTTCTGGAGCTGTTCTATTACACGCCGATG 7360  
Db 5257 ATGAGTTTCTCTGGCGCCAAATGCTCTATTTCTGGAACTGTTCTATTACACGCCGATG 5316  
Qy 7361 ATGTTGTTCCAGGGTTGTCAGGACAGCACTTCCCGAAGCCACCCGCTGGCTGCAG 7420  
Db 5317 ATGATGGCTCATCGTTGTTGTCAGGAACAGAAATTTGATGCGGCGAACCATTGGTTCCGT 5376  
Qy 7421 TATGCTGGAACCCCGCGGCGACGTTGTAACCGGGTCTGTCAGAAATTTACACCTGGAAT 7480  
Db 5377 TATGCTGGAGTCCATCCCGTTATATCGTTGATGTTAAATTTGCTATCTACCACATGAAC 5436  
Qy 7481 GTCCGCTCGCTGGAGAGGACACCGGCTGGAACGACTCCCGCTGGACTCTCATTTGACCCC 7540  
Db 5437 GTGCGACCGCTGGAAGAGACACCACTGTTGGAATGACAACTGAGCTCCACCGATCCA 5496

Qy	7541	GATGCAATAGCCCGNATGACAGCCCAATGCAATTACAGGTCCCACTTTATATGTGCTACCTC	7600
Db	5497	GATGCTGATGCCCAAGATGATCCGATGCACACTCAAGGTGGCTACTCTTTATATGGCGACGTTG	5556
Qy	7601	GACCTGCTGATTGCCCCGGTGTATGCGCGCTACCGGTGCTCGAGCGGGACACCCCTTAAC	7660
Db	5557	GATCTGCTAATGGCCCGTGGTGTATGCTGCTTACCGCCAGTTAGAGCGTGAATAGTTGGCT	5616
Qy	7661	GAGGCCCGATGTGTTAGCTCCAGGCCCTGAACTCTTGGGCGACGAGCCCTATATTTCC	7720
Db	5617	GAAGCTAAATGTGGTATACACAGGCGCTTAATCTGTTGGTGATGAGCCACCAAGTGATG	5676
Qy	7721	TTTGAAGCCCACTGCTGGCGGTGACCTCGGTGTACGACGACGAGGAGTGACGAGCGC	7780
Db	5677	CTGAGTACGACTTGGGCTAATCCAACATATGGGTAAATGCTGCTTTCAAAAAACACACAGCAG	5736
Qy	7781	GATTACCAGAGG-----CCCTGCTGGCGTGGCCGGTTGTTGTCGCTCCCGAGACA	7834
Db	5737	GTTGCTCAGCAAGTGCTTACCCAGTTGCGTCTCATAGAGGGTAAMAAACCCCGTTGCTTA	5796
Qy	7835	CGACCGCGAATTCCTTGACGCACTGTTCTCCCGCAGCAGAACGAGTGCCTCAAGGC	7894
Db	5797	GGAACGCCAATTCCTTGACGCTTATTCCTGCCGAGGAAATAGCAAGCTCAAGGC	5856
Qy	7895	TACTGGCAAACTTTGGCAGACGGCTCCATAAACCTGGGCCAACACTCTCCATTGACGC	7954
Db	5857	TACTGGCGGACACTGGCGGACGCTATGTTTAAATTTACGTCAATAATCTGTGCAATGACGC	5916
Qy	7955	CAGCGCTTTCCGTCCGCTAGCCCAAGCGCTGCGAACCGTCCGCTCGCAGAGTGCC	8014
Db	5917	CAGCGCTCTCTTTGCCGCTGATGCTTAACCGGCTGATCAAAGCTTTACTGAGTGG	5976
Qy	8015	GTCGTCAAAGCGCAGGGTGCTGCAGCACTGCGCGCCGGTGATGCCGCTTTACAGT	8074
Db	5977	GCGETTCAGTCTCTCAAGGGGAGCCGACTTGCCGAGGGCGCGCTGACTATTCACGC	6036
Qy	8075	TTCCCGGTATGTGGAGAACGCCCGGGGATGGTGAGCTGTGTGACCGGGTTTCGGAAC	8134
Db	6037	TTCCCTCAAAATGCTAGAAGGGCACGGGCTTGCTTAAACAGCTTATACAGTTTCGGTAGT	6096
Qy	8135	ACATGCTCCGTATTACCGAGCGTCAGGATGCGGAGGCGTGGCCAACTGCTGCAGACC	8194
Db	6097	TCACTATTGGGTACAGTGAGCGTCAGGATGCGGAAGCTATGAGTCAACTACTCTGCAAAAC	6156
Qy	8195	CAGGGCAGTGAACTGATACGCCAGGCGCTTTGCCAGCAGATAACGCTCTCGAGGAAATC	8254
Db	6157	CAAGCCAGCAGTTAATCTGACCAAGTATTCGTATGCAGATTAACCAATTCGCAGAGCTG	6216
Qy	8255	GATGCGGATATTGCCGCCCTGGAGGAGCGCCGCGCGCAGATGCGTTTGAACGT	8314
Db	6217	GATTCGGAAAAAACCGCTTTGCAAGTCTCTTTAGCTGAGTGCAACAAACGGTTTGACAGC	6276
Qy	8315	TACAAAGTGTGTACGAGGCGGACGTCAACACCGGCGAAAAACAGGCCATGGAATTGTATC	8374
Db	6277	TATAGCAACTGTATGAGAGAACATCAACGCAGAGTGAGCAGCGCGCTGGCGTTACGC	6336
Qy	8375	CTCAGTTCTGTCGCTGTGCGGCATCAACCGCGCGCTCTTTTGGCCGAGGCCGCGGCC	8434
Db	6337	TCAGATCTGCTATTGAGTCTCAGGAGCGCAGATTTCCGCTATGGCAGCGCGGTGTT	6396
Qy	8435	GATATGTCGCCCAATATTACGGGCTGGCGGTGGGGGCTCCCGCTATGGGGCACTATTT	8494
Db	6397	GATATGCCACCAATATCTTCGGCTTGCTGTATGGCGGCATGCATTATGTGCTATTGCC	6456
Qy	8495	AAAGCCACCGGCATCGGCATCAGGTGCTCCGTCCGATGCCACCCGCAATCAGCGGACAA	8554
Db	6457	TATGCCATCGCTGACGGTATTGAGTTGAGTGTGCTCTGCCAAGATGGTTGATGGGAGAA	6516
Qy	8555	ATCAGCAGTCCGAAGTGTAACCGCTGCGCGGAGGAGTGGGAATTCACGCGGACAA	8614
Db	6517	GTTGCTCAGTCGGAAATATATTCGGCTGCGCGTCAAGAAATGGAAAAATTCAGCGTGAAC	6576
Qy	8615	GCGCAGTCTGACGTGGCGCAGATTGATGCCACAGCTGCGCGGCATGGCAGTGGCGCGGAA	8674

Db	6577	GCACAAAGCGAGATTAAACAGTTTAAACGGCGAACTGGAATCACTGCTTATTGC	CGCGTAA	6636
Qy	8675	GGGGCTGAGCTGCAGAAAACTTACCTTTGAGACCCAGCAGACCCAGGCACAGGCGCAGTTG	8734	
Db	6637	GCGCTGAAATGCAAAAAGATACCTGAAACCCAGCAGCTCAGGCGCAGGCACAACTT	6696	
Qy	8735	GCATTCTGCAGAGTAAGTTCAACAATACGGCTCTGTACAGCTGGCTGCGGGGCAGGTTG	8794	
Db	6697	ACTTTCTTAAGAAAGCAAAATTCAGTAATCAAGCGTTATATAGTTGGTTACGAGGGCGTTTG	6756	
Qy	8795	TCCGCCATTATTATACAGTTCTATGACCTGGCAGTATCCGCTGCCTGATGGCGCAACAG	8854	
Db	6757	TCAGGTATTATTTCAGTTCTTAAGACTTGCGCGTATCAGTTGCCCTGATGGCAGAGCAA	6816	
Qy	8855	GCCTGGCAGTGGGA---TAAATTCGAGACTAGGTCGTTTATCCAGCGGGGCGCTGGATG	8911	
Db	6817	TCCTATCAATGGGAAGCTAATGATAATTCCATTAGCTTTGTCAAACCGGTGCATGGCAA	6876	
Qy	8912	GGGGCAAAATGCCGGTCTGCTGGCGGGGAAACCTTGATGCTGNAATCTGGCGCAGATGGAG	8971	
Db	6877	GSAACTTACGCGCGCTTATTTGTGTGGAGAAGCTTTTGATACAAATATTCGCACAAATGGAA	6936	
Qy	8972	CAGGCTGGCTGACGGGGATGACGGGCAATAGAGGTGACGCGACGGTCTGCGCTGTCTG	9031	
Db	6937	GAGGCATACTGAAATGGGNAATCTCGCGCTTTTGGAGTAGAACGCACGGTTTCATTGGCA	6996	
Qy	9032	GAGGTCTATACAGCTTCGCGGAGGATGCGGCATTTCTCTGGCCGACAAAGGTGGTGGAA	9091	
Db	6997	GTGGTTTATGATTTCACTGGAAGGTAATGATCGTTTTTAAATTTTAGCGGAACAAAATACCTGCA	7056	
Qy	9092	CTGGTCAGTAACGGTTTGGCGAGTCGGGTACGAAAGCAACGGATTACAGATGGATCAA	9151	
Db	7057	TTATTGGATAAGGGGAGGGAACAGCAGGAATTAAGAAATAAGGTTTTCATTGGGCTAAT	7116	
Qy	9152	CAGCAACTCGAGGCCACCTCGAACTGGGTGACCTCGGTATCGGCAACGATTACCCGGTTC	9211	
Db	7117	GCTATCCTGTCAGCTTCGGTCAAATTTGTCGACTTGAACTGGGAACGGATTATCCAGAC	7176	
Qy	9212	TCGCTTGG-----CACCATGAGCGGATCAAAACAATAAGCGTCAAGTCCCGGG	9262	
Db	7177	AGTATCGTTGGTAGCAACAAAGGTTCTGCTGTTTAAAGCAAAATCAGTGTTCGTACCTGCA	7236	
Qy	9263	CTGGTCGGCCCTTATCAGGACGTCGCTGGGTTCTCAGCTACGGCGGAAGTATGGTCAATG	9322	
Db	7237	TTGGTTGGGCTTATCAGGATGTTTACGCTATGCTCAGCTATGGTGGCAGTACTCAATTTG	7296	
Qy	9323	CCCCGGGGTTGACGCGCTGGCGGTCTCACAGGAATGAACGACAGCGGCCCAATTCCAA	9382	
Db	7297	CCGAAAGGTTGTTTCAGCGTTGGCTGTGTCATGGTACCAATGATAGTGTGATGTTCCAG	7356	
Qy	9383	CTGGATTCAATGACCGCGTTTACCTGCGGTTTGAAGGACTTCCAGTTGATGACACAGGG	9442	
Db	7357	TTGGATTCAATGACGGCAAAATACCTTGGCAATTTGAAGGTTATGCTCTTGATGATCAGGGT	7416	
Qy	9443	ACGCTGACACTGAGCTTCCGGATGCTGACGGCAAAACAACAGGCGATGCTCTCTCAGTCTG	9502	
Db	7417	ACACTGAACTTCAAATTCGGAATGCTACCGAAGCAGGAAAGCAATATTGCAAACTATG	7476	
Qy	9503	AGGCAATCAATCTGATATTCGTTACCCAT	9534	
Db	7477	AGGCAATTAATTTTGATATTCGTTATACAT	7508	

RESULT 14  
US-08-051-567B-11  
: Sequence 11, Application US/008051567B  
: Patent No. 6528484  
: GENERAL INFORMATION:  
: APPLICANT: Ensign, Gerald C  
: APPLICANT: Bowen, David J  
: APPLICANT: Pettell, James  
: APPLICANT: Fatig, Raymond

APPLICANT: Schoonover, Sue  
APPLICANT: ffrench-Constant, Richard  
APPLICANT: Rocheleau, Thomas A.  
APPLICANT: Blackburn, Michael B.  
APPLICANT: Hey, Timothy D.  
APPLICANT: Merlo, Donald J.  
APPLICANT: Orr, Gregory L.  
APPLICANT: Roberts, Jean L.  
APPLICANT: Strickland, James A.  
APPLICANT: Guo, Lining  
APPLICANT: Ciche, Todd A.  
APPLICANT: Sukhapinda, Kitiseri  
TITLE OF INVENTION: Insecticidal Protein Toxins From Photorhabdus  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dow AgroSciences Patent Department  
STREET: 9330 Zionsville Road  
CITY: Indianapolis  
STATE: IN  
COUNTRY: US  
ZIP: 46268  
COMPUTER READABLE FORM: disk  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,567B  
FILING DATE: 05-MAY-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/063,615  
FILING DATE: 18-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/395,497  
FILING DATE: 28-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/007,255  
FILING DATE: 06-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/608,423  
FILING DATE: 28-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/705,484  
FILING DATE: 28-AUG-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J  
REGISTRATION NUMBER: 27386  
REFERENCE/DOCKET NUMBER: 960296.93804  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 608-251-5000  
TELEFAX: 608-251-9166  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7515 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..7515  
US-08-851-567B-11

Query Match 4.1%; Score 781.2; DB 4; Length 7515;  
Best Local Similarity 60.2%; Pred. No. 2e-206;  
Matches 1356; Conservative 0; Mismatches 878; Indels 18; Gaps 3;

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Qy 8855 GCCTGGCAGTGGGA---TAAATTCGAGACTAGTCTGTTATCCAGCGGGGCTGGATG 8911
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Qy 8972 CAGCGCTGCTGACGGGGATGACGGGCAATAGAGTGACCGCGAGCTGCTGCTGTCG 9031
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Db 7477 AGCGATATTTTGGCATATTTCTGTTATACCAT 7508
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## RESULT 15

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US-09-637-048C-2
; Sequence 2, Application US/09637048C
; Patent No. 6590142
; GENERAL INFORMATION:
; APPLICANT: Patell, Jim
; APPLICANT: Merlo, Donald
; APPLICANT: Herman, Rod
; APPLICANT: Roberts, Jean
; APPLICANT: Guo, Lining
; APPLICANT: Schafer, Barry
; APPLICANT: Sukhapinda, Kitiieri
; APPLICANT: Owens Merlo, Ann
; TITLE OF INVENTION: Transgenic Plants Expressing Photorhabdus Toxin
; FILE REFERENCE: 50698
; CURRENT APPLICATION NUMBER: US/09/637,048C
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/148,356
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 7515
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(7512)
US-09-637-048C-2
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Query Match 4.1%; Score 781.2; DB 4; Length 7515;

Best Local Similarity 60.2%; Pred. No. 2e-206; Matches 1356; Conservative 0; Mismatches 878; Indels 18; Gaps 3;

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Db 5257 ATGATTTCTCTGGCCCAATGCTCTATTTCTGGCACTGTTCTATTACACCCCGATG 5316
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Search completed: January 27, 2005, 05:49:12  
Job time : 1755 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 06:07:24 ; Search time 75282 Seconds  
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11895.606 Million cell updates/sec

Title: US-10-070-489A-1

Perfect score: 18937  
Sequence: 1 ggatccgagtggaaggaatca.....cgtgcccgagcgagcgatggc 18937

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 segs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	4541.8	24.0	7122	1	AY220302 Yersinia
4	3419.8	18.1	4302	1	AY220492 Yersinia
5	2368.8	12.5	37948	6	AR166758 Sequence
6	2368.8	12.5	37948	6	BD136648 Insectici
c 7	2357.8	12.5	349519	1	BX571862 Photorhab
8	2348.2	12.4	127816	1	AF346500 Photorhab
c 9	1845	9.7	38457	1	XNE308438
10	1658.8	8.8	38258	6	A69711
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c 12	1640.4	8.7	313050	1	AJ414152 Yersinia
13	1367.8	7.2	38457	1	XNE308438
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21	1108.8	5.9	4431	6	AY427908	Sequence
22	1091.2	5.8	8757	1	AY282763	AY282763 Xenorhabd
23	1046.4	5.5	4425	6	CQ824616	Sequence
24	969.8	5.1	4458	6	AR285416	Sequence
c 25	968.6	5.1	349287	1	EX571860	Photorhab
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28	903.4	4.8	11421	1	AY545599	Yersinia
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30	880.2	4.6	10964	1	AE013618	Yersinia
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35	848.8	4.5	7551	6	AR285419	Sequence
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DEFINITION Sequence 1 from Patent WO0116305.  
ACCESSION AX092884  
VERSION AX092884.1 GI:13444936  
KEYWORDS Serratia entomophila  
SOURCE Serratia entomophila  
ORGANISM Serratia entomophila  
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
Enterobacteriaceae; Serratia.  
REFERENCE 1  
AUTHORS Glare,T.R., Hurst,M.R. and Jackson,T.A.  
TITLE Nucleotide sequences encoding an insectidal protein complex from  
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JOURNAL Patent: WO 0116305-A 1 08-MAR-2001;  
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Qy	3121	TGTGGCGAGCTATGAGCCCTGCTCATGCTGGCCATTGAAGCGGATATTCACCGGA	3180	Qy	4201	TATCGCGGCTACTACGAGTGAAACTCTCTGGCTGACATCCACGACCTATCCGCTGTGA	4260
Db	3121	TGTGGCGAGCTATGAGCCCTGCTCATGCTGGCCATTGAAGCGGATATTCACCGGA	3180	Db	4201	TATCGCGGCTACTACGAGTGAAACTCTCTGGCTGACATCCACGACCTATCCGCTGTGA	4260
Qy	3181	GCTGTATCAGATCTGCGGAGAAATACGACAGACAGTACGAAAGCACTCTGGAGTAA	3240	Qy	4261	GCTGTCAATGTTGCTGCTCCCTCTTTCAGCGGGTGGCGCGGCTCGCTGTGTCGA	4320
Db	3181	GCTGTATCAGATCTGCGGAGAAATACGACAGACAGTACGAAAGCACTCTGGAGTAA	3240	Db	4261	GCTGTCAATGTTGCTGCTCCCTCTTTCAGCGGGTGGCGCGGCTCGCTGTGTCGA	4320
Qy	3241	GAAATTTGGTGATGCTCCCTCTCCTGTTTATCTTATGATGACCTTGCAACATTTTA	3300	Qy	4321	TAATGAGCTGACGCGATTTCTGTACAGACACACCTGGCTACGAGACAGGCTGGAC	4380
Db	3241	GAAATTTGGTGATGCTCCCTCTCCTGTTTATCTTATGATGACCTTGCAACATTTTA	3300	Db	4321	TAATGAGCTGACGCGATTTCTGTACAGACACACCTGGCTACGAGACAGGCTGGAC	4380
Qy	3301	TGATCTTGATGAGTACGCTTCTGTTTATGTTGATTAAGGCTGGCTTTTCAATCC	3360	Qy	4381	GCTCAGCGATGTTCTGATGCTGACGACGAGTACGCTGCTGACCCCTGACCCCGACAT	4440
Db	3301	TGATCTTGATGAGTACGCTTCTGTTTATGTTGATTAAGGCTGGCTTTTCAATCC	3360	Db	4381	GCTCAGCGATGTTCTGATGCTGACGACGAGTACGCTGCTGACCCCTGACCCCGACAT	4440
Qy	3361	AAACAATGATATCTACATTAATAGTCAATTAAGTCTGTAACCTGTAAGTAAAGCACTGG	3420	Qy	4441	TGAGAACCTGCTCGCTTCCCTGCGCAACGAGCTGTGCGGCGTGGAGCTTCCCGGAAAC	4500
Db	3361	AAACAATGATATCTACATTAATAGTCAATTAAGTCTGTAACCTGTAAGTAAAGCACTGG	3420	Db	4441	TGAGAACCTGCTCGCTTCCCTGCGCAACGAGCTGTGCGGCGTGGAGCTTCCCGGAAAC	4500
Qy	3421	TTTAAATGATATCATCATTTTAAAGCGCTAGCGGAGACTCACAGCATTAACCC	3480	Qy	4501	GCTCCCGCGATGCGGCTCCCTTTATTCGCCCGCATGACGCTGGAGCGCACCGATAC	4560
Db	3421	TTTAAATGATATCATCATTTTAAAGCGCTAGCGGAGACTCACAGCATTAACCC	3480	Db	4501	GCTCCCGCGATGCGGCTCCCTTTATTCGCCCGCATGACGCTGGAGCGCACCGATAC	4560
Qy	3481	TGAGCTTATACCTTATGGGATGGAACATATCTTTATATTTTACGGTGGTCAACGAT	3540	Qy	4561	GGCGAAGCGGATGCTGACCTTGGCGGAGCCAGTGTGAAGCCAGAGGGGCTGACGCTGACGGA	4620
Db	3481	TGAGCTTATACCTTATGGGATGGAACATATCTTTTATATTTTACGGTGGTCAACGAT	3540	Db	4561	GGCGAAGCGGATGCTGACCTTGGCGGAGCCAGTGTGAAGCCAGAGGGGCTGACGCTGACGGA	4620
Qy	3541	ATCAGAGGATGTTTCAAACTAGGCTGTTAGGTTCTAAACAGTACCACTTTTACTCTGG	3600	Qy	4621	ATTTATTTCTTTTGGTGAATGCGCCCAAAATGACGAGCGGCGGCGAGATGSCAGG	4680
Db	3541	ATCAGAGGATGTTTCAAACTAGGCTGTTAGGTTCTAAACAGTACCACTTTTACTCTGG	3600	Db	4621	ATTTATTTCTTTTGGTGAATGCGCCCAAAATGACGAGCGGCGGCGAGATGSCAGG	4680
Qy	3601	GGATTTACGCTTCAAAAGGGTTCGCTATAGCATTCCTGTTGAAATAGATGAAGAAA	3660	Qy	4681	GTTTCCCAAGCCCTGTGGCAACTGGCACTGATCATCCGACGACCGGCTCAGCACGG	4740
Db	3601	GGATTTACGCTTCAAAAGGGTTCGCTATAGCATTCCTGTTGAAATAGATGAAGAAA	3660	Db	4681	GTTTCCCAAGCCCTGTGGCAACTGGCACTGATCATCCGACGACCGGCTCAGCACGG	4740
Qy	3661	GTTAAATGAGGATCACAATAGGATGAGTGAAGGAGGGGGATTTTACTCAACAGT	3720	Qy	4741	CGAGCTGACGCTGCTGCTCAGCGAGCGGAGCGCTTCCCGCACAGGATGGCACCTGCTGC	4800
Db	3661	GTTAAATGAGGATCACAATAGGATGAGTGAAGGAGGGGGATTTTACTCAACAGT	3720	Db	4741	CGAGCTGACGCTGCTGCTCAGCGAGCGGAGCGCTTCCCGCACAGGATGGCACCTGCTGC	4800
Qy	3721	AAACTTCACTCTGATTAATGATGATCTGCGATATTTCAATTTAAATTAAGTAT	3780	Qy	4801	CCATGACCTGCGCGCTTTCGCGACATTAACGCGTTCATGCGCTGTTTAAACGCGACGG	4860
Db	3721	AAACTTCACTCTGATTAATGATGATCTGCGATATTTCAATTTAAATTAAGTAT	3780	Db	4801	CCATGACCTGCGCGCTTTCGCGACATTAACGCGTTCATGCGCTGTTTAAACGCGACGG	4860
Qy	3781	CGGCTTATACAAGCCACGGGCTATGACCGGCGGAAATATATCAATCAACCAATTTCT	3840	Qy	4861	CHAGCCTGCGGGGAGGCTCTGACCGACTTGAAGCGGAGGAGTCTGCTGAGCCCTGCT	4920
Db				Db	4861	CAGCCATGCGGGAGGCTCTGACCGCACTTGAGACCGGAGAACTGCTGCTGAGCCCTGCT	4920

QY	4921	GGCCCGGCGCCTGTCTACAGAAATGAGCAGGATGTGACCGGCGCCTTGGCGCAGGTGAGGGG	4980	QY	6001	CTACGACGGTACATGAGGTTCGCCGCTGCTGCGATTCGACATTTACCGGCAACATCGCATTTCC	6060
DB	4921	GGCCCGGCGCCTGTCTACAGAAATGAGCAGGATGTGACCGGCGCCTTGGCGCAGGTGAGGGG	4980	DB	6001	CTACGACGGTACATGAGGTTCGCCGCTGCTGCGATTCGACATTTACCGGCAACATCGCATTTCC	6060
QY	4981	GGCCCGGTGAACAGGACAAACAGCGTGTTCACCTCTCTGGGAAGAGGTGGACAGGCTGAGCA	5040	QY	6061	GGAAACGCGAGGGCATGCTGTAATCCCTGACCTGAGCTGAGCAGCTCTATTGCGCGTT	6120
DB	4981	GGCCCGGTGAACAGGACAAACAGCGTGTTCACCTCTCTGGGAAGAGGTGGACAGGCTGAGCA	5040	DB	6061	GGAAACGCGAGGGCATGCTGTAATCCCTGACCTGAGCTGAGCAGCTCTATTGCGCGTT	6120
QY	5041	GTGGCTGGACATGAGTGAGACCTGTCCATTAGCCATCCGCTGGCTAGCCTGATTC	5100	QY	6121	TTACTCCGTCACCGCAAGCCGACCTTTGATACGCTCAGCTGATTTCTGTGATTAATGA	6180
DB	5041	GTGGCTGGACATGAGTGAGACCTGTCCATTAGCCATCCGCTGGCTAGCCTGATTC	5100	DB	6121	TTACTCCGTCACCGCAAGCCGACCTTTGATACGCTCAGCTGATTTCTGTGATTAATGA	6180
QY	5101	CCTGAAGTACATCAATGTGTCCGATGACAGTGCACCGTGTGACAGCAGTGGCAGGTGGT	5160	QY	6181	TATGACGCTAAATGTCTCATCTCAGATATAGGGATTTTAAAGAGCGTCAGTCACCAATTTAA	6240
DB	5101	CCTGAAGTACATCAATGTGTCCGATGACAGTGCACCGTGTGACAGCAGTGGCAGGTGGT	5160	DB	6181	TATGACGCTAAATGTCTCATCTCAGATATAGGGATTTTAAAGAGCGTCAGTCACCAATTTAA	6240
QY	5161	ATCCGCTCTGCTCGAGCGCGGTGAAAGACGACCGAGCTCGCGCTGCGACGATATCT	5220	QY	6241	TACGAGCATCTGAGAAATTTAATAATGTGTTTTTTCAGACCTTCCGCTTAATTTTGT	6300
DB	5161	ATCCGCTCTGCTCGAGCGCGGTGAAAGACGACCGAGCTCGCGCTGCGACGATATCT	5220	DB	6241	TACGAGCATCTGAGAAATTTAATAATGTGTTTTTTCAGACCTTCCGCTTAATTTTGT	6300
QY	5221	GGAGGAGGACACGACGCGCCCTTTGTGCGTATTATCTCGTAAATCTGSCACCGAACAT	5280	QY	6301	CAGTGCACAGGTTTAAATGATGATTTTCAAGATTCCTCTCTTTTTCAGCGGATTTCTCATCTTAAATCTAA	6360
DB	5221	GGAGGAGGACACGACGCGCCCTTTGTGCGTATTATCTCGTAAATCTGSCACCGAACAT	5280	DB	6301	CAGTGCACAGGTTTAAATGATGATTTTCAAGATTCCTCTCTTTTTCAGCGGATTTCTCATCTTAAATCTAA	6360
QY	5281	GGTATCCGGCGCGATGACCTCTTTCGGGTATCTGCTGGATAATCAGGTGTCAGCCAA	5340	QY	6361	AACTACAAGTACTGTTTTTACTAAATGAAGATTCCTCTCTTTTTCAGCGGATTTCTCATCTTAAATCTAA	6420
DB	5281	GGTATCCGGCGCGATGACCTCTTTCGGGTATCTGCTGGATAATCAGGTGTCAGCCAA	5340	DB	6361	AACTACAAGTACTGTTTTTACTAAATGAAGATTCCTCTCTTTTTCAGCGGATTTCTCATCTTAAATCTAA	6420
QY	5341	GGTAAAAACACCCGATTCGAGGCGCATCGCGGCTGATATCAACCGGGC	5400	QY	6421	TACAGCAAAATGTTTCTGTTTTTGTAGTACTGCTGGCATCGCCACTCAATCTACCATAGA	6480
DB	5341	GGTAAAAACACCCGATTCGAGGCGCATCGCGGCTGATATCAACCGGGC	5400	DB	6421	TACAGCAAAATGTTTCTGTTTTTGTAGTACTGCTGGCATCGCCACTCAATCTACCATAGA	6480
QY	5401	CTTTAACGGAATAGAACTAGCGCCATGCGCAGAGGTGAGGGCGCTCAGTTTTTCTAGTA	5460	QY	6481	AAAAATTCGTTTCAGGCGAGGATAGAAATTTGAGGAAATTAATTTTATGCGAGCCAGGCGCG	6540
DB	5401	CTTTAACGGAATAGAACTAGCGCCATGCGCAGAGGTGAGGGCGCTCAGTTTTTCTAGTA	5460	DB	6481	AAAAATTCGTTTCAGGCGAGGATAGAAATTTGAGGAAATTAATTTTATGCGAGCCAGGCGCG	6540
QY	5461	CTGGGATACGTTCAACAAAGTTTACAGACCTCGGGGGGCTCTCAGAGCTGTTTTACTA	5520	QY	6541	CGCGGATTTGACGGATTTGTTGGAGTGGATGTTCTAAATTTCAAAAAGTATACACAGGTCGG	6600
DB	5461	CTGGGATACGTTCAACAAAGTTTACAGACCTCGGGGGGCTCTCAGAGCTGTTTTACTA	5520	DB	6541	CGCGGATTTGACGGATTTGTTGGAGTGGATGTTCTAAATTTCAAAAAGTATACACAGGTCGG	6600
QY	5521	TCCGGAAACTACCTCGACCCGAGTCCGATTCGGGCGACCGGATGATGACACCCCT	5580	QY	6601	AAAAAGCAGTTGGTGTCACTGTAAATCTTATTCGGTCACTGGCGTTAGTGGTTCTGT	6660
DB	5521	TCCGGAAACTACCTCGACCCGAGTCCGATTCGGGCGACCGGATGATGACACCCCT	5580	DB	6601	AAAAAGCAGTTGGTGTCACTGTAAATCTTATTCGGTCACTGGCGTTAGTGGTTCTGT	6660
QY	5581	GCTGCGAGTCTGTCAGCCAGAGATCAACCGCGATACCGTGAGAGTGCCTTTTAAAC	5640	QY	6661	TGAGTTTATTTATGATTCATCAATAACTTTCAGCGGAAATTTTGTGAGTAAATGAT	6720
DB	5581	GCTGCGAGTCTGTCAGCCAGAGATCAACCGCGATACCGTGAGAGTGCCTTTTAAAC	5640	DB	6661	TGAGTTTATTTATGATTCATCAATAACTTTCAGCGGAAATTTTGTGAGTAAATGAT	6720
QY	5641	CTATCTGACCACTTTGAGCAGATTCGCAATCTGAACTGTCAGCGGATCACGATAA	5700	QY	6721	AACCGCTTTAAATTTAGCGGAGTACATCAAAAGTAAATTAAGTGTCTATTCGGCTCTCA	6780
DB	5641	CTATCTGACCACTTTGAGCAGATTCGCAATCTGAACTGTCAGCGGATCACGATAA	5700	DB	6721	AACCGCTTTAAATTTAGCGGAGTACATCAAAAGTAAATTAAGTGTCTATTCGGCTCTCA	6780
QY	5701	CGCCAGCATGACGAGGAGTACATGTTGTTGCGGATCGAGCATCACAGATCAGACTAA	5760	QY	6781	AGATTTTGGAGTGTAAAGTCTGCTCATGCGGCACTTCAGATATATGAATTAATCGATGA	6840
DB	5701	CGCCAGCATGACGAGGAGTACATGTTGTTGCGGATCGAGCATCACAGATCAGACTAA	5760	DB	6781	AGATTTTGGAGTGTAAAGTCTGCTCATGCGGCACTTCAGATATATGAATTAATCGATGA	6840
QY	5761	CTGGTACTGGCGGACGCGCAACCAAGCAAAATTCGAAGTCAATGATGCCCGGAAATGC	5820	QY	6841	TATCATCTGACATCCGCGTAAATCGGACTGAAATTAATTCCTGGGCTTCCGCTGATG	6900
DB	5761	CTGGTACTGGCGGACGCGCAACCAAGCAAAATTCGAAGTCAATGATGCCCGGAAATGC	5820	DB	6841	TATCATCTGACATCCGCGTAAATCGGACTGAAATTAATTCCTGGGCTTCCGCTGATG	6900
QY	5821	CTGGACCGGATGACAAATTAACCTGCGGAATGAATCCGTTGATCTGATCTGTTGCTC	5880	QY	6901	GTATATGATAGCTCAGTCTGCAATCCCGGAAATTAATCTTTTCAACACCAAAATCGCTGAG	6960
DB	5821	CTGGACCGGATGACAAATTAACCTGCGGAATGAATCCGTTGATCTGATCTGTTGCTC	5880	DB	6901	GTATATGATAGCTCAGTCTGCAATCCCGGAAATTAATCTTTTCAACACCAAAATCGCTGAG	6960
QY	5881	GGTGTGTTTCAACAGTCCGCTTTATGTCGTCTGGGTGCAAGAGAAATCAGTCTGCTGATC	5940	QY	6961	TTTTTACCGTTAATPACAGTGATATCTGTAAGATGAGTTTGGAGTAAATGATGATG	7020
DB	5881	GGTGTGTTTCAACAGTCCGCTTTATGTCGTCTGGGTGCAAGAGAAATCAGTCTGCTGATC	5940	DB	6961	TTTTTACCGTTAATPACAGTGATATCTGTAAGATGAGTTTGGAGTAAATGATGATG	7020
QY	5941	GGAGGACAGAGCAGCAACACCGCAGCAGAGCTACACGCTGAAATCTGTTTCGGCG	6000	QY	7021	CGCTGTCGATCAGATAAAGTGTGCTGCTGGCGCGCCGAGCGGCCATATTAACCGCTATTCG	7080
DB	5941	GGAGGACAGAGCAGCAACACCGCAGCAGAGCTACACGCTGAAATCTGTTTCGGCG	6000	DB	7021	CGCTGTCGATCAGATAAAGTGTGCTGCTGGCGCGCCGAGCGGCCATATTAACCGCTATTCG	7080
				QY	7081	AAACATTAATATGACACTTCGCTTATCGCATTTACGTAATAAATACGCGTGGCGCGAGTA	7140





QY	9301	CTACGGCGGAAGTATGGTCAATGCCCCGGGGTTGACGGCGCTCGCGGTCTCACACGGAAT	9360	10381	CTGTTTATCTGGTGTGTTGATTATAGTGAGCGTAGCTCGGTGCTGTCTGAAGCGCGGGCC	10440
DB	9301	CTACGGCGGAAGTATGGTCAATGCCCCGGGGTTGACGGCGCTCGCGGTCTCACACGGAAT	9360	10381	CTGTTTATCTGGTGTGTTGATTATAGTGAGCGTAGCTCGGTGCTGTCTGAAGCGCGGGCC	10440
QY	9361	GAACGACAGCGGCCAATTCGAATGATTTCAATGATACCCCGGTTACTCGCGGTTGAAGG	9420	10441	TGGCAACACCAAGAGTGGGAGTGGCTGTGTCTGTCAGGATGTTTTCGCGGTATGAG	10500
DB	9361	GAACGACAGCGGCCAATTCGAATGATTTCAATGATACCCCGGTTACTCGCGGTTGAAGG	9420	10441	TGGCAACACCAAGAGTGGGAGTGGCTGTGTCTGTCAGGATGTTTTCGCGGTATGAG	10500
QY	9421	ACTTCCAGTTGATGACACAGGAGCCCTGACACTGAGCTTCCGGATGCTGACGGCAACA	9480	10501	TTTGGTTTAAACCTGCGGACTCGCCGCTGTGCCGTGAGTTTGTGATTTGATTTACCTA	10560
DB	9421	ACTTCCAGTTGATGACACAGGAGCCCTGACACTGAGCTTCCGGATGCTGACGGCAACA	9480	10501	TTTGGTTTAAACCTGCGGACTCGCCGCTGTGCCGTGAGTTTGTGATTTGATTTACCTA	10560
QY	9481	ACAGGCGATCTCTCTAGTCTGAGCGACATCATCTCTGATATCCGTTTACACCATATCAG	9540	10561	GGTGTCTGCGGGAGTTTCGGAGCGAATGATGCGCCAGCATTTGATTTCTGCCCTGTTG	10620
DB	9481	ACAGGCGATCTCTCTAGTCTGAGCGACATCATCTCTGATATCCGTTTACACCATATCAG	9540	10561	GGTGTCTGCGGGAGTTTCGGAGCGAATGATGCGCCAGCATTTGATTTCTGCCCTGTTG	10620
QY	9541	CTGATAGGTATCAACATAGCGAGGCCCCCGAAGAGGGGCTCGAGGAGACTGAGCATG	9600	10621	CTGGACTACAGGGAAGTCTTCTACTCAGTCTGCTCGAGAACGTGACACAGGTGGCTTAT	10680
DB	9541	CTGATAGGTATCAACATAGCGAGGCCCCCGAAGAGGGGCTCGAGGAGACTGAGCATG	9600	10621	CTGGACTACAGGGAAGTCTTCTACTCAGTCTGCTCGAGAACGTGACACAGGTGGCTTAT	10680
QY	9601	CAAAATCATCAAGACATGGCCATTACTGCCCCCAGCTTGCCTTCCGGGGCGGTGCGGTC	9660	10681	GAGTCGGAACGGACGCTTGTGCTTGGCGGCACTGGCATTTGGGGTGGCAAACTTTACC	10740
DB	9601	CAAAATCATCAAGACATGGCCATTACTGCCCCCAGCTTGCCTTCCGGGGCGGTGCGGTC	9660	10681	GAGTCGGAACGGACGCTTGTGCTTGGCGGCACTGGCATTTGGGGTGGCAAACTTTACC	10740
QY	9661	ACCGGGCTCAAGGGTGATATCGCGGGCGCAGGGCCGGATGGTGGCGGACCTTGAGTATT	9720	10741	CCGCCGACATTTGTCGGCATGGCAGACGCGTGACGATATGGCAAGTTGAGTTGCTTCAA	10800
DB	9661	ACCGGGCTCAAGGGTGATATCGCGGGCGCAGGGCCGGATGGTGGCGGACCTTGAGTATT	9720	10741	CCGCCGACATTTGTCGGCATGGCAGACGCGTGACGATATGGCAAGTTGAGTTGCTTCAA	10800
QY	9721	CCCTTCCGGTTAGCCCCGGTGGGTTACGCCCCCACTGGGGGACTTAATATCAAGC	9780	10801	CCCTATCAGTTGTAGACCTTAAACGGCGAAGGTGTGGTGGGTATCTGTATCAGGACAGC	10860
DB	9721	CCCTTCCGGTTAGCCCCGGTGGGTTACGCCCCCACTGGGGGACTTAATATCAAGC	9780	10801	CCCTATCAGTTGTAGACCTTAAACGGCGAAGGTGTGGTGGGTATCTGTATCAGGACAGC	10860
QY	9781	CGGTGCGGGAAACGGCCCTTTGGCATTTGGCTGGGGTATCGCGGTGCTGTGTCAGCGT	9840	10861	GGTCCCTGTGTGTTACCGGTAAACGGGTACCGGTACCGGTACCGGTACCGGTACCGGTAC	10920
DB	9781	CGGTGCGGGAAACGGCCCTTTGGCATTTGGCTGGGGTATCGCGGTGCTGTGTCAGCGT	9840	10861	GGTCCCTGTGTGTTACCGGTAAACGGGTACCGGTACCGGTACCGGTACCGGTACCGGTAC	10920
QY	9841	CGTACGCGCAACGGAGCACCTACTACGATGATGATGATGATGATGATGATGATGATGAT	9900	10921	TGGGGGCGGCTGCGGCCCTGCGGCAATTCGCCGCTTTGATTAACAGCGCATCTTGGCG	10980
DB	9841	CGTACGCGCAACGGAGCACCTACTACGATGATGATGATGATGATGATGATGATGATGAT	9900	10921	TGGGGGCGGCTGCGGCCCTGCGGCAATTCGCCGCTTTGATTAACAGCGCATCTTGGCG	10980
QY	9901	GAGGTGCTGGTGGGCACTACGGCTGTGGGCAACCGAAGACAGCGAGGCACTCTCA	9960	10981	GATCTTAATGGGAGTGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGG	11040
DB	9901	GAGGTGCTGGTGGGCACTACGGCTGTGGGCAACCGAAGACAGCGAGGCACTCTCA	9960	10981	GATCTTAATGGGAGTGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGG	11040
QY	9961	CTACTGGGATAAACCCAGCGGAAGCTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAG	10020	11041	TATGATCGCACCCCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	11100
DB	9961	CTACTGGGATAAACCCAGCGGAAGCTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAG	10020	11041	TATGATCGCACCCCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	11100
QY	10021	GGTAGTCTCAGCGCCCTTGAAGCTTGGCTGCGCGCGGACGAGACAGAAACGGAAATTTGG	10080	11101	GAATATGCGCATCCAAAGACAGTGTCTGCGGATATCTTGGGGCTGGGTTTAAACGACATG	11160
DB	10021	GGTAGTCTCAGCGCCCTTGAAGCTTGGCTGCGCGCGGACGAGACAGAAACGGAAATTTGG	10080	11101	GAATATGCGCATCCAAAGACAGTGTCTGCGGATATCTTGGGGCTGGGTTTAAACGACATG	11160
QY	10081	GTGTTATATACCCCTGACGACAGGTGGCTGCTGCTGCGGCGGAAATGCGAGGCTCGATC	10140	11161	GTGCTTATCGGGCGGCGAGTGTTCGCTCTATTCGGGCAAAACGATGTTGGATATAA	11220
DB	10081	GTGTTATATACCCCTGACGACAGGTGGCTGCTGCTGCGGCGGAAATGCGAGGCTCGATC	10140	11161	GTGCTTATCGGGCGGCGAGTGTTCGCTCTATTCGGGCAAAACGATGTTGGATATAA	11220
QY	10141	AGCAACCCACAGCCCCAACACAGAGCGGGTTGGCTGATGATGATGATGATGATGATGAT	10200	11221	GGGGAGACCGTGCAGCAAAACGGAAAGACTCTCTCCGGTCCCGGGGTTGACCCACGCT	11280
DB	10141	AGCAACCCACAGCCCCAACACAGAGCGGGTTGGCTGATGATGATGATGATGATGATGAT	10200	11221	GGGGAGACCGTGCAGCAAAACGGAAAGACTCTCTCCGGTCCCGGGGTTGACCCACGCT	11280
QY	10201	ACCGGGCAACAGATGTATTACCAATACCGTGGCGAAGATGATGATGATGATGATGATGAT	10260	11281	ACCTCGTGGCTTACGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	11340
DB	10201	ACCGGGCAACAGATGTATTACCAATACCGTGGCGAAGATGATGATGATGATGATGATGAT	10260	11281	ACCTCGTGGCTTACGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	11340
QY	10261	GAGCGGACCGGCAACCGGAGGCGCGGCAACGTTATCCGGTGGCGGTCTGGTATGGT	10320	11341	GCTAATGGAGTACGTTTACGTTGATGATGATGATGATGATGATGATGATGATGATGATG	11400
DB	10261	GAGCGGACCGGCAACCGGAGGCGCGGCAACGTTATCCGGTGGCGGTCTGGTATGGT	10320	11341	GCTAATGGAGTACGTTTACGTTGATGATGATGATGATGATGATGATGATGATGATGATG	11400
QY	10321	AACCGTCAGCGGCTCGGACCTACCGGCGGTGTCGACACCATCAATGATGATGATGATG	10380	11401	ATTCCCGGTTTACGAGTACGTTTAAACCTGACCCAGATATTTGCTGGCGGAT	11460
DB	10321	AACCGTCAGCGGCTCGGACCTACCGGCGGTGTCGACACCATCAATGATGATGATGATG	10380	11401	ATTCCCGGTTTACGAGTACGTTTAAACCTGACCCAGATATTTGCTGGCGGAT	11460
				11461	ACCGCGGTTCCGGTACCGGACCTGATTTTATGCGATGATGATGATGATGATGATGATGAT	11520

11461	Db	 ACCGCGGTTCCGGTACCA	CGGACCTGATTTATGCGATGAGTGACCGGTTAGTCAITTTAT	11520
11521	Qy	TTCAACACAGAGTGGTAATTTATTTTCGCCAGCGCATACGCTGCTCTTCCGCCAAAGGTGTG	11580	
11521	Db	TTCAACACAGAGTGGTAATTTATTTTCGCCAGCGCATACGCTGCTCTTCCGCCAAAGGTGTG	11580	
11581	Qy	CGCTATGATCGCACTGCGAGTCTGCAAGTGGCGGATATCCAGGGGCTGGGGTGCCTAGC	11640	
11581	Db	CGCTATGATCGCACTGCGAGTCTGCAAGTGGCGGATATCCAGGGGCTGGGGTGCCTAGC	11640	
11641	Qy	CTGTACTGACGGTCCCCCATGTCGCGCTCATCACTGGGTGCGCATTTATCGCGAGAC	11700	
11641	Db	CTGTACTGACGGTCCCCCATGTCGCGCTCATCACTGGGTGCGCATTTATCGCGAGAC	11700	
11701	Qy	AAACCCCTGGTTGTTGAATGGCATGAACAAACAATATGGGGGCCCGGCATGCACTGCATAT	11760	
11701	Db	AAACCCCTGGTTGTTGAATGGCATGAACAAACAATATGGGGGCCCGGCATGCACTGCATAT	11760	
11761	Qy	CGCAGTTCGGTGCAGTTCCTGGCTGGATGAGAAAGCCGAGCACTGGCGGAGGAGTCC	11820	
11761	Db	CGCAGTTCGGTGCAGTTCCTGGCTGGATGAGAAAGCCGAGCACTGGCGGAGGAGTCC	11820	
11821	Qy	CTGCTCTGTACTCTGCGCAATTTACATTTGCATACCCCTGTGGCGTTCCGTTGGTGCAGAGTAG	11880	
11821	Db	CTGCTCTGTACTCTGCGCAATTTACATTTGCATACCCCTGTGGCGTTCCGTTGGTGCAGAGTAG	11880	
11881	Qy	ATCACCGGTAAACCGTCTGGTACGCAAGTGTCTTTATTCGCGACCGGGTCTGGGACGGGAG	11940	
11881	Db	ATCACCGGTAAACCGTCTGGTACGCAAGTGTCTTTATTCGCGACCGGGTCTGGGACGGGAG	11940	
11941	Qy	GAACGCGAGTTTCGGGGGTTTCGTTTGTGTAGATCAGGGATACCGATACCTTGGCAAGC	12000	
11941	Db	GAACGCGAGTTTCGGGGGTTTCGTTTGTGTAGATCAGGGATACCGATACCTTGGCAAGC	12000	
12001	Qy	CAGGGTACGCGACGAACTGAGTATGCCCTCTGTGAGCCGGAACTGATATGCCACCGGG	12060	
12001	Db	CAGGGTACGCGACGAACTGAGTATGCCCTCTGTGAGCCGGAACTGATATGCCACCGGG	12060	
12061	Qy	GTACCGGCAGTAGACAGAGCGTCTGCCGAGACGTTATTCGCAAAAGATGCGCGCTTTT	12120	
12061	Db	GTACCGGCAGTAGACAGAGCGTCTGCCGAGACGTTATTCGCAAAAGATGCGCGCTTTT	12120	
12121	Qy	GCCGATTTCCGCAACCCGTTTCACTGTCTGGTTTTCAGGAGAGGATGAGCAGACATATACCTCG	12180	
12121	Db	GCCGATTTCCGCAACCCGTTTCACTGTCTGGTTTTCAGGAGAGGATGAGCAGACATATACCTCG	12180	
12181	Qy	GACGACGCAAGACATTCGTGTTCAGCAGACCGCTTAAAGGCATCTCTCTCGCAGTAG	12240	
12181	Db	GACGACGCAAGACATTCGTGTTCAGCAGACCGCTTAAAGGCATCTCTCTCGCAGTAG	12240	
12241	Qy	TTATACGGTCCGATGGCAGCAGCCAGGCCGATATCCCTTACAGCGTCACCTGAGTCTCGC	12300	
12241	Db	TTATACGGTCCGATGGCAGCAGCCAGGCCGATATCCCTTACAGCGTCACCTGAGTCTCGC	12300	
12301	Qy	CCGCAAGTACGGCTAGTTGAAAGCGAATGAGACTACCCGGTGGTGTGCGCGATGGGCGCG	12360	
12301	Db	CCGCAAGTACGGCTAGTTGAAAGCGAATGAGACTACCCGGTGGTGTGCGCGATGGGCGCG	12360	
12361	Qy	GAAGCCGTACGTTCAGTTTATGAAAGGTCACCAATGATCTCTCAATGCCACAGCAGCGC	12420	
12361	Db	GAAGCCGTACGTTCAGTTTATGAAAGGTCACCAATGATCTCTCAATGCCACAGCAGCGC	12420	
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Qy	5445	GTCAAGTTTTTCACTGACTGGGATACGTTTCAACAAACGTTTACAGCACCTGGCGGGGGTCT	5504	Qy	6525	ATGACGCCAGCGCCGCGGCGGATTTGACGGAATTTGCGGAGTGGATGTTTCTAAATTTCAA	6584
Db	52315	GTCAAGTTTTTCACTGACTGGGATACGTTTCAACAAACGTTTACAGCACCTGGCGGGGGTCT	52374	Db	53395	ATGACGCCAGCGCCGCGGCGGATTTGACGGAATTTGCGGAGTGGATGTTTCTAAATTTCAA	53454
Qy	5505	CAGAGCTGGTTTACTATCCGGAATACTACCTCGACCGCAGCGTCCGTATCGGGCAGACCG	5564	Qy	6585	AGATATACAGGTTCGGAAAAGACGAGTTGGTGTCTACTGTAAATCTTATTCGTCACCTG	6644
Db	52375	CAGAGCTGGTTTACTATCCGGAATACTACCTCGACCGCAGCGTCCGTATCGGGCAGACCG	52434	Db	53455	AGATATACAGGTTCGGAAAAGACGAGTTGGTGTCTACTGTAAATCTTATTCGTCACCTG	53514
Qy	5565	GCATATGAGACCCCTGCTGAGTCTGTGACGACGACGACTATCAACCGCGATACCGTGG	5624	Qy	6645	GCCTTAGTGGTCTGTTGAGTTATTTATTTGATTTCATCAATAATAATACTTCAGCGGAATTT	6704
Db	52435	GCATATGAGACCCCTGCTGAGTCTGTGACGACGACGACTATCAACCGCGATACCGTGG	52494	Db	53515	GCCTTAGTGGTCTGTTGAGTTATTTATTTGATTTCATCAATAATAATACTTCAGCGGAATTT	53574
Qy	5625	AGGATGCTTTTAAAAACCTATCTGACCACTGTTTACGACGATTTGCAACACTGTCTCA	5684	Qy	6705	TGTCAGATAAATGATAACCGCTTTAATTTAGCGGCAGTACATCAAAAGTTTAAATTCGTTGT	6764
Db	52495	AGGATGCTTTTAAAAACCTATCTGACCACTGTTTACGACGATTTGCAACACTGTCTCA	52554	Db	53575	TGTCAGATAAATGATAACCGCTTTAATTTAGCGGCAGTACATCAAAAGTTTAAATTCGTTGT	53634
Qy	5685	GCGGATATCAGATAACGACGATGACGACGAGGAGTCAATGATATGTTGGGTGCGAGCA	5744	Qy	6765	CGTCTATTGGCTCTCAAGATTTTGGAGTGTAAAGTGGCTCATGCGCGCATCTTCAGATAT	6824
Db	52555	GCGGATATCAGATAACGACGATGACGACGAGGAGTCAATGATATGTTGGGTGCGAGCA	52614	Db	53635	CGTCTATTGGCTCTCAAGATTTTGGAGTGTAAAGTGGCTCATGCGCGCATCTTCAGATAT	53694
Qy	5745	TCACAGATCAGACTAATCTGTTGCTGCGCAGCGCCACACACAGCAAAATCCAGACTCAA	5804	Qy	6825	ATGAATTAATTCAGATGATATCATCTACATCCGCGGTAAATGGAGCTGAAATTTAAATTCCT	6884
Db	52615	TCACAGATCAGACTAATCTGTTGCTGCGCAGCGCCACACACAGCAAAATCCAGACTCAA	52674	Db	53695	ATGAATTAATTCAGATGATATCATCTACATCCGCGGTAAATGGAGCTGAAATTTAAATTCCT	53754
Qy	5805	TGATGCCCGCGAATTCCTGGACCGGATGGACAAAAATTAATCTGCGGAATGAATCCCGTGT	5864	Qy	6885	GGCCTTCCGCTGAATGGTATAATGTAAGCTGCTGCAATCCGGGAATAATCTTTTCA	6944
Db	52675	TGATGCCCGCGAATTCCTGGACCGGATGGACAAAAATTAATCTGCGGAATGAATCCCGTGT	52734	Db	53755	GGCCTTCCGCTGAATGGTATAATGTAAGCTGCTGCAATCCGGGAATAATCTTTTCA	53814
Qy	5865	CAGATCTGTGCTCGGTGTTTTTCAACAGTCCGCTTTATGTCGTGCGGTGCAAGAGA	5924	Qy	6945	ACACAAATTCGCTGAGTTTACCGTTAATACAGTGATATTTGTTGAAGATGAGTTTGACG	7004
Db	52735	CAGATCTGTGCTCGGTGTTTTTCAACAGTCCGCTTTATGTCGTGCGGTGCAAGAGA	52794	Db	53815	ACACAAATTCGCTGAGTTTACCGTTAATACAGTGATATTTGTTGAAGATGAGTTTGACG	53874
Qy	5925	ATCAGTCTGCTGATACGGAGCAGAGACGACGACCAACCGCAGCAGACTACCGCTGA	5984	Qy	7005	TGACGTTTACGTTTACCGCTGTCGATCAGAAATACCGTCTGTCGCGCGCCGCGACCGCCA	7064
Db	52795	ATCAGTCTGCTGATACGGAGCAGAGACGACGACCAACCGCAGCAGACTACCGCTGA	52854	Db	53875	TGACGTTTACGTTTACCGCTGTCGATCAGAAATACCGTCTGTCGCGCGCCGCGACCGCCA	53934
				Qy	7065	TATTAACCGCTCATTCGAAAACATTAATAATGACACTTCCGTTTATTCGCTTACGTAATAATA	7124

Db 53935 TATTACCGCTCAATTCGAAACATTAAATGACACTTCCGTTATCGATTACGTTAAATAA 53994  
 QY 7125 CGGCTGGCGGAGTATATTCGTTTCACTTCGGGTAAACATGTGGGCTTATTCGGCTCA 7184  
 Db 53995 CGGCTGGCGGAGTATATTCGTTTCACTTCGGGTAAACATGTGGGCTTATTCGGCTCA 54054  
 QY 7185 ACACCTCTTTTGGCCGCCAACTGGTCGACCGGCGGAATACCGGGATGTGACACATCTTT 7244  
 Db 54055 ACACCTCTTTTGGCCGCCAACTGGTCGACCGGCGGAATACCGGGATGTGACACATCTTT 54114  
 QY 7245 CCATGAGACCCAGAGGCTTACCGAACCCGCCCTCGAAGAGGGAGTGATGTGTTATGG 7304  
 Db 54115 CCATGAGACCCAGAGGCTTACCGAACCCGCCCTCGAAGAGGGAGTGATGTGTTATGG 54174  
 QY 7305 ACTTCTCGGAGCAATGCTCTATTTCTGGAGCTGTCTATTAACGCGCATGATGG 7364  
 Db 54175 ACTTCTCGGAGCAATGCTCTATTTCTGGAGCTGTCTATTAACGCGCATGATGG 54234  
 QY 7365 TGTTCAGCGGTGTTGACAGAACAGCACTTCCGGAAGCCACCCGCTGGCTGCAGTATG 7424  
 Db 54235 TGTTCAGCGGTGTTGACAGAACAGCACTTCCGGAAGCCACCCGCTGGCTGCAGTATG 54294  
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 Db 54295 TCTGGAACCCGCGCGGCACTGGTAAACCGGGTGTCTGAGAAATTAACCTTGAATGTCC 54354  
 QY 7485 GTCCGCTGGAGGAGACCGGCTGGAACGACTTCGCGCTGACTCCATTAAGACCCGATG 7544  
 Db 54355 GTCCGCTGGAGGAGACCGGCTGGAACGACTTCGCGCTGACTCCATTAAGACCCGATG 54414  
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 Db 54415 CAATAGCCAGTACGACCCCATGCAATTACAAGTTCGCCACCTTTATGTCGTACCTCGACC 54474  
 QY 7605 TGTGTATTCGCGCGGTGATGCGCCTACCGGCTGTCTGAGCGGACACCTTTAAACGAGG 7664  
 Db 54475 TGTGTATTCGCGCGGTGATGCGCCTACCGGCTGTCTGAGCGGAGACACCTTTAAACGAGG 54534  
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 Db 54535 CCGGATGTGGTACGTCACGAGCCCTGAACCTTCTGGCGACGACCCCTATATTCCTTTG 54594  
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 Db 54595 AGCCGACTTGGTCGGCGTTGACCTGGGTGACGACGACGAGGTGACGACGCGATT 54654  
 QY 7785 ACAGAGGCGCTGTGCGCGTGTGGCGGTGGTGGTCCGCTCCGAGACACGAGCGGCA 7844  
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 QY 7845 ATTCTGTGACGACGCTTCTCCCGCAGCAGAACGAGGTGCTCAAGGCTACTGGCAA 7904  
 Db 54715 ATTCTGTGACGACGCTTCTCCCGCAGCAGAACGAGGTGCTCAAGGCTACTGGCAA 54774  
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 Db 54775 CTTTGGCACAGGGCTTCCATAACCTTCGCGCAACCTTCCATTTGACGCGCCAGCGCTTT 54834  
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 Db 54835 CCTGTCCGTCTACGCGACCGGTTCGAAACCGTTCGCGCTTCGAGAGTCCGTCGTCACA 54894  
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 Db 54895 GCGCGCAGGCTGTGACGACGCTTCGCGCGCGGTGATGCGGCTTTACGTTTCCCGGTCA 54954  
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Db 55015 GTATTACCGAGCGTCAGGATCGGAGCGCTGCCAAAACCTGCTGCAGACCCAGGCGAGTG 55074  
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 Db 55075 AACTGATAGCCAGGCGCTTCGCCAGCAGGATAAAGTCTCTCAGGAAATCGATCGCGATA 55134  
 QY 8265 TTGCGCGCTTCGAGGAGAGCGCGCGCGCGCAGATGGTGTGAAAGCTTACAAAGTGT 8324  
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 Db 55255 CCGTCTGTGCGCATCAACCGCGCGCTCTTTTGGCGAGCGCGCGCGATATGCTCG 55314  
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 Db 55315 CCAATATTTACGGGCTGGCGGCTCGCGGCTCCCGCTATGGGCACTATTTAAAGCCACCG 55374  
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 Db 55375 CCATCGGCATCCAGGTGTCTCCGATGCCACCCGATATCAGCGACAAAATCAGCCAGT 55434  
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 Db 55435 CGGAGTGTACCGCGCTCGCGGAGGAGTGGGAATCCAGCGTATAGTGCAGTCTG 55494  
 QY 8625 AGTGGCGCAGATTGATGCCAGCTGGCGGCTCATGCGAGTGGCGGAGGCGGTGAGC 8684  
 Db 55495 AGTGGCGCAGATTGATGCCAGCTGGCGGCTCATGCGAGTGGCGGAGGCGGTGAGC 55554  
 QY 8685 TGCAGAAACCTTACTTGGAGACCCAGCAGACCCAGCGCAGCGGCAAGTTGCAATCTCTG 8744  
 Db 55555 TGCAGAAACCTTACTTGGAGACCCAGCAGACCCAGCGCAGCGGCAAGTTGCAATCTCTG 55614  
 QY 8745 AGAGTAAGTTCAACAACTACGCTCTGATACAGTCTGCGGGGAGGTTGTCGCCATTT 8804  
 Db 55615 AGAGTAAGTTCAACAACTACGCTCTGATACAGTCTGCGGGGAGGTTGTCGCCATTT 55674  
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 Db 55675 ATTACAGTTCTATGACCTTGGCAGTATCCCGTGTCTGATGCGCAACAGAGGCTGCGAGT 55734  
 QY 8865 GGGATAAATTCAGACTAGGTCTGTTATTCAGCGCGGGGCTTGGATGGGGGCAATGCGG 8924  
 Db 55735 GGGATAAATTCAGACTAGGTCTGTTATTCAGCGCGGGGCTTGGATGGGGGCAATGCGG 55794  
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 Db 55915 GCCTCGCGGAGATCGGCAATTTCTCTGCGCGCACAAGTGTGTGAACTGAGTCAAGG 55974  
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 Db 56035 CCACCTGAAACTGCTGACCTCGGTATCGGCAACGATTTACCCGCTCTCCCTTGGCACCA 56094  
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 Db 56095 TGAGCGGATCAAAACAAATAGCTCACTCCCGCGCTGCTCGGCGCTTATCAGGAG 56154

Qy	9285	TCGCTGCGGTTCTCAGCTACGGGGAAGTATGCTCATGCCCGGGTTGCAGCGCGTGG	9344	10365	ATCAATGAGTAGCTGCTGTTATCTCTGCTGTTGATTATGAGCTAGCTAGCTCGTCT	10424
Db	56155	TCCGTGCGGTTCTCAGCTACGGCGGAAGTATGCTCATGCCCGGGTTGCAGCGCGTGG	56214	57235	ATCAATGAGTAGCTGCTGTTATCTCTGCTGTTGATTATGAGCTAGCTAGCTCGTCT	57294
Qy	9345	CGGTCTCACACGGAAATGAACGACACGCGGCAATTCGAATCTGATGATTTCAATGACCGCGTT	9404	10425	GTCCTGAAGCGCGCGCTTGCAGAAACACACAGGAAGTGGGAGTGGCTGTCTGCTCAGGATTG	10484
Db	56215	CGGTCTCACACGGAAATGAACGACACGCGGCAATTCGAATCTGATGATTTCAATGACCGCGTT	56274	57295	GTCCTGAAGCGCGCGCTTGCAGAAACACACAGGAAGTGGGAGTGGCTGTCTGCTCAGGATTG	57354
Qy	9405	ACCTGCCGTTTGAAGGACTTCCAGTTGATGACACAGGAGCCCTGACACTGAGCTTCCCGG	9464	10485	TTTTTCCGGGTATGAGTGTGTTTAACTGCGGACTCGCGCGCTGTGCGCGTCAGGTTTT	10544
Db	56275	ACCTGCCGTTTGAAGGACTTCCAGTTGATGACACAGGAGCCCTGACACTGAGCTTCCCGG	56334	57355	TTTTTCCGGGTATGAGTGTGTTTAACTGCGGACTCGCGCGCTGTGCGCGTCAGGTTTT	57414
Qy	9465	ATGCTGACGGCAAAACACAGCGGATGCTCTCAGTCTGAGCGACATCATCTCTGCATATCC	9524	10545	GATGTTCCATTACTAGGTGTTCTGCGCGGAGTTCGGGAGCGAATGATGCGCCAGCATT	10604
Db	56335	ATGCTGACGGCAAAACACAGCGGATGCTCTCAGTCTGAGCGACATCATCTCTGCATATCC	56394	57415	GATGTTCCATTACTAGGTGTTCTGCGCGGAGTTCGGGAGCGAATGATGCGCCAGCATT	57474
Qy	9525	GTATACACCATATCAGCTGATGATGATCAACATAGCGAGCGCCCGGACGAGGCGCTGC	9584	10605	GATTTCTCGCTGTTGCTGGAATAAGGAAAGTCTTCACTCAGTCTGCTCAGAACGT	10664
Db	56395	GTATACACCATATCAGCTGATGATGATCAACATAGCGAGCGCCCGGACGAGGCGCTGC	56454	57475	GATTTCTCGCTGTTGCTGGAATAAGGAAAGTCTTCACTCAGTCTGCTCAGAACGT	57534
Qy	9585	GAGGAGACTGAGCATGCAAAATCATCAAGACATGGCCATTACTGCCCCACGTTGCTTTC	9644	10665	GCACAGGTGGCTTATGAGTCGGACGGGACGCTTGTGCTTCCCGGACCTGCGATTGGG	10724
Db	56455	GAGGAGACTGAGCATGCAAAATCATCAAGACATGGCCATTACTGCCCCACGTTGCTTTC	56514	57535	GCACAGGTGGCTTATGAGTCGGACGGGACGCTTGTGCTTCCCGGACCTGCGATTGGG	57594
Qy	9645	CGGGGCGGTGCGGTCAACCGGGTCAAGGGTGATATCGCGCGGCGAGGCGCGATGGTGC	9704	10725	GTGGCAAACTTTTACCCCGCGACATTTGTGCGCATGCGCAGACGCTGACGATATGGCAA	10784
Db	56515	CGGGGCGGTGCGGTCAACCGGGTCAAGGGTGATATCGCGCGGCGAGGCGCGATGGTGC	56574	57595	GTGGCAAACTTTTACCCCGCGACATTTGTGCGCATGCGCAGACGCTGACGATATGGCAA	57654
Qy	9705	GGGACCCCTGAGTATCCCTTGGCGGTTAGCCCGGTGCGGGTTAGCCCCCACTAGGGC	9764	10785	GTTGAGTTGCTTCAACCTTATCAGCTTGTAGACCTTAACGGCGAAAGTGTGGTAT	10844
Db	56575	GGGACCCCTGAGTATCCCTTGGCGGTTAGCCCGGTGCGGGTTAGCCCCCACTAGGGC	56634	57655	GTTGAGTTGCTTCAACCTTATCAGCTTGTAGACCTTAACGGCGAAAGTGTGGTAT	57714
Qy	9765	ACTTAATTATCAGCGGTCGGGACCGCCCTTGGCATTTGGCTGGGGTATCGCGG	9824	10845	CCTGTATCAGGACAGCGGTGCTTGTGAGTACCGTAACCGGTACGCCAGTTCGGGGATGA	10904
Db	56635	ACTTAATTATCAGCGGTCGGGACCGCCCTTGGCATTTGGCTGGGGTATCGCGG	56694	57715	CCTGTATCAGGACAGCGGTGCTTGTGAGTACCGTAACCGGTACGCCAGTTCGGGGATGA	57774
Qy	9825	TGCTGCTGTCAGCGTCTGAGCGCAACGGAGCACCTACCTACGATGATACTGATGAAT	9884	10905	TCGGATGCTGTGACCTTGGGGGCGGCTGCGGCCCTGCGGACAAATGCCCTTTGCAATA	10964
Db	56695	TGCTGCTGTCAGCGTCTGAGCGCAACGGAGCACCTACCTACGATGATACTGATGAAT	56754	57775	TCGGATGCTGTGACCTTGGGGGCGGCTGCGGCCCTGCGGACAAATGCCCTTTGCAATA	57834
Qy	9885	CACCGTCCGGAAGGTGAGTGTGTGCGCGCATCTACCGGCTGCTGGCAACCAAGAACG	9944	10965	CAGCGCATCTGCGCGGATCTTAAATGGGATGCTGCGCTGGAGTGGGTCTTACCGCCC	11024
Db	56755	CACCGTCCGGAAGGTGAGTGTGTGCGCGCATCTACCGGCTGCTGGCAACCAAGAACG	56814	57835	CAGCGCATCTGCGCGGATCTTAAATGGGATGCTGCGCTGGAGTGGGTCTTACCGCCC	57894
Qy	9945	ACGCGAGCCACTCACTACCTGGGATAAACCGAGCGGAGCTTCAACGTTTACGTTTA	10004	11025	CGGTGCGGGGATGATGATCGCACCCCGCGCGACTGCTGATTTACCCCGCT	11084
Db	56815	ACGCGAGCCACTCACTACCTGGGATAAACCGAGCGGAGCTTCAACGTTTACGTTTA	56874	57895	CGGTGCGGGGATGATGATCGCACCCCGCGCGACTGCTGATTTACCCCGCT	57954
Qy	10005	CCGTTACGTAACGAGGAGTGTCTCAGCGCTTGGAGCTTGGCTGCGCGACGAGAC	10064	11085	GTGAGCTTTGCCCGTAGAATAATGCGCATCCAAAGCAGTGTCTGCGGATATCTTGGGGC	11144
Db	56875	CCGTTACGTAACGAGGAGTGTCTCAGCGCTTGGAGCTTGGCTGCGCGACGAGAC	56934	57955	GTGAGCTTTGCCCGTAGAATAATGCGCATCCAAAGCAGTGTCTGCGGATATCTTGGGGC	58014
Qy	10065	AGAAACGGAATTTGGGTGTTATATACCTGACGACAGGTGCTGCTGGGCGGAAA	10124	11145	TGGGTTAAACGGAATTTGGGTGTTATCGGGCGCGAGTGTGCTCTTATTTCCGGCAAAA	11204
Db	56935	AGAAACGGAATTTGGGTGTTATATACCTGACGACAGGTGCTGCTGGGCGGAAA	56994	58015	TGGGTTAAACGGAATTTGGGTGTTATCGGGCGCGAGTGTGCTCTTATTTCCGGCAAAA	58074
Qy	10125	TGCGAGGCTCGCATCAGCAACCCACAGCCCAACACAGACGCGGTTTGGCTGATGA	10184	11205	CGATGCTCGAATAAAGGGAGACCGTGCAGCAAAACGGAAAGACTCACTCTGCGGTC	11264
Db	56995	TGCGAGGCTCGCATCAGCAACCCACAGCCCAACACAGACGCGGTTTGGCTGATGA	57054	58075	CGATGCTCGAATAAAGGGAGACCGTGCAGCAAAACGGAAAGACTCACTCTGCGGTC	58134
Qy	10185	GTCTCTCGGTATCACTTACCGGCAACAGATGTATTACCAATACCGTCCGGAAGATGA	10244	11265	GGGGTTGACCCACGTAACCTCTGCGGCTTCACTGATATGCGCTGGCAGTGGACAGACGA	11324
Db	57055	GTCTCTCGGTATCACTTACCGGCAACAGATGTATTACCAATACCGTCCGGAAGATGA	57114	58135	GGGGTTGACCCACGTAACCTCTGCGGCTTCACTGATATGCGCTGGCAGTGGACAGACGA	58194
Qy	10245	CGGTGTGACAGCGGAGCGACGCGCAACCGCGAGCGCGCCCAACGTTATCCGGT	10304	11325	TTTGAACGAGGTGCTGCTTAATGAGTACGTTACTGGCCAAACCTTGGGCGACCGGT	11384
Db	57115	CGGTGTGACAGCGGAGCGACGCGCAACCGCGAGCGCGCCCAACGTTATCCGGT	57174	58195	TTTGAACGAGGTGCTGCTTAATGAGTACGTTACTGGCCAAACCTTGGGCGACCGGT	58254
Qy	10305	GGCGGTCTGATGCTGAACCGTACGCGGCTCGACCGCTACCGCGCTGTGTGACACC	10364	11385	CGGTGACCGGTGAATATTTCCCGTTTTAGCCAGTCACTACGTTTAACTTAACTTAACT	11444
Db	57175	GGCGGTCTGATGCTGAACCGTACGCGGCTCGACCGCTACCGCGCTGTGTGACACC	57234	58255	CGGTGACCGGTGAATATTTCCCGTTTTAGCCAGTCACTACGTTTAACTTAACTTAACT	58314
				11445	GATATTTGCTGGCGGATACCGACCGTTTCCGGTACCGGACCTGATTTATTCGATGATGA	11504

Db 58315 GATATTGCTGGCCGATACCGACGGTTCCGGTACACCGACCTGATTTATGCGATGAGTGA 58374  
QY 11505 CCGGTTAGTCATTTATTTTCAACAGAGTGGTAATTAATTTTCGCGACGCGCATACGCTGCT 11564  
Db 58375 CCGGTTAGTCATTTATTTCAACAGAGTGGTAATTAATTTTCGCGACGCGCATACGCTGCT 58434  
QY 11565 CTTGCCGAAGGTGTCGGCTATGATCGACCTGCACTGCGAGTGCAGTGCAGGATATCCAGG 11624  
Db 58435 CTTGCCGAAGGTGTCGGCTATGATCGACCTGCACTGCGAGTGCAGGATATCCAGG 58494  
QY 11625 GCTGGGGTGCCTAGCCTGTGTTACTGACGGTCCCGCATGTCGCGCTCATCACTGGGTGTG 11684  
Db 58495 GCTGGGGTGCCTAGCCTGTGTTACTGACGGTCCCGCATGTCGCGCTCATCACTGGGTGTG 58554  
QY 11685 CAAATTTATCGGACAGAAACCCCTGGTTGTAATGGCATGAACAAATATGGGGGCCCG 11744  
Db 58555 CAAATTTATCGGACAGAAACCCCTGGTTGTAATGGCATGAACAAATATGGGGGCCCG 58614  
QY 11745 GCATGCACTGCATATCGCAGTTCCGGTGCAGTTCTGCTGGATGAGAAAGCCGAGCACT 11804  
Db 58615 GCATGCACTGCATATCGCAGTTCCGGTGCAGTTCTGCTGGATGAGAAAGCCGAGCACT 58674  
QY 11805 GCGCGGAGGAGTTCCCTGCTGCTACCTGCGCAATTTACATTCATACCCCTGTGGCGTTTC 11864  
Db 58675 GCGCGGAGGAGTTCCCTGCTGCTACCTGCGCAATTTACATTCATACCCCTGTGGCGTTTC 58734  
QY 11865 GGTGGTGCGAGATGAGATCAACCGGTAAACCGTCTGCTGTCGAGCGTCTTATCGCACCG 11924  
Db 58735 GGTGGTGCGAGATGAGATCAACCGGTAAACCGTCTGCTGTCGAGCGTCTTATCGCACCG 58794  
QY 11925 CGTCTGGGAGGCGAGGACCGCAGTTTCGGGGTTTGGTTTGGATCAGGATAC 11984  
Db 58795 CGTCTGGGAGGCGAGGACCGCAGTTTCGGGGTTTGGTTTGGATCAGGATAC 58854  
QY 11985 CGATACCTTTGGCAAGCCAGGTTACCGCGACGGAACCTGAGTATGCCCTTCTGTGAGCCGGAA 12044  
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QY 12045 CTGGTATGCCACCGGGTACCGGAGTACGAGCGTTCGCGGAGACGTTATGGCAAAA 12104  
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QY 12225 CTTGCTGCGCAGTATGATATACGGTCCGATGCGAGCGCCGATATCCCTTACAG 12284  
Db 59095 CTTGCTGCGCAGTATGATATACGGTCCGATGCGAGCGCCGATATCCCTTACAG 59154  
QY 12285 GPTCACTGAGTCTCGCCCGCAGTACGGCTAGTTGAAAGCAATGGAGACTTACCCGTTGGT 12344  
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QY 12345 GTGCGCGATGGGCGCGGAAACCGCTAGCTGAGTTTATGAACGGTACCAATGATCCTCA 12404  
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QY 12405 ATGCCAACAGCAGCGGTACTCTCTCAGTATGATAGCTTCCCACTGCGTCAGTCTAG 12464  
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QY 12465 TGTCAATTTATCCACGAGCCCTCGCTCGGCGCAATCCATATCCGCGCTCTTACCGGC 12524  
Db 59335 TGTCAATTTATCCACGAGCCCTCGCTCGGCGCAATCCATATCCGCGCTCTTACCGGC 59394  
QY 12525 GACGCTGTTCCGCAACAGTTTATGACGAGCAGCAGATATTAACGCTCGGGTTGCAACA 12584

Db 59395 GACGCTGTTTCGCAACAGTTATGACGAGCAGCAGAGATATTACGCTCGGGTTGCAACA 59454  
QY 12585 GACGAGTGCACATCACTTGTGTTTCACTGTCGAGGGGCAATGGTTGTTGGGGTTGGCGGA 12644  
Db 59455 GACGAGTGCACATCACTTGTGTTTCACTGTCGAGGGGCAATGGTTGTTGGGGTTGGCGGA 59514  
QY 12645 GCGCTCGGGGACGATGATTTACGCTTACTCTCGGACACGTCGCGGAAGGGGCTCTGAC 12704  
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QY 12705 GCTGGAACACCTGTTGGGCCCGAAAGCCTGCTCTCGGATAGTCAGGTCCGTACGCTGCG 12764  
Db 59575 GCTGGAACACCTGTTGGGCCCGAAAGCCTGCTCTCGGATAGTCAGGTCCGTACGCTGCG 59634  
QY 12765 GGTTCAGCAGCAAGTCTGATCTGGAATTCACAGACGTTGCGACCGTCTGCTCCGCG 12824  
Db 59635 GGTTCAGCAGCAAGTCTGATCTGGAATTCACAGACGTTGCGACCGTCTGCTCCGCG 59694  
QY 12825 ACTCCCCCACAAGGTAGCTTTTATCGAAACGGCGCTGCTGGATGAGGGTATGGTCAAGTTTC 12884  
Db 59695 ACTCCCCCACAAGGTAGCTTTTATCGAAACGGCGCTGCTGGATGAGGGTATGGTCAAGTTTC 59754  
QY 12885 ACTGCTGCTCTACATTTGTTGATGAACATCTCGAGCAAGCCGGTTACCGCAATCCGGATA 12944  
Db 59755 ACTGCTGCTCTACATTTGTTGATGAACATCTCGAGCAAGCCGGTTACCGCAATCCGGATA 59814  
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Db 59995 CGCAGGATTTGTCACACAGCGCATTTGACCTGCGCTTCTGACGCGCGCTCGGGTGAC 60054  
QY 13185 GGACCCCAATGATATCTGACGTCGCTCACTCTGATGCTCTGCGCGCGGTGACCAACCTT 13244  
Db 60055 GGACCCCAATGATATCTGACGTCGCTCACTCTGATGCTCTGCGCGCGGTGACCAACCTT 60114  
QY 13245 GCGATTTCTGGGGCAGCGAGATGGTATTCGCCACCGGTTACAGTGATGCCACGTTGCCGT 13304  
Db 60115 GCGATTTCTGGGGCAGCGAGATGGTATTCGCCACCGGTTACAGTGATGCCACGTTGCCGT 60174  
QY 13305 TCCGGAACGCGCAGCAGCGCTCTGGCGTTGACGCGCGCCCTACCAATGACAGTGTCT 13364  
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QY 13425 CGTGTGCTGCTACCGATCTGATGACAGTATTCGCGACAGCAGGTCCGCGCAACAGGTGAC 13484  
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Db 60355 ATTCAGTGAACGTTTGGCGGTGAGTTGCAATCGGCAACCGCGCAGCGCGAGGCAACGC 60414  
QY 13545 CTGGCAACGAGGACGCGCAACTGGTGAACGCGCAGTGAAGTTCCCGGTCACTGT 13604  
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QY 13605 AGCAACGAATTTCCGCTGGCGGTTCACCGGGAGGGCGGATGATGACAAATAAGGTCTGCC 13664  
Db 60475 AGCAACGAATTTCCGCTGGCGGTTCACCGGGAGGGCGGATGATGACAAATAAGGTCTGCC 60534

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Db	60535	TGTTGGGTTTATCAGCGGTATTTCTGGACAGTTGGCAATATGTCAGTGATGACAGTGC	60594	Db	61615	ATTTACAGTACCTGAATAGCCTGACCGGACAGTACTGACAGCGGTGAGCGCCGATGCCG	61674
QY	13725	CCGCAGGACCTGTATGCCAGACAGCACTTTTACGATCCGACGCGAGGAAATGGCAGGT	13784	QY	14805	GTACGTGCGTGGAACTGAGCGATGCGCGGGGGGGGCTTTCTGGCGGTACCGGGGCTG	14864
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QY	13845	AGACGAAATGATACCGTTGGCTAAACGACGATCCTGACTGGGAAGAGGGGGGACG	13904	QY	14925	CGCTGAGCATCACCGGACAGTTTACCGGTGAAGCCGCCCAAAATTACGGAAACGTTCTGT	14984
Db	60715	AGACGAAATGATACCGTTGGCTAAACGACGATCCTGACTGGGAAGAGGGGGGACG	60774	Db	61795	CGCTGAGCATCACCGGACAGTTTACCGGTGAAGCCGCCCAAAATTACGGAAACGTTCTGT	61854
QY	13905	GTGATGATCGTCCGCCCTGACAGCGCTGCCCTGATGAGACAAAGATGAAATACAC	13964	QY	14985	ACGCTGGCAATACGGATGCGGAGAAATTCTCAATCTGGCTGGCCAGTGTGTCAGTCATT	15044
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QY	14085	AGGGCGATCGTTGGCCCTCTGGAGAGAAACCCGGGAAAGAAAGTGGGAGAGCAA	14144	QY	15165	CCTGGAAATGACCTGCTGGATGGGAGACGTTCTTCAACAGACCCACGCTGATGCGACCG	15224
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QY	14145	CGACAGACTCACATGAACAGGTGGCTATACATGCTGAAGAACTGGCTGCTGCGCGT	14204	QY	15225	GGCGCTCTGAGCATCACCGATGCAAAAGGTAATCTGCAGCGGTGGCATATGATGTGG	15284
Db	61015	CGACAGACTCACATGAACAGGTGGCTATACATGCTGAAGAACTGGCTGCTGCGCGT	61074	Db	62095	GGCGCTCTGAGCATCACCGATGCAAAAGGTAATCTGCAGCGGTGGCATATGATGTGG	62154
QY	14205	GACGCTGCCCTGATGCTCAGCGCACTGGTTCAGCGCTGACAGCAACCGTTACACCCCTC	14264	QY	15285	CTGGGCTGCTATCGGGCAGTTGGTTGACGCTGAAGACCGGACGAGCAGGTCATCGTGG	15344
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QY	14265	CAGCGCAACTTGGCAGTCTGAAACCCGCGGCTTTCCGACGACTACCGCTATCGGTACA	14324	QY	15345	CCTCCCTGACGTAATCGGCGCGGGGAAAGTTGGTGGTGAAGAACACGCGCAACGCGGTGG	15404
Db	61135	CAGCGCAACTTGGCAGTCTGAAACCCGCGGCTTTCCGACGACTACCGCTATCGGTACA	61194	Db	62215	CCTCCCTGACGTAATCGGCGCGGGGAAAGTTGGTGGTGAAGAACACGCGCAACGCGGTGG	62274
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QY	14385	AGAGCGGGAGCTGGCAGCGTATGCTGACAGGACAGAGTGAATGGCAGGCTTCGCGG	14444	QY	15465	CGTCTGGGCACTGTCGGGAGCAAAAGTGTCTGCAGGACCTGCGCTATACGTATGACCCCG	15524
Db	61255	AGAGCGGGAGCTGGCAGCGTATGCTGACAGGACAGAGTGAATGGCAGGCTTCGCGG	61314	Db	62335	CGTCTGGGCACTGTCGGGAGCAAAAGTGTCTGCAGGACCTGCGCTATACGTATGACCCCG	62394
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QY	14505	AAGTGAAGGTTTTCGCGATTATTAACAGGATACATGAGCACATCCTCTTCA	14564	QY	15585	AAGTGTATCCGAGAGATACGTATCTACGACGCTGTACAGCTGGTTCAGCGCCACAG	15644
Db	61375	AAGTGAAGGTTTTCGCGATTATTAACAGGATACATGAGCACATCCTCTTCA	61434	Db	62455	AAGTGTATCCGAGAGATACGTATCTACGACGCTGTACAGCTGGTTCAGCGCCACAG	62514
QY	14565	GTAGCACCCCGTTCGCGTGTCTGACAAACCGCGGCTTGTGGTGGGAGCTGCAGT	14624	QY	15645	GGCGTGAGATGGCCAATGCGGCGCAGCAGGCAACGACTTTACCATCCGCTACAGCCCCC	15704
Db	61435	GTAGCACCCCGTTCGCGTGTCTGACAAACCGCGGCTTGTGGTGGGAGCTGCAGT	61494	Db	62515	GGCGTGAGATGGCCAATGCGGCGCAGCAGGCAACGACTTTACCATCCGCTACAGCCCCC	62574
QY	14625	ACTACGCCATCCGGATACACCGGAGAGACGAGCGGTATCACTGCGCATCAGCAG	14684	QY	15705	TTCTTACAGACAGCTCTGCTTACCAATTAACGCGGCACTTACCGGTATGACCGTGGTG	15764
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QY	14685	ATGAGCGCGGCTGTCTCAAAAGCGCGGCTTACACGCGGCGGTCTACAA	14744	QY	15765	GCAACTGACGAGATGCGGCGCAGTCCCTGCCACGAACTAATTAATACGACAGACA	15824
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				QY	15825	TACGCTTAGTGACGCGCAATAGGCGGCTACTGAGCAGCTTGGCGGGAAGTCCCGTCAG	15884



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Qy	15945	TGTTGTGAGCGCACGCTGAGAACTGCAAAAGGTGACACGGGTGCTGCTGATGCGGGGG	16004
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Db	62875	CGGACACAGCAAGAACTGCTGATGATGCGGCGAGTCAAGCTATTTACAAACCGGCA	62934
Qy	16065	CGCGGCAAACTGGCAACAACTGTTACAGACACAGCGGCTAGTGTACTGCGCGGGCTGGAGT	16124
Db	62935	CGCGGCAAACTGGCAACAACTGTTACAGACACAGCGGCTAGTGTACTGCGCGGGCTGGAGT	62994
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Db	63175	ACAGAGGGTTTACCTTATCAGTGAGGAGGTTCTACCGTATGCGGAAACGGCTGTTTC	63234
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Db	63235	TGACGGCGCAAGTGAGGTTGAGGCTGACTACAAACTATCCGATACTCAGGCAAGGAGC	63294
Qy	16425	GTACGCGACGGGGCTGGATTATACGGTTATCGGTATACAGGCAATGCGGACGGCGCT	16484
Db	63295	GTACGCGACGGGGCTGGATTATACGGTTATCGGTATACAGGCAATGCGGACGGCGCT	63354
Qy	16485	GGCTCTCCAGGACCGGCGGACGCGTGGACGGGCTGAACCTGTTCCGATCGTGGCA	16544
Db	63355	GGCTCTCCAGGACCGGCGGACGCGTGGACGGGCTGAACCTGTTCCGATCGTGGCA	63414
Qy	16545	ATAATCCCGTCACGCTGTTTGACAGCAACGGGCGGATCAGTACTGGTCAGGAGGCCAGAC	16604
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Qy	16605	GATTAGTGGGGGAGCAATTTGTTTCATCCGTTACATGCTGTTTGTGAAGAATTTCTG	16664
Db	63475	GATTAGTGGGGGAGCAATTTGTTTCATCCGTTACATGCTGTTTGTGAAGAATTTCTG	63534
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Db	63535	TAGAGAAAGATTTCATCAGCGTGAAGCAAGCTGCAATTTATCTATTTACGCGCTGG	63594
Qy	16725	GTAGGTGACGACGCAAAAGGCCATTAATTTCTAGAGAAACCATTTAAACCCGGTTCCC	16784
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Qy	16845	TCGTTGCCGAGTAGGACAGTGGGATGCATCAGGTGACGTGGAATTTATGCGCAACA	16904
Db	63715	TCGTTGCCGAGTAGGACAGTGGGATGCATCAGGTGACGTGGAATTTATGCGCAACA	63774
Qy	16905	GACCGGTGTGAGGATTTGGTTTATCTGTGACCTGCGAAGATACCTTCTGCGCAATGAAA	16964

Db	63775	GACCGGTGTGAGGATTTGGTTTATCCTGTGTCAGCTCGAGAATACTTCTGCGCAATGAAA	63834
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Db	63835	TTGTTAATGTCATGGATAAAATTTAAATCATACGCCCTACACCGGGGATTTATGACATGC	63894
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Qy	17325	GTGAGAACTGTTTAAATTTCTATTAATCTACAAATACACCTCTTCTGAACTGTTCTTG	17384
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Qy	18585	GCTACCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	18644
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Qy	18705	GGCAGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	18764
Db	65575	GGCAGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	65634
Qy	18765	ACCTCTTCTTTTAAAGAACAGCTGCGCGCAGAGCTGCTGCTGCTGCTGCTGCTGCT	18824
Db	65635	ACCTCTTCTTTTAAAGAACAGCTGCGCGCAGAGCTGCTGCTGCTGCTGCTGCTGCT	65694
Qy	18825	CGGTAACGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	18884
Db	65695	CGGTAACGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	65754
Qy	18885	CGGCAAAATTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	18937
Db	65755	CGGCAAAATTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	65807
RESULT 3	AY220302	7122 bp DNA linear BCT 01-DEC-2003	
LOCUS	AY220302	Yersinia frederiksenii plasmid pMYF1 putative insecticidal toxin	
DEFINITION		TcYf1 (tcyF1) gene, complete cds.	
ACCESSION	AY220302		
VERSION	AY220302.1	GI:32699983	
KEYWORDS		Yersinia frederiksenii	
SOURCE		Yersinia frederiksenii	
ORGANISM		Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	
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SGRFSSEBELSTAAAPLVNAQTQSDTSAGMLDADVLQEGULTADFISLITD			
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QDGQVFTTWKEDQADLMGAVSLVTPSGLARLALYINVDNAPGSYEWLAYS			
GLQSLGSLSLTATLSAALDEESTSALCAVYLRLNAPNMVSGRDDLFGYLLDNQVA			
OKMTPEANAGIOLYVNRILSGOERGADSTLTTPQFTDMDYKRYKSSWAGISEL			
VYPENLPTVRIGQNMDSLLQSVSSVNTDVEDAFKNYLITFPGQVVMNLITIS			
GHDXISMTQSGASWYGRNTPDMEWYRCANHSKIOERVMGALATGWTKNLSGMP			
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FDTGQMSPATLGHVTCNPLSEELYCAFYPTIGIPDIGNTVLVSVDMSKMLTVSD			
TNMSNWNPEFNIAVSCTFNSSLSVDEYVNYFMGVEPERKNFYVAINDRPG			
GFIGVDVNSKIYQVGKASDVIHKTFVSVGVQGIELNVHSGKHLFGTLTIDMVA			
LNNGSTITSLINGATITASFGLVFPVNVANDLIDITLTARMNGTEIKSWPSEEVY			
NRELNTQVGNLNFNTALSFTDSDITDDEFDVTTLTFAVGENDAVLAARTYIMNVR			
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TORLTPEALESGDVFMDGSANALYFWELFYTPMVFQRLQEQFPEATLQVY			
WNPAGHYVGMQLQNTWYRPLEEDTSWNSDPLSDVDPDAVAQNEPMHYKVAIFMRML			
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DGQLLSVYATPAETALNAAVSQSSSLSPVAMPYLPFRVPMLENARGOVSLIQ			
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GSRYGALFNATAGIQVSSDAFRISADKISQSEMYRRREDWEIQRDGASDVGTMDA			
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LAVSHCMNSDGGQQLDFDNRWLFPFSGIPVGDSGTTLTSPFDADGRQAMLLSLSDII			
LHRYTILIS"			
Query Match	24.0%;	Score 4541.8;	DB 1; Length 7122;
Best Local Similarity	78.5%;	Pred. No. 0;	
ORIGIN			

Matches 5605; Conservative 0; Mismatches 1507; Indels 29; Gaps 13;			
QY	2414	ATGAGCGAAGACATTATGATATATATGATGATATTTCTGGAGAAAGTGAATGCTCACGA	2473
Db	1	ATGAGCGAAGACATTATGATATATGATGATATATTTCTGAAAGTCAATATCCACAAC	60
QY	2474	GCACGCTGTCAGAAAGAAACAGATACAGCGGTGACGCTGACGGATTTATTTCTCGCCTTCG	2533
Db	61	GAACGCGAGTCTGAGGAAAGCGTCAACGAGAGACTCTGGCGGATTTTTTCTCACGTTCT	120
QY	2534	TTTTCCGAGGTCAAAAAATCACTGGCGACAGCTCTCATGGGAGAGGTCCTGCTATCTG	2593
Db	121	CTCTCTGAAGTTAAAAAATCACCGGAGCAATCTGTCTATGGGAGAGGTCGCTATCTG	180
QY	2594	TACAGTCAGGCGAGCAGCAAGAAAGAAACCGGCTCACCGAATCCCGTATTTCTGGCC	2653
Db	181	TACCGTCAGGCACAAAGAGGCAAAAGAAACCGGCTCACTGAGTCAGCTATTTCTGGCC	240
QY	2654	CGGGCGAATCCCTCACTGGTGAATGCGTTTCGGCTGGGAATACGGCAGGCGAGCCGCACT	2713
Db	241	CGGGCCAAATCCCACTCAGCCGGTGGCGGCGCTGGGAATACGGCAGGTCGAGATACC	300
QY	2714	CGCAGCTATGATGACTGGTTTGCTCCGCGCAGACCGTTTCGCCGCCCGGCTCGGTG	2773
Db	301	CGCAGCTATGATGATGGTGGTTTCGGCTCCCGTGCAGAACGTTTCAACCGGCGCTGATTCGGTG	360
QY	2774	GCCTCCATGTTCTACCGGGCGGTATCTGACCGAGCTGTACCGTGAGGCGGAGGACCTG	2833
Db	361	GCATCCATGTTTCCCGCGGGCGGTATCAGACAGAGCTGTACCGTGAGGCGAAAGACCTG	420
QY	2834	CATCCGGAACCTCGCTGTTCCGGCTGGACATCCGGCGTCCGACCTGGCGGCGCTGGCC	2893
Db	421	CATCCGGAACCTCGCTGTTACCGGCTGGACCAACCGCGCTTGACCTGGCACAACCTGGC	480
QY	2894	CTTAGCCAGAAATATATGACAGCAGAGCTCTCCACCTGAGCTGTCCAATGAGTACTG	2953
Db	481	CTCAGCCAGAGCAATATGATAGAGAAATCACCACTTGGTCTCTCCAGTGAGCTGCTG	540
QY	2954	TATCGCGGTATCGGGCAGCGGAAGGCTTGACGACGACAGCGTCAGGGAGCTGCTCGCC	3013
Db	541	CTCCGAGTATCGGGCAGCGGAAGGCAATGACGTGACAGCGTCAGGAGTCTGCTCGCG	600
QY	3014	GGGTATCGCTGACCGGCTGACCCCTATCACTGGGCGGTACGAGCGGCGCCGCCAAGCC	3073
Db	601	GAGTATCGCTCACAGGCTGTCCCGGATCACACAGCGTA-TAGGCGGCGCCGCCAAGCC	659
QY	3074	ATTCTGGTCAGAACCGGCTGATGGGTTTCCGCGTTCAGCGGTAACTCCGATGTGGCGAGCTT	3133
Db	660	ATTCTGTGAGGTGCCCGACGCTGCTGGGTTTTAGCAGGAATCCGAGCGTGGCGCAGCTT	719
QY	3134	ATGGACCTGCTCCATGTCGCCATTGAAGCCGATATTTACCGGAGCTGTATCAGATA	3193
Db	720	ATGGGCCCTCGCTCCATGTCGGCTTTCAAGCCGATATTT-TGCGAGCTGTATCAGATA	778
QY	3194	CTGGCCGAAGAAATTACGACAGACAGTTACGAAGCACTCTGGAAGTAAAGAAATTTGGTGAT	3253
Db	779	CTGGCCGA--ACCTTAGCACACACAGACAGCAAGCAGCGCTGGAGTAAAGAAATCTGCTCAT	836
QY	3254	ATGCTCCCTCCTCACTGTATCTTATGATGCACTTGGCAACATTTATGATCTTGATTAC	3313
Db	837	ATGCGTCCCTCAGCACTGTATCTTATG-TCGACTTGCACGTTTTACGATCTTCATTAC	895
QY	3314	GATGAGCTAACTCTGTTATGTCATTAAGGCTCGACTTTTCAAAATCCAAACAAATGAATAC	3373
Db	896	GATGGTCTAACTTCGTTATTTAGTTAAGGCTGGACTTTTCCAAATCCAAACAAATGTTATAC	955
QY	3374	TACATTAATAGTCAATTAAGTGTGTAATCTCTGAATGAAGCACTGGTTTAACTATA	3433
Db	956	TACCTTATTATTCAAGTAAGTGTGTAACGC-GAATGAAGAAACTGTTTATACAACACTATG	1014
QY	3434	CATCATTTATTAGAACGCTAGGCGGAGACTCACAGCAGATTAACCTGAGCTTTACCT	3493
Db	1015	CA-AGTTATTAAGATCGTTACCGGAGATTTCAGCAGATTAACCATCGCTTATACAT	1073

QY	3494	TATGGGATGGAACATATCTTTATAATTTACGGTGGTCTCAACGATATACAGAGTATAGT	3553
Db	1074	TATCGGATGGAAAC-----ATAAATGGAGCGTGGTCTCGAGATATACAGAGGTATT	1125
QY	3554	TTCAAACATAGGTCGTTAGGTTCTAACAGTAGCAATCTTTT-ACCTCTGGGATTTATCAGCT	3612
Db	1126	TTCAAACATACGACGCTTAGGTTCTAACAGTAGCAATCTTTGCTCTGGGATTTATCAGCT	1185
QY	3613	TCAAAAGGGGTCGCTATAGCAATTCCTGTTGAAATAGATAGAGAAAGTTAAATGATGG	3672
Db	1186	TCAGAAGGGGTCGCTACAGCAATTCGTTGTTAATAGAGAAACGAAAGTTAAATGTTGG	1245
QY	3673	GATCACAATAGGATTGAGTAGGAAGGGGGGATTAATCTCAACAGTAAATCTTCACTCT	3732
Db	1246	CATCACAATAGGACAGAGTTGGAATCGGGGGTATATTAATCTC-ACAGTATACATCACTCA	1304
QY	3733	GATTGAATATGATCCCTGCGATATTCATTCTTAAATTTAAATAAAGTTATCCGCTATACAA	3792
Db	1305	GATTCAATATGTCCTGCGATATACATTCCTTACTCGAAATATGTTTATCCGCTGTACAA	1364
QY	3793	GGCCACGGGCATGACACCGCGGAATATATCAATCAACAATATTCCTTAATAACGGTCT	3852
Db	1365	GCCACGGGCATCCCATGCGGGAATATATCAAAATCACCCATATTTCTTAATAACGGTCT	1424
QY	3853	CACCAATTGACCATGGGTCCTGAGTAAATCTTCTGGTCCGTTACCTGATGCGTCACTA	3912
Db	1425	CACTATTGACCAATGCGTCTGAGCAAAATCTTCCAGGTTGTTACTGATGAGTCACTA	1484
QY	3913	TCAGCTTGATGTGGCCCGGTCTCATGATTTGTGCAACGGAACCATCAGTGACAGCGGTT	3972
Db	1485	TCAGCTTGATGTGGCCCGGTCTACTGTTATTTGTGCAACGCGCACCATCAGTGACCGGCTT	1544
QY	3973	CAGCGCGAAGAACGGGCTGTTCAACACGCTGTTCAACACCCACCGCTGAAACGGCCAGCT	4032
Db	1545	CAGCGCGAAGAACGGGCTGTTCAACACGTTGTTCAACACCCCGCGCTGAAACGGCCAGCA	1604
QY	4033	GTTTTCTGACAGATGATFACCCCTCGACTTACGCTCTGAAGCACCGGAGGATGCTTTCG	4092
Db	1605	GTTCTCTGGGACGATACCGCCCTCGACTTACGCTCTGAAGCACCGGAGGATGCTTTCG	1664
QY	4093	TCTACGCTACTGAAACCGCGCAATTAACATCAGCGCTCGGGGCTTTCACGCTGTGGCA	4152
Db	1665	CCTCAACGTTACTGAAGCGCGCATTTAAACGTCAGCGCTCGGGCTTTTCCACACTGTGGCA	1724
QY	4153	GTTGGCAGCGGTGACAGCAGCGCTGGGTTTAGCTCTGCTGCTGACAAATATCGCGCACT	4212
Db	1725	GCTGGCTAGGGGCAACAGCAGCGCGGGTTTACCTGCTCTGCGGCAAAATATCGCGCCCT	1784
QY	4213	CTACCGAGTGAATCTCTGGCTGACATCCACGACCTATCCGCTGGTGAGCTGTCAATGTT	4272
Db	1785	CTACCGGTTAAACTCTTAGCGGATATCCATGACCTGTCGTTGGTGAGTTGGCGATGTT	1844
QY	4273	GCTGTCGCTCTCCCTTTTCAGCGGGGTGGCCGCGGCTCGCTGTCCGATAAATAGCTGAC	4332
Db	1845	GCTGTCGCTCTCCCTTTACGACAAAGTTCGCCATCGACACCCCTGTCCGATGATGAGCTGAC	1904
QY	4333	GCAGTTCTGTACGACACCAACCTGCTCATCGGAGCAGGCTGGAACGCTCAGCGATGT	4392
Db	1905	GCAGTTCTGTACGACACCAACCTGCTCATGGCTCAGGGCTGTGCTGGTTCAGCGATGT	1964
QY	4393	GTTTCTGTGCTGACGACGAGTACCGTACCTGCTGACCCCGCAATTTGAGAAACCTGCT	4452
Db	1965	CTTTCTGTGCTGACAAACAGCGTACAGTACCTGCTGACCGCGGAGATGCAAAATCTGTT	2024
QY	4453	CGCTTCCCTCGGCAACGAGCTGTGGGCGGTGAGCT---GTTCCCGGAAACGCTCCCGG	4509
Db	2025	CGCCACGCTCGCTCTGGTCTGTGGGACGTTTCAATTTCTTCTTCTGACGAACTGTCCAC	2084
QY	4510	CGATGCGCTCCCTTTTATTTGCGCGCATGAGCTGGAACGACCGATACGCGGAAGGC	4569
Db	2085	CGAGCTGACCACTGGTTGCGCGCTTCCACGAGCTGGATTTCAACCGACAGTCCCGGGC	2144



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 Qy 6904 TAATGATAGCTGAGTCTGCAATCCGGGAATTAATCTTTTCAACACAAATCGCTGAGTTT 6963  
 Db 4482 TAACAGAGAGCTGAATCTACAGGTGCGAAATAATCTTTTCAATACGAATGCACTGAGTTT 4541  
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Db 4261 GATACCTGACG 4271
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## RESULT 5

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AR166758 LOCUS 37948 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 11 from patent US 6281413.
ACCESSION AR166758
VERSION AR166758.1 GI:16242227
KEYWORDS Insecticidal toxins from Photorhabdus luminescens and nucleic acid
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 37948)
AUTHORS Kramer, V.Cary., Morgan, M.Kent., Anderson, A.Robert., Hart, H.Prim.,
Warren, G.W., Dunn, M.M. and Chen, J.Shong.
TITLE Insecticidal toxins from Photorhabdus luminescens and nucleic acid
sequences coding therefor
JOURNAL Patent: US 6281413-A 11 28-AUG-2001;
FEATURES Location/Qualifiers
source 1..37948
/organism="unknown"
/mol_type="unassigned DNA"
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## ORIGIN

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Query Match 12.5%; Score 2368.8; DB 6; Length 37948;
Best Local Similarity 54.0%; Pred. No. 0;
Matches 6358; Conservative 0; Mismatches 4747; Indels 671; Gaps 47;
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Db 5569 CGTGATGATCTATCAATACCTATTGATCGATAACCAAGTTTCGCCGACATTAACCT 5628
QY 5351 ACCCGATTTCGGAGGCCATCGCCGCATACGCTGTATATCAACCGGGCCCTTAACCGA 5410
Db 5629 ACAGAGATCGCTGAAGCTATCGTAGTATCCAACTGATATTAACCGCGGTTGAAAAT 5688
QY 5411 ATGAACTCAGCGCCCATGGCAGAGGTGAGGGGCGTCACTGTTTCACTGCTGGATACG 5470
Db 5689 ATGAGGAGGAGATCTGTCTCAAGTGTCCACGCGCTCATTTCTTCCAACTCGGATAAA 5748
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Qy	13443	CTATGACAGTATACCGGACAGAGTCCGCCAACAGGTGACATTCAGTGAACGGTTTGG	13502
Db	14162	TTATGACCGGATCTTTAAGCAACAGATTCGTCAACAGTAGTATTTCAGTATGGCTTTGG	14221
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RESULT 6  
BD136648  
LOCUS BD136648 37948 bp DNA linear PAT 18-SEP-2002  
DEFINITION Insecticidal toxin from Photobhabdus.  
ACCESSION BD136648  
VERSION BD136648.1 GI:23231593  
KEYWORDS JP 2002504336-A/6.  
SOURCE Photobhabdus luminescens  
ORGANISM Photobhabdus luminescens  
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
Enterobacteriaceae; Photobhabdus.  
Kramer, V.C., Morgan, M.K., Anderson, A.R., Hart, H.P., Warren, G.W.,  
Dunn, M.M. and Chen, J.S.  
Patent: JP 2002504336-A 6 12-FEB-2002;  
NOVARTIS AG  
OS Photobhabdus luminescens  
PN JP 2002504336-A/6  
PD 12-FEB-2002  
PF 18-FEB-1999 JP 2000532529  
PR 20-FEB-1998 US 09/027080, 20-JAN-1999 US 60/116439 PI  
VANCE CARY KRAMER, MICHAEL KENT MORGAN, ARNE ROBERT ANDERSON, PI  
HOPE PRIM HART,  
PI GREGORY WAYNE WARREN, MARTHA MARY DUNN, JENG SHONG CHEN PC  
C12N15/09, A01H5/00, A01N63/02, C07K14/24, C12N1/15, C12N1/19 PC

, C12N1/21, C12N5/10,  
PC C12P21/02, C12N15/00, C12N5/00  
CC orf5  
CC hph2  
CC orf2  
FH Key Location/Qualifiers  
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FT CDS (23768)..(31336)  
FT CDS (31393)..(35838).  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:29488"  
ORIGIN  
Query Match 12.5%; Score 2368.8; DB 6; Length 37948;  
Best Local Similarity 54.0%; Pred. No. 0;  
Matches 6358; Conservative 0; Mismatches 4747; Indels 671; Gaps 47;  
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Db 5569 CGTGATGATCTATCAATACCTTATGATGATAACCAAGTTTCGCGGACATTAACAACT 5628  
QY 5351 ACCCGAATGCGGAGGCCATCGCGGCATACGGCTGTATATCAACCGGGCCCTTAACGGA 5410  
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Db	9702	GAATGACAGCGGTCAGTTCCACTGATTTCAACGATGGCAAAATCTCTGCGTT	9761
QY	9421	ACTTTCAGTTGATGACACAGGAGCCCTGACACTGAGCTTCCCGGATGC-----	9468
Db	9762	AATCAAAATCGATGA---AGGTACGCTGACATTTAGCTTTCCCAATGCAATTA	9818
QY	9469	-----TGACGGCAAAACAACAGGCGATGCTCTCTCAGTCTGAGCGACATCAT	9513
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QY	9514	CTGTCATATCCGTTTACACCATTTACAGTGTATAGGTATCAACATAGGGCA---	9569
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QY	10050	GCCCGCGGACGAGACAG-----AAACGGAAATTTGGGTGTTATATACCC	10097
Db	10400	ACCCAAGGCAACACCCCAAGACAACTGGCAAAACAGATTTTGGCTGATAT	10459
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[illegible]

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Db	15059	ATTACCTACTACAACATTTGTTAGAAAACGA	15094
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Qy	15114	AGTTGTCGCCGAGCGCGGGGCCAACTGGATGGGTGAGATGCTCGGCTGGGTAATG	15173
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Db	15796	ACATGCTGGCTGATGACATCTACAAACCTGAGCGCCTTGTGATGCAACCGCGCGCTTAC	15855
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Qy	8261	GATATTTGCCCGCTGGAGGAGAGCGCGCGCGCGCAGATGCGTTTTCGAACGTTTACAAA	8320		
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Query Match	12.58;	Score	2357.8;	DB	1;	Length	349519;
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Matches	5313;	Conservative	0;	Gaps	35;		
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Qy 9098 AGTAACGTTTCGGGCTGCGGTACGAAAGCAACGGATTACAGATGGAT----- 9148
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Qy 95515 AAGAAATAATTAGTCACTGCGGTAGCGGAAATAACACCTGAAATTTGGTACCGGAAAT 95456
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Qy 9437 ACAGGACCTGACACTGAGCTTCCCGATGC-----TGACGGCAA 9478
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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9479 CAACAGCGCATGCTCCTCAGTCTGAGCGACATCATCTGCAATCCGTTACACCATATC 9538
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95098 CAAAAAACCATGCTGGAGAGTCTAAGGACATCATTTCTGCAATTCGTACACCATTCG 95039
Qy 9539 AGCTGATAGTATCAACATAGCGCA-----GGCCCCGACAGAGGCTCGGAGAGACTG 9594
Db 95038 CAATAACGATTTCAATTAAGTGTCTAAACAGGCCCCCTAAATGGGGCTCTCAAGAGTCT- 94980
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Qy 9835 CAGCGTCTGACGCGCAACCGAGCACCTACCTACGATGATACTGATGAATTCACCGGTCG 9894
Db 94739 CGCGCGCGCACCCATTTTGGTGTCCCAATTAACGAAACCGATACCTTCTTGGGCGC 94680
Qy 9895 GACGCTGAGGTGCTGGTCCGCGCACTCAACGCTGTGGCAACCCAGAGACACGCGAGCC 9954
Db 94679 GAAGGCGAAGTACTGCT-----AGTCGCGGATCAACCGCGGTGATGAA 94638
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Db 94637 TCAGCATTCAGGGTATCAACCTAGGCGCTACCTTACCGTTACCGGATACCGTTCCCGT 94578
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Db 94397 TCACCACATGTTGAGCAAAATTTATTCAGTACCGGCGCAAGATAACTTAGATTGTGAA 94338
Qy 10255 GAGCGGAGCGGACCGGCAACCGCAGGCGCGGCGCAAGCTTATCCGTTGGCGGTCTGG 10314
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Db 94277 TACGCAACCGACAGCAGCGGAAAGTTTACCGGCTCTGAATGGTGGCGGCCCATCAAA 94218
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Db 94217 GCAGACTGTTGTTCTTACCTGTTATTGATTACCGGAAACGAGTAACACCTGAAATG 94158
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Db 94103 CGTTATGAATATGGCTTTGCAATTCAGTACTCGCGGTTTATGCCGTGAGATGATGAT 94044
Qy 10552 CATTACCTAGTGTCTTGGCGGGAGTTTCGGGAGCGAATGATGCCGAGCAATTGATTTCT 10611
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Db	94043	CACCTGCTGCAAGCGCTGGATTAATAAGATAAAGAACACAAACGACCAACGCTGGTTTCA	93984	Db	92963	GTGCCAGCGCTGACTGAGCGTGCCACATATGACCCCCCATCACTGGCGTTGTGATCTA	92904
Qy	10612	CGCCTGTTGCTGACTACAGGGAAGTCTTCACTCAGTCTGCTCGAAGAACGTGACACAG	10671	Qy	11692	TCGGCAGACAAACCTCGTGTGTAATGGCATGAACAAATATATGGGGCCCGGATGCA	11751
Db	93983	CGCCTGATATCAATTAATGACGAAGCGCAATCGCCAGCACGCTGGTATTCGTTCTGTCGA	93924	Db	92903	ACCAGGCAAAACCGTGGTTACTCAGCAAAATGAACAAATATATGGGAGCCACCAAC	92844
Qy	10672	GTGGCTTATGATCGACGGGAGCTTGTGCTTCCCGGCACTGCAATTTGGGGTGGCAA	10731	Qy	11752	CTGCACATATCGCAGTTCGGTTCAGTTCCTGGGTGATGAGAAAGCGAGCACTGGCGGA	11811
Db	93923	GTAGGACATGAGCAAGCGGTACTGCGCTCACCTGCCACCATTAAGATTTGGCGTATCAA	93864	Db	92843	TTGCGTTACCGCAGTTCCTCCAGTTCCTGGCTGGATGAANAAGCCGCGCACTGGTTGCC	92784
Qy	10732	ACCTTTACCCCGCGCATTTGTCCGCATGSCAGACGCGTGCAGATATGGGCAAGTTGAGT	10791	Qy	11812	GGCAGTTCCTCTGCTGCTACTCTGCCATTTACATTTGATACCTCTGTGGGTTCGGTGGTG	11871
Db	93863	GAATTTTTCACCGCAACATAACACTGACTGGCAACCGATGATGTGCTGCAAACTTCAAT	93804	Db	92783	GGACAAACACCGGTTTGTATCTCCCTTCGCGGTACACACCTATGCAAAACGGAACA	92724
Qy	10792	TTGCTTCAACCCCTATCAGCTTTAGACCTTAACGGGGAAGGTGTGGGTATTCCTGTAT	10851	Qy	11872	CAGGATGAGATCACCGGTAAACGCTGCTGCTCAGCGAGCTGCTTATTCGCCACGCGCTCTGG	11931
Db	93803	GCCATTCAGCGCTGGCAGCTAGTCGATCTAAAGGCGAAGGATTAACCGGCGCTGTATAT	93744	Db	92723	GGCGATGAATCAGCGGCAACAAATAGTCACACACTGCGTTATGCTGTGGGCCCTTGG	92664
Qy	10852	CAGGACAGCGTCCCTGGTGGTACCTGAAACCGGTACGCGTACGCGGAGTATCCGGAT	10911	Qy	11932	GACGGCGAGGAACGCGAGTTTCGGGGTTCGGTTTGTGTGAGATCAGGATACCGATACC	11991
Db	93743	CAGGATAAAACCTTTGGTGGTACCCTTCGCGACAGCTCTGGGTGAATTTGCTCAGAT	93684	Db	92663	GATGGCGTGAACGGGAATTTTCGCGGATTTGGTTATGTTGAGCAGACAGACCATCAA	92604
Qy	10912	GCTGTGACCTTGGGGGGCGGTGCGGCCCTGCCACAATGCCCGCTTTTGCATTAACAGCGC	10971	Qy	11992	TTGGCAAGCAGGGTACGGGACGGAACGTAGTATGCCCTTCTGTGAGCGGAACTGGTAT	12051
Db	93683	ACCGTCACTTGGGAAAAATACAGCCTTTGTCTGTATCCCTTCCTTGCAAAAGCAAGCC	93624	Db	92603	CTGGC---CCAAAGGCAACGCGTCAAGACGCCACCCACCGCGATGACCAAAACCTGGTAT	92547
Qy	10972	ATCCTGGCGATCTTAATGGGGATGTGCGCTGGAGTGGTTCGTTACCGCCCGCGTGTG	11031	Qy	12052	GCCACCGGGGTACCGGCACTAGACGAGCTCTGCCGGAGACGTATTGGCAAAACGATGCC	12111
Db	93623	TCGCTGTGATATCAACGGAGACGGCAACTTGTATGGGTATATCAACCGGACCGGATTA	93564	Db	92546	GCCACCGGGCTACCGGTAATAGTAACATTTATCAACAGATTTTGGGTGGTGAATAT	92487
Qy	11032	GCGGGATGTATGATCGCACCCCGCGCGAGCTGTGTGATTTACCCCTGTCCAGCC	11091	Qy	12112	GCGCGTTTTCGCGATTCGCGACCCGCTTCTACTGTCTGGTTTCAGGAGAGATGAGCAGACA	12171
Db	93563	CGGGATATCATAGTCAACGTCCAGATGGCAGTTTGACAGCTTTTACCCCACTCAATGCT	93504	Db	92486	CAGGCTTTTTCGCGGTTTTTACCACGCTTTTACGACTTGGCAAGATGGCAAGATATCTG	92427
Qy	11092	TTGCCGTAGATATGCGATCCAAAAGCAGTCTCCCGCATATCTGGGGGCTGGTTA	11151	Qy	12172	TATACTCG---GACACAGCAGACATCTGTGTTGACGAGCCCTTGAAAGGCATCTG	12228
Db	93503	CTGCCGTGGAATATATCATCTACATCCAGCTGCGCAACTCGCGATTTAATGGGAGCGCGCTC	93444	Db	92426	TTAAACCGGAAGATGATAACAGCCAGTATTTGGCTAAACCGGGCACTGAAAGGTCAACTG	92367
Qy	11152	ACGCAATGCTTATTCGGGCGCGCAGCTGTGCTGCTTACCCCTGTCCAGCC	11211	Qy	12229	CTGCGCAGTGTATATACGGTCCGATGGCAGCAGCGCCGATATCCCTTACACGCTC	12288
Db	93443	TCGTGTTAGTGTGATCGGCCCTTAATAGTGTGCTTTATATGCCAATACTCTGACGCGC	93384	Db	92366	CTACGTAGTGTGCTGACGATTTGACGACAGTACAAATAACAGTTCCTTACTGTCT	92307
Qy	11212	TGGAATAAAGGGGAGACCGGTGACGAAACGGAAGAAGTCACTCTGCGGTCGCCGGGGTT	11271	Qy	12289	ACTGAGTCTCGCCCGAGGTACGGC---TAGTTGAAGGAATGGAGACTACCCCGTGGTG	12345
Db	93383	TTGCCAAAGGAAAGATGTGGTGAATCCGGTGATCTCAGCTGCGCAGTACCGGTGCC	93324	Db	92306	ACTGAATTTCTGTCACAGTACGTCTGATTTACAGCAGGAGATAACCAATACCCCGTACTT	92247
Qy	11272	GACCCAGTACCTCTGCGGTTCACTGATATGGCTGGCAGTGGACAGCAGCATTTGACG	11331	Qy	12346	TGCGCAGTGGGCGCGCAAGCCGTACGTCAGTTCATTTAGACGCTACCAATGATCCTCAA	12405
Db	93323	GATCCGCGTAAGCTGGTGGCGTTTAGTGATGTATTTGGGTTCCGCTCAGGCACATCTGGTT	93264	Db	92246	TGGTCATCTGTAGTTGAAAGCCGAGCTATCAATTACGAGCGTATCGCAGCGACCCACAA	92187
Qy	11332	GAGTGGCTTAATGGAGTACGTTACTGGCCAAACCTGGGCAAGCTGCTTTCGGTCCAG	11391	Qy	12406	TGCCAAACAGCAGCGCGTACTCCTCAGTGTATGATACGGTTTCCCACTGCGTCAGGTCACT	12465
Db	93263	GAAGTGAGCGCAATAAAGTCACTGCTGGCCCTAATCTGGGGCATGGACGTTTGGTCAA	93204	Db	92186	TGCAGCCAGATATTAACGCTATCCAGTATCTATTTTGGCCAAACCGTAAACAGGTTTCG	92127
Qy	11392	CCGCTGAATATTCGGGTTTAGCCAGTCACTGACTACGTTTAAACCTGACCAAGATATTG	11451	Qy	12466	GTCAATATATCCAGCAGCCCTCGTCCGGCGGACATTCCTATTCGGCGTCTTACCGGCG	12525
Db	93203	CCCATTAACCTGCGGATTCAGCCAGCAGAGGCTATATTTAAACCGGCTCAAGTTAT	93144	Db	92126	GTACAGTATCCAGCGCGGAAGCAACCCAGCAATCAGTCCGATCTCTGATACGCTGCTGAT	92067
Qy	11452	CTGCGCATACCGACGTTCCGGTACACCGACTGATTTATGCGATGAGTGAACCGGTTA	11511	Qy	12526	ACGCTTTCGCCCAACAGTTTATCAGCAGCAGCAGAGATATTAACGCTGGGGTTGCAACAG	12585
Db	93143	CTGGCCCATCTGGATGCGCGGCCCAACCGATCTGATTTATGTTTACACCAACCCGCTG	93084	Db	92066	GAAATTTAGCCCAACAGCTATGATGAACAGCAACGCCAATTAAGGCTCACTTATCAACA	92007
Qy	11512	GTCAATTTATTAACACAGTGTGTAATTTATTCGCGAGCGCATACGCTGCTTTCGCCG	11571	Qy	12586	AGCAGTGACATCACCTGTTTTCCTGCTGAGGGGCAATTTGTTTGGGGTTGGCGGAG	12645
Db	93083	GACATCTTCTGTAATAAAGTGGCAACCGTTTTCGCCACCGATGATCAATTTGCCCTTCCCA	93024	Db	92006	TCCAGTTGGCATCATCTGACTGACAATACCG-----TTCGGGTGTTAGGATTAACGGAT	91953
Qy	11572	AAAGTGTGGCTATGATCGCACCTGCGAGTCTGCAAGTGGCGGATATCCAGGGGCTGGGG	11631	Qy	12646	GGTTCGGGGAAGTGTATTAACGTTACTCTGCGGCAACAGCTGCGGAAGGGGTCTGACG	12705
Db	93023	GAAGGCTTGGTTTTGACCATACTGTCAGTTTACAGTGGCCGATATFACAAGGTTAGGT	92964	Db	91952	AGTACCGCAGTGATATCTTCACTTATGAAGCTAAATAATGTAACCTGCTGGTGTAAAT	91893
Qy	11632	GTGCTTAGCCTGTACTGACGGTCCCGCATGTCCGCGCTCATCACTGGGTGTGCCATTTA	11691	Qy	12706	CTGGAACACCTGTTGGCGCCCGAAAGCCTGCTCGGATAGTCAGTCCGTACGCTGGCG	12765
				Db	91892	CTGGAACCTACTGATGATTAAGATAGCTGATTTGGGATTAATAACCGCGTGAATATCTC	91833

Qy	12766	G	G	T	C	A	G	C	A	A	G	T	C	T	G	G	T	A	T	C	T	G	A	T	T	C	A	A	G	A	G	T	T	G	C	A	C	G	T	C	G	C	T	G	C	T	G	C	C	A		12825
Db	91832	G	G	C	C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A		91773			
Qy	12826	C	T	C	C	C	C	C	C	A	A	G	T	A	G	T	T	T	T	T	T	C	G	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A		12885			
Db	91772	C	G	A	C	A	G	C	G	T	A	G	C	T	T	T	A	C	C	G	A	C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A		91713			
Qy	12886	C	T	G	G	T	G	C	C	T	A	C	A	N	T	T	G	T	G	A	T	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----		12933		
Db	91712	T	T	T	G	A	T	G	G	A	G	C	A	T	C	C	A	T	C	T	G	C	T	C	A	A	T	T	G	T	C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A		91653		
Qy	12934	C	A	A	T	C	G	G	A	T	A	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T		12993			
Db	91652	C	A	A	A	A	A	A	T	A	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T		91599			
Qy	12994	C	A	G	G	A	T	A	T	T	A	C	T	A	T	C	G	C	G	C	G	C	A	G	A	C	A	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T		13053			
Db	91598	C	A	T	G	T	T	A	C	C	A	T	T	A	C	G	T	A	C	G	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T		91539			
Qy	13054	A	G	T	A	T	T	G	A	C	G	G	C	C	A	G	T	T	A	C	G	T	A	C	G	T	A	C	G	T	A	C	G	T	A	C	G	T	A	C	G	T	A	C	G	T	A	C		13113		
Db	91538	A	C	C	A	A	C	T	A	C	G	G	C	A	A	A	T	T	A	C	A	C	T	T	G	G	A	T	T	A	C	A	C	T	T	G	G	A	T	T	A	C	C	T	A	T	T	T		91479		
Qy	13114	T	G	S	C	A	G	A	T	T	G	C	C	A	G	G	A	T	T	G	T	C	A	C	C	A	C	A	G	C	C	G	A	T	A	G	A	T	A	G	A	T	A	G	A	T	A	G		13173		
Db	91478	A	C	C	G	A	G	A	T	G	C	T	G	G	G	C	T	G	A	C	A	C	C	T	C	A	G	C	C	A	A	T	A	T	A	G	A	T	A	G	A	T	A	G	A	T	A	G		91419		
Qy	13174	G	T	C	C	G	G	T	A	C	G	A	C	C	C	A	A	T	A	T	C	T	G	C	A	G	T	C	C	G	T	C	G	A	G	T	C	C	G	T	C	T	G	A	T	C	T	T		13233		
Db	91418	G	T	C	A	A	C																																													

Qy	13821	TACCCCGTGGTTTGTGGTCAGTGAAGACGAGNAATACACGTTGGGCTAAACGACGCAATC	13888
Db	90767	CAGCCCTATTTTCCCTCAATGACTGGCGGATACGTTAGCAATGACAGTGC--CCGCGCAGGAAA	90710
Qy	13881	CTCACTGGGAAGAGGGGGGACGGTGAATAGTCTCGTCGCCCTCGACAGGCGCTGCCCTG	13940
Db	90709	AAGAAGCTTATGCAGATACCCATGCTATGATCCCGTTGGTCGAGAAATCAAGGTTATCA	90650
Qy	13941	ATGGAGACAAAGATGAANAATACATCTACAGGTTGCGCGGTTGTGCTGACAGGTGTTATG	14000
Db	90649	CGCAAAAGGTTGGTTGACCCGAACTTGTTCACTCCTTGTTTACTGTCATGAGGATG	90590
Qy	14001	GTTTGGGGGCTTCCCATTTGGCGGTTACACCGTCGGTTACACGCGCGCAGATACATCAATGG	14060
Db	90589	AAAATGACACGCGCTGCTGAGGTGAATAGGTGAATATGTAATCTTGATCAATTCGCGCCCTGC	90530
Qy	14061	CAACAACGCGCAGCGCAACAGGAAAGGCGGATGGTTGGCCCTCTCGGACGACGAAACC	14120
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Qy	14121	CGGGAAAGAAAGTGGGAGCAGCAACGACAGACTGACATGAACAAGAGTGGCTATACATGCT	14180
Db	90469	CAACTTATCATCTGTTGATCATTTGTTTATTGCGGCCCTGGGCGGCCCTCGTAAGGTAC	90410
Qy	14181	GAAGAAAGACTGGCTGCTCGCGGTGACCGTGCCTGTATGCTCAGGCACATGGTTCAGGCG	14240
Db	90409	CTCATTTGATATCAAAACAAACAAATATAAATGGAGTTGGATCAACGTAATTTCTGTCAACTC	90350
Qy	14241	CTGCAGCACCGGTTTACCACCTCCAGCGGCAACTTGCAGCTCGTGAACCCGCGGCTT	14300
Db	90349	ATCATCTCTGCTTTACCGGTTGTACTAGAGGATTTGCTGAGTTTGAAGTGGCGGCGAGT	90290
Qy	14301	TCC-----GCAGCTACCGCTATCGGTACAGACGACCTCGGAGGCCAACCCGGCGGTTTTG	14354
Db	90289	ATCTATGACTTTTGCAAATTCAGGTTTATTGCGCAACAACGAGNATACCGGATGNAAC	90230
Qy	14355	TTTGCCGAACGTGTTCCGCGCGCTGACACAGAGAGCGGAGAGCTGGCAGCGTATGCTGAC	14414
Db	90229	TGGCTCTGGCGCGCGCTCATTAACGTATCATCATGATCATGGAAGGAAGCAATAAGGCCCC	90170
Qy	14415	AGACACAGATGNAATGGCAGACCTCGCGGCGCGCTATCAGGCGGCTACGCACGAAGCA	14474
Db	90169	ACTGCCACAATAAACCATCAGTCTCTAGTTAACCTGCAAAATATTCGACTACACTATCGA	90110
Qy	14475	GAATAATAAGGGGATTTAGCCGTTAAGGAAAGTACGCGTGTTCGCGATTAATATTA	14534
Db	90109	CTATCTGAGAAAATCAATACATACAGACAACAATTCGATTCGAGATTGCAAGAAAGATTACACAA	90050
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ORGANISM Photorhabdus luminescens  
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AUTHORS Waterfield,N.R., Bowen,D.J., Fetherston,J.D., Perry,R.D. and ffrench-Constant,R.H.  
TITLE The tc genes of Photorhabdus: a growing family  
JOURNAL Trends Microbiol. 9 (4), 185-191 (2001)  
MEDLINE 21185117  
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REFERENCE 2 (bases 1 to 127816)  
AUTHORS Waterfield,N.R., Daborn,P.J. and ffrench-Constant,R.H.  
TITLE Genomic islands in Photorhabdus  
JOURNAL Trends Microbiol. 10 (12), 541-545 (2002)  
MEDLINE 22454990  
PUBMED 12564983  
REFERENCE 3 (bases 1 to 127816)

AUTHORS ffrrench-Constant,R.H., Bowen,D.J. and Waterfield,N.R.  
TITLE Direct Submission  
JOURNAL Submitted (19-JAN-2001) Biology and Biochemistry, University of Bath, Claverton Down, Bath BA2 7AY, UK

REFERENCE 4 (bases 1 to 127816)  
AUTHORS Waterfield,N.R. and ffrrench-Constant,R.H.  
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REMARK Sequence update by submitter  
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Query Match

Best Local Similarity

Matches 7327; Conservative

0; Mismatches 6235; Indels 1161; Gaps 58;

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Pred. No. 0;

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28867 TCAGAAACAAACAAATCAGCGCCATGAAACTGAGGGGTGGATGGAAGTCCACGATG 28808
Qy 6514 AATTAATTTTATGACGCGCAGCGCGGATTTGACGGATTTGTGGGAGTGGATGT 6573
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
28807 GCAATGCAATTTATCATCGCAATACCGTTAAACATTTATGCGGTTACTCTGATCTGG 28748
Qy 6574 TTTCTAATTCAAAAGTATACAGGTTCGAAA-----AGAACGAGTTGGTGTCTACTG 6623
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
28747 GCGCGATCAACCGTTTATAATAAAACGAAAAATATATTGTCATCAGTTCAAGGCCACT 28688
Qy 6624 TAAATCTTATTCGCTCACTGCGTTAGTGTCTGTTGATTTATTTGATTTCACTCA 6683
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
28687 TGAACCGAGATACACTAGCGTTTGAATTAACCAACGAGTTGAAAAATTAATTTATGCC 28628
Qy 6684 ATAAATCTTTCAGCGGAATTTTGTGAGATAAAATGATAACCGCTTTAATTTAGCGG 6743
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
28627 GATTGTTGAGTTTCCATTTTCTCGAAACACAAATTTTAAACACCGTTTTCACCGTTG 28568
Qy 6744 CATCAAAAGTTAATACGTGCTCTATTGGCTCTCAAGATTTTGGAGTGTAAAGTCCG 6803
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
28567 GCAATAAAACCACTGATTTTAAAAAGTGCAGTTATGCTGTTGATGTTAATAATTTCTC 28508
Qy 6804 TCATGCGGCACCTTCAGATATATGAATTAATCAATGATATCATACTGACATCCGCGTAA 6863
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
28507 GCTTCAGATATTTAGTTCCTTCAATCATCCGCGTGGGATATTTGACACAGGTATTA 28448
Qy 6864 ATGGGACTGAAATTAATCTCGCCCTTCCGCTGATGTTGTTAATGATGAAGCTGATCTG 6923
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Db	28447	ACAACTACTGATGTCACAAATTAACGGTGGTAGCTGGCAGTAACACCCACACTTTACGGCCA	28388
Qy	6924	AATCCGGGAATATCTTTTCAACACCAATCGCTGAGTTTACCAGTAAATACACAGTGATA	6983
Db	28387	GTGACCATATGCTCTCTTCCCGGCAACAGTTTTGATGCTATGCCGTACACCTTTAAGC	28328
Qy	6984	TTGTTCAAGATGAGTTGACGTGACGTTTACGTTTACCGCTGTCAGATCAGATAACGTCG	7043
Db	28327	CACGTGAATTCGATGCTCATCGTTGGCCTTTACCAATTAATATGCTCTCTGGATATCG	28269
Qy	7044	TGCTGCCCGCCCGGACGGCCATATTAACCGTCAATTCGAAACATTAATAATGACACTTCGG	7103
Db	28267	TTTTTGAGACCAAGCAAGACGGCGGAGTGCTGGTGAAGATCAAGCAAAACATTAATCG	28208
Qy	7104	TTATCGCATTAACGTAAAAATACCGTGGCGCGCAGATATATCGTTTTCAC-----	7152
Db	28207	TGAACGGGTAAATTAATTCGGAAGATATCTGTTCTGCGTGAATCTCATTCGGGTG	28148
Qy	7153	-----TGCGGTAAAGATGGCGCTTATTCGCTCAACACCTCTTTGCGCGCAAC	7205
Db	28147	CCCAATATATGACGCTCGGGGTATCGTATTGCTTAAATACCTGCTGGCTTCTCAAC	28088
Qy	7206	TGCTCGACCGGGCAATACCGGATTGACACCAATCTTTCCATGGAGACCCAGAGCTTA	7265
Db	28087	TGGTATCCAGAGCAACACCGGCATTGATACTATCTTGACATGGAAACCCAGCGTTAC	28028
Qy	7266	CGAAACCGCCCTGGAAGA-----	7284
Db	28027	CGAAACCTCGTTGGGAGAAGGCTCTTTGCCAACTTTGTTCTGCTCAATATGACCCCTG	27968
Qy	7285	-----	7284
Db	27967	CTGAACATGGCGATGAGCGGTGTTTAAATCCATATCGGGAATGTTGCGGTAAACACGG	27908
Qy	7285	-----	7284
Db	27907	GAAAGCAGCTTATTACAGCGGAATGTTATCCGATACGTCGGAACCAAGTATGACACTGT	27848
Qy	7285	-----	7284
Db	27847	TTGTCCTTATGCCGAAGGATATTACATGCATGAAGGTGTGAGATTGGGGTTGGATACC	27788
Qy	7285	-----	7284
Db	27787	AGAAATACCTATGACACACTTGGGAATCTGCTTTCTTTTATTTTGTATGAGACAAAC	27728
Qy	7285	-----	7284
Db	27727	AGCAATTTGTTAATTAACGATGCTGATCATGATTCAGGAATGACCAACAGGGGATCG	27668
Qy	7285	-----GGGAGTGTATG	7295
Db	27667	TGAAAAATACAGAAATACAAAGGATTTTGAATGTTTCTATCGCAACGGGCTATTCCG	27608
Qy	7296	TGTTTATGACTTCTCGGAGCAATGCCCTCTATTCTGGAGCTGTTCTATTACACGC	7355
Db	27607	CCCCGATGGAATTTCAATAGTGCAGCGCCCTTATTACTGGGAATGTTCTATTATACACC	27548
Qy	7356	CGATGATGTTGTTCCAGCGGTTGTCGAGAACAGCACTTCCCGGAAGCCACCCTGGC	7415
Db	27547	CGATGATGCTTCCAGCGTTTCTACAGGAATAAATTCAGAGAACCCACACATGGA	27488
Qy	7416	TGCAGTATGTCGGAACCCCGCGGACAGTGGTAAACGGGGTGTGTCAGAAATTAACCTT	7475
Db	27487	TAAACTACGCTCTATAATCCCGCGGCTATATCTGTTAAACGAGAAATCGCCCCCTGATCT	27428
Qy	7476	GGAACTCCGCTCGCTGGAGGAGACACCGCTGGAACGACTCGCCGCTGGACTCCATTTG	7535
Db	27427	GGAACTGCGCGCGCTGGAGAGACCACTCTCTGGAAATGCCAATCCGTTGGATGCCCATTG	27368
Qy	7536	ACCCCGATGCAATAGCCCACTAGACCCCATGATTTACAAGTTCGCCACCTTTATGTCGT	7595
Db			
Db	27367	ATCCGATGCCGTGCACAATATGACCCGACACACTATAAAGTTGCCACCTTTATGCGGC	27308
Qy	7596	ACCTCGACTGCTGATTTCCCGGGGTGATGCCCTTACCGGTGCTTCGAGCGGGACACCC	7655
Db	27307	TGTTGATCAACTTATTCGCGCGGATATGCGCTTATCGGAACCTGACCCCGATGCGT	27248
Qy	7656	TTAAAGAGCCCGGATGTTGATGCTCCAGGCCCTGAACTTCTTGGCGACGAGCCCTATA	7715
Db	27247	TGAATGAAGCAAGATGTTGATGCTGCTTTGGAATGCTGGGTATGAGCGGAGG	27188
Qy	7716	TTTCTTTTGAACCCGACTGTCGCGGTGAACCTGGGTGACGACGAGAGGTGACGC	7775
Db	27187	ATTACGGCAGCAACAGTGGGCGCACCGTCTCTTCCGTGGCGGCACCACTGTGC	27128
Qy	7776	GAGCGATTACAGAGGCCCTGCTGGCGGTGGCGGTGTTGTCCTCCGCTCCCGACAC	7835
Db	27127	AGCGGCGCTTATCAGCAGGACCTTACGGCGCTAGACAAACGAGAGGTGTCCTACAGCCC	27068
Qy	7836	GGACGGCGAATTCCTTGACGGCACTGTTCTCCCGCAGCAGAACGAGGTGCTCAAGGCT	7895
Db	27067	GCACGCTTAACCTGTTGGTGGTGTGTTCTCTCGCGGAATATAACCGGCACCTCACGAT	27008
Qy	7896	ACTGGCAACCTTTGGCAGCGGCTCCATAACCTCGCGCACCAACCTCTCCATTGACGGC	7955
Db	27007	ACTGGCAACCTTGCGTTTGGCGCTTTTAACTCGCGCATATCTTTCCATTGACGGAC	26948
Qy	7956	AGCGGTTTCCCTGCTCGCTACGCCACGCGCTCGAACCGCTCCGCCCTCGCAGAGTCCG	8015
Db	26947	AGCGGTTATCGTGGCGATTTACGCGGAGCTTACCGAATCCGAAAGCGCTGCTCCCAGTA	26888
Qy	8016	TGCTCAACAGCGCGCAGGCTGTCAGCACTCCCGCGCGCGGTGATGCGCTTTACAGTT	8075
Db	26887	TGTTACAGGCTTCTCAGGCGGTAGTGCAGTGTCTGCCCGCACATTTGTTATACCGCT	26828
Qy	8076	TCCCGTCTATGCTGGAGAACGCCCGGGGATGCTGAGCTGTGCTACCGGTTTCGCAACA	8135
Db	26827	TCCCGTGTATGCTGGAGCGGCGCCCAATCTGTGTAGCGCAATTAACCCAGTTTCGGCACCT	26768
Qy	8136	CACTGCTCGTATTACCGAGCGTCAGGATGCGGAGCGCTGGCCAACTGCTGCAGACCC	8195
Db	26767	CTCTGCTCAGTATGTCAGAGCATGATGATGCCGATGAATCTCACCAGCTGCTACTACGC	26708
Qy	8196	AGGCGAGTGAATGATACGCCAGGCGCTTCGCCAGCAGGATAAAGCTCTCGAGGAATCG	8255
Db	26707	AGGTTATGGAATTCGGGACACAGAGCATCCGTATTTCAGCAACGAACTGTCGATGAGTG	26648
Qy	8256	ATCCCGATATCCCGCCCTGGAGGAGCGCGCGCGCGCGCAGATGCGTTTGAACGTT	8315
Db	26647	ATGCTGATATTGCTGTTTGGCAGAGAGCGCGCGCAGTGCACAAATTCGCTGGAAAAAT	26588
Qy	8316	ACAAAGTGTGACAGGCGGACGTCACACCGCGGAAAAACAGGCCATGAGCTGTACC	8375
Db	26587	ACCAGCAGCTGATGACGAGGATATCAACCCAGGAAACAGCGTGCATGTCTACTTTG	26528
Qy	8376	TCAGTTGCTGCTGCTGCTCGGCATCAACCGCGCGCTCTTTTGGCGGAGCGCGCGCGC	8435
Db	26527	ATGCGCGCAGGTGATGCTCTGCGCGGACGCGCTCTCAGTAGCAGAGGGTGGCTG	26468
Qy	8436	ATATGCTGCCAATATTTACGGCTGCGCTGCGGGTCTCCCGCTATGCGGCACTATTATA	8495
Db	26467	ACTTAGTTCCAAACGTTTCCGTTTCTGCTGTTGCGCGCAGTCTGTTGGGGGCGACACTGC	26408
Qy	8496	AAGCCACCGCATCGGCATCCAGGTGCTCTCCGATGCCACCGCATATCAGCGGACAAA	8555
Db	26407	GTGCTTCCGCTCCGCTGATGCTGCTTCTGCGCACAGCTTCCCAATATTCGCGAGACAAA	26348
Qy	8556	TCAGCAGTTCGGAAGTGTACCGCGCTGCGCGGAGGAGTGGGAAATTCAGCGCTGATGTG	8615
Db	26347	TACGCGTTTCGAGAGCTTACCGCGCGCGCTCAGAGTGGGAAATTCAGCGTGAATG	26288
Qy	8616	CGCAGTCTCAGCTGGCGCAGATTGATGCGCAGCTGGCGGCTATGCGCAGTGGCGCGGAAG	8675
Db	26287	CTGACGCTGAAAGTCAAAACAAATGGATGCCAGCTGGAAAGCCTGAAATAACGCCGGAAG	26228



QY	8676	GGGCTGAGCTGCAGAAAACCTTACCTTGAGACCCAGCAGACCCAGGCACAGCGCAGTTGG	8735
Db	26227	CAGCAGATGCGAGTGAATATACAGAGACCCAGAGGCCATCTACTCAGGCTCAGTTAG	26168
QY	8736	CATTCTGCAGAGTAAGTTCAACAATACGCTCTGTACAGCTGCTGCGGGCAGGTTGT	8795
Db	26167	AGCTGTTACAGCGTAATTCACAAAACAAAGCGCTTTACAGTTGATGCGCGCAAGCTGA	26108
QY	8796	CCGCCATTATACCACTTCTATGACCTGCGAGTATCCCGCTGCTGATGCGCCACAGG	8855
Db	26107	GTGCTATCTATACCACTTCTTGAACCTGACCCAGTCTCTCTGCTGATGGCAGGAAG	26048
QY	8856	CCTGGCAGTGGGATAAATTCGAGA---CTAGGTGCTTTATCCAGCGCGGGGCTGGATGG	8912
Db	26047	CGTGCGCCCGAGCTGACCGACAAACGGTGTATCTTTATCCGGGTGGGGCTTGAAACG	25988
QY	8913	GGGCAATGCGGCTGCTGCGCGGGGAAACCTGTATGCTGAATCTGTGGCAGATGAGC	8972
Db	25987	GTACGACTGCGGGTTTATGCGGGTGAACAGTGTGCTGCTGAATCTGGCAGAAATGGAA	25928
QY	8973	AGGCTGGCTGACGGGGGATGCGGCAATAGAGGTGACCGGACGGTCTGCTGCGG	9032
Db	25927	AAGTCTGGCTGGAGCGTATGAGCGGCACTGGAAGTGACCCGTACCGTCTCGTTGGCAC	25868
QY	9033	AGGTCTATACAGCCTCGCGAGGATGCGGCATTCTCTGGCGCAAGGTGGTGAAC	9092
Db	25867	AGTTCTATCAGGCTTATCATCAGA---CAACTTAACTGACCGAATACTCAGCAAT	25811
QY	9093	TGCTCAGTAACGTTTCGGCAGTGCAGGTTACGAAAGCAACGATTAAGATGATGATCAAC	9152
Db	25810	TCCTGCTGAAGGAAAGGCAACGTTAGGAGCTTCGGCAATGAATTAATACTCAGTAACC	25751
QY	9153	AGCAACTCGAGGCCACCTGAAACTGCTGACCTCGGTATCGGCAAGATTAACCGGTCT	9212
Db	25750	GCCAGATAGAAGCCTCAGTCCGATTTGCTGATTTGAAATTTTCAGCGCATCCCCGAAA	25691
QY	9213	CCCTTGACCATGAGCGCATCAACAAATAGCGTCAAGCTCCCGGGCGCTGGTGGCC	9272
Db	25690	GCTTTGCAATACCCGTCAGTTGAAACAGTGAAGTGTACCTTCCCGGCGCTGGTGGTC	25631
QY	9273	CCTATCAGGACGTCGTCGCGGTTCTCAGCTACGCGCGGAAGTATGCTCATGCCCGGGTT	9332
Db	25630	CGTATGAAGATATCCGGCGGCTGCTGAATTTACGCGCGCAGCATCGTATGCCACGGGTT	25571
QY	9333	GCAGCGCTGGCGGTTCTACACGGAATGAACGACGCGCCCAATCCCACTGATTTCA	9392
Db	25570	GCAGTGTATTTGCTCTCTCCACGCGCGTGAATGACACAGTGTCAATTTATGCTGGATTTCA	25511
QY	9393	ATGACCGCGTTACTTCCCGTTTGAAGGACTTCCAGTTGATGACACAGGAGACCTGACAC	9452
Db	25510	ACGATTCCTGTTATCTCCGTTTGAAGTATTTCCGTTGAATGACAGCGGTAGCTGACGT	25451
QY	9453	TGAGCTTCCCGATGCTGACCGCAACAAACAGCGGATGCTCTCAGTCTGAGCGACATCA	9512
Db	25450	TGAGTTTCCCGGATGCGACTGATCGACAGAAAGCGTGTCTGGAGAGCTTGAGCGATATCA	25391
QY	9513	TCCTGCATATCCGTTACACCATATCAGCTGATAGGTATCAACATAGCGCAGGCCCGCA	9572
Db	25390	TTCTGCATATCCCGTATACCATTTGTTCTTAAATTAACCAATTTGTGATAGCAGGCTCCTG	25331
QY	9573	ACGAGGCGCTGCGAGGAGATGAGCATGCAAAATCATCAAGACATGGCCATTACTGCCCC	9632
Db	25330	A-GGAGCCTGTTTAAAGAGTTTATGAGGGTTTCAACACCTTTGAACTTGAAATACC	25272
QY	9633	CAGCTTCCCTTCGCGGCGGTCGCGTCAACCGGCTCAAGGGTATATCCGCGCGCAGG	9692
Db	25271	GTCAATGCCCTCTCGGGCGGATCACTAAAGGAATGGGAGAGCACTCAATGCCGTCGG	25212
QY	9693	GCGGATGTTGCGGCGACCTGAGTATTCCTTCCCGGTTAGCCCCGGTTCGGGTTACGC	9752
Db	25211	AGCGAAGGCGGAGCGTCATTTTCACTGCCCTTCCCGATCTCTGTCGCGGCTGCTGCT	25152
QY	9753	CCCCACTGGGCGACTTAATTAATCAACAGCGGTCGGGGAACGGCCCTTTGGCATTTGGCTG	9812
Db	25151	GGCGGTGCTATCACTGAATTAACAGCAGTACTGCTGCAATGGTCAATTCGGATGGGTG	25092
QY	9813	GGGTATCGCGGTCGCTGCTCAGCGTCGTACGCGCAACGGAGCAACCTACCTACGATGA	9872
Db	25091	GCAATGCGGGTTGGTTTATCAGCCTGCGGTACCGCAAGGGGCTTCGCACTATACGGG	25032
QY	9873	TACTGATGAATTCACCGGTCGGACGGTGAAGTGTGCTGCGGCACTCAGCGCTGCTGG	9932
Db	25031	ACAGATGATGATCTCGGGCCGGATGGGAAGTGTGAGTATTTGTCGGGACAGCAAGG	24972
QY	9933	CACCAAGAGACAGCGCAGCCACCTCACTACTGGGGATAAAACCCAGGGGGAAGCTTCAA	9992
Db	24971	GCAACAGAGCAACGACCGCAACCTCACTGTTGGGACGGTCTGACACAGCGCATAC	24912
QY	9993	CGTTCAGGTTTACCGTTACGTACGAGGGTGTCTCAGCGGCTTTGAGGTTGGCTGCC	10052
Db	24911	TGTTACCCGCTATCAGTCCCGGTGCGCAAAAAATCGTTCTGTTTAAACACACTGGCAGCC	24852
QY	10053	CGCCGAC-----GAGACAGAAACGGAATTTTGGGTGTTATATACCCCTGACGACAGGT	10106
Db	24851	ACAGCAGACGTTGAGGAAGAGACGTCCTTTTGGGTACTTTTACTGCGGATGGTTAGT	24792
QY	10107	GGCTCTGCTGGGCGGAAATCGCAGGCTCGCATCAGCAACCCCAACCCCAACACAGAC	10166
Db	24791	GCACCTATTTCGTTAAGCATCATCATGACGTATTTGCTGACCCGCGAGATGAACAGAAAT	24732
QY	10167	GGCGGTTTGGCTGATGGAGTCTCGGTATCACTTACCGGGGAACAGATGATTTACCAATA	10226
Db	24731	TGCCCCGCTGGCTGATGGAGGAACCGCTCAGCATACCGGGGAACATATTTACTATCACTA	24672
QY	10227	CCGTGCGGAAGATGATGACGTTGTGACGAGCGGAGCGACCGCCACCCGAGCCCGG	10286
Db	24671	TCGGGCGAAGAGCATGTTGACTGTGATGAGCAGTAACCTTGTCTCAGCA--TTCACTGTTA	24614
QY	10287	CGCCCAACGTTATCCCGTGGCGGCTCTGGTATGATAACCGTCAGCGCGGCTCGGACGTACC	10346
Db	24613	CGGCCACGTTATCTCTG-GCAAGTCCAGTATGSCATATCTCAGCGGGAACCGCTTTT	24555
QY	10347	GGCGCTGGTGTGACACCATCAATGGAATA---GCTGGCTGTTTATCTCGGTGTTGATTA	10403
Db	24554	CGCGGTAATAATCAGGTATCCCTGTTGATAATGACTGTTGTTTTCATCTGGTATTTGATTA	24495
QY	10404	TGCTGAGCGTGTGCTCGTCTCTCAAGCGCGGCTGCGCAACACCCAGGA--	10456
Db	24494	CGGTGAGCGCTTATCTTCGCTGAACCTCCGTAACCCGAAATCAATGTGTGAGAAACAAATGT	24435
QY	10457	-----GTGGGAGTGGCTGCTGCTCGTCAAGGATTTGTTTTCGGGTATGA	10499
Db	24434	GTCTGAAAACAATGTCTCTGAAAAATGGCGTTGTCTCGGACAGTTTCTCCGCTATGA	24375
QY	10500	GTTTGGTTTAACTCGGACCTCGCGCTGTGCGCTCAGGTTTGTGATTTTCATTTACCT	10559
Db	24374	ATATGGGTTTGAATAATCGAACCCGCTGTGTGTCGCCAAGTTCTGATGTTTTCATCAGCT	24315
QY	10560	AGGTGTTCTGGCGGGAGTTCCGGACGGAATGATGCGCAGCATTCGATTTCTCGCTGTT	10619
Db	24314	GAAAGCGTGGCAGGGGAAAAGGTTGCAAGAAACACCGCGCTGGTTTCCGCTCTAT	24255
QY	10620	GCTGGAATACAGGAAAGTCTCTTCACTCACTGTCTGCTCGAGAACGTGCACAGGTGGCTTA	10679
Db	24254	TCCTGATTATGACCTGAAACAAAGGTTTCTTGTCTGCAAAACGCGCCGAGACTGGCCCA	24195
QY	10680	TGAGTCGAGCGGACGCTCTTGTGCTTCCGCGCATCTGGCAATTTGGGGTGGCAAACTTTAC	10739
Db	24194	TGAAACGAGCGGTACGCCAGTGTATGTGTCCCGCTGGAAATGGATTATCAACGTGTATA	24135
QY	10740	CCGCGCGCATTTGTCGGCATGGCAGACGCTGACGATATGGGCAAGTTGAGTTGCTTCA	10799
Db	24134	TCATGCGGTGAATCTGAACCTGGCAGTCCCATGCGCAGTTAGAAAAAATGAACACGTTGCA	24075
QY	10800	ACCCTATCAGCTTGTAGACCTTAACCGCGAAGGTGTGGGTATCTCTGTATCAGGACA-	10858



Db 24074 GCCATACCAATTGGTTGATTTATATGAGAAGGAATTCGGCGCTACTTTATCAGGATAC 24015  
 Qy 10859 --CGGTGCTGTGTGATCGGTGAACCGGTACGCCA---GTCCGGGGATGATCCGGATGC 10913  
 Db 24014 TCAGAAAGCCGTGTGTGATCCGTCTCCGGTACCGGATATCACTGCCGAAAGGAACGAATGC 23955  
 Qy 10914 TGTGACCTGGGGGGCGCTGCCGCCCTGCCGACAATGCCCGCTTTTCATAAACAGCGCAT 10973  
 Db 23954 GGTACCTATGAGGAGCGGAACCACTGCCACATATTCGGGCACAACAGGAAGCCGAT 23895  
 Qy 10974 CTTGGCGGATCTTAAATGGGGATGGTGGCTGGAGTGGGTGCTTTACCGCCCGCGGTGGC 11033  
 Db 23894 GTTGTGGACATCAATGGTGAACGGCGTCTGGATTGGGTGATTAACGGCATCAGGTTACG 23835  
 Qy 11034 GGGGATGTATGATCGCACCCCGCGCGAGCTGGTGGCATTTACCCCGCTGTACGCCCTT 11093  
 Db 23834 GGGCTACCAACCATGTCAACCGAAGTGAATGGACACCCCTTTATTCCTATATCCGCTGT 23775  
 Qy 11094 GCCCGTAGAATATGCCATCCAAAGCAGTGTCTGCCGATATCTCGGGGCTGGGTAAAC 11153  
 Db 23774 GCCAATGGATATTTCAATCCGAGCGCAAACTGGCTGATATTGATGGGCTGGGCTGCC 23715  
 Qy 11154 GGCATGGTCTTATCGGCGCGCAGTGTTCGCCCTCTATTCCGGCAAAAACGATGGTTG 11213  
 Db 23714 TGACTTAGCGCTTATCGGCGCAATAGTGTACGTGTCTGTCGTCAAATAATCCGCGAGATG 23655  
 Qy 11214 GAATAAGGGGACCGTGCAGCAAAACGGAAGACTCACTCTGCCGCTCCGGGGGTGGA 11273  
 Db 23654 GGATCGCGCTCAGGATGTTATTCAATTTGTCAATAAGCACTGCCGCTTCCGGCAAAA 23595  
 Qy 11274 CCCAGCTACCTCGTGGCGTTAGTGTATGCTGGCTGGCAGTGGACAGCAATTTGACGA 11333  
 Db 23594 TAAGCTCATCTTGTGCAATCAGTGTATGATGATGACAGCTCGGGCAATCATCTGTGGA 23535  
 Qy 11334 GGTGCGTGTAAATGGAGTACGTTACTGGCCAAACCTGGGCGACGCGTGTTCGGTCAGCC 11393  
 Db 23534 AGTTACGGCAATAGCGTGGCTACTGGCGCAACCTGGGCGATGGAAATTTGGTGAGCC 23475  
 Qy 11394 GGTGAATATCCCGGTTTTAGCCAGTCACTGACTAGTGTAAACCTGACCAATATGCT 11453  
 Db 23474 TCTGATGATAACAGG--CTTCCAAATTTACGGGGAAACGTTTAAACCCCAACAGACTGTATAT 23416  
 Qy 11454 GGCGGATACCGAGGTTCCGGTACCA--CGACCTGATTTATGCGATGAGTGACCGGTTAG 11512  
 Db 23415 GGTACACCTACATGGCTCAGGACACACCGATTTTATGCGCCCAATACTTACCTTG 23356  
 Qy 11513 TCATTTATTTCAACAGAGTGGTAATTTTTCGCGAGCGCATACGCTGCTTTGCCGA 11572  
 Db 23355 AACTCTATGCCAATGAAGCGGCAATCAATCTGCTGAACCTCAGCGTATTGATCTGCCGG 23296  
 Qy 11573 AAGGTGCGCTATGATCGCACTCGAGTCTGCAAGTGGCGATATCCAGGGGCTGGGG 11632  
 Db 23295 ATGGGTGACGTTTGTATGATCTTGTGCGTTACAAATAGCGGATACACAAGGATTAGGA 23236  
 Qy 11633 TGCTAGCTGTTTACTGACGCTCCCGCATGTCCGCGCTCATCACTGGGTGTCATTTAT 11692  
 Db 23235 CTGCCAGCATATTTTGAAGATCCCGCATATGAAGGTGAGCACTGCGCATTTGGATGA 23176  
 Qy 11693 CGGCAGACAAACCTCGTGTGTAATGGCATGAACAAATATGGGGGCGCGGCATGCAAC 11752  
 Db 23175 CCATATTTCAAGCTTGGCTGCTGAATGCCGTCAATAAACAATATGGGAACAGAAACCAACGC 23116  
 Qy 11753 TGCACTATCGAGTTCGGTGCAGTCTGCTGGTGGATGAGAAAGCCAGGCACTGGCGGAC 11812  
 Db 23115 TGTATATCGAGCTCTGCCAGTCTTGGCTGGATGAGAAATTTACAGGCTTCTGAATCCG 23056  
 Qy 11813 GCAGTTCCTCGCTGCTACCTGCCATTTACATTTGCATACCTCTGGCGCTTCGGTGGTGC 11872  
 Db 23055 GGATACGGTGGTCACTACTTACCGTTCCCGGTGATGTGTGTGCGCAACGGAATGC 22996  
 Qy 11873 AGATGAGATCACCGGTACCGTCTGGTGCAGCACTGCTTTATCGCCACCGCGTCTGGG 11932

Db 22995 TGGATGAATTTCCGTAACCGATTGACCCAGCAATTTATCATTTACTCACAATGTCCTGGG 22936  
 Qy 11933 ACGGCGAGAAACGCGAGTTTCGGGGTTTGGTTTGTTCAGATCAGGATACCGATACCT 11992  
 Db 22935 ATGGTCTGGAACCGGAGTTTCGTGTTTGGCGGGGTGACGCAAACTGATATTTGATTCAC 22876  
 Qy 11993 TGGCAAG-----CAGGGTACGGGACGGAACCTGAGTATGCTTCTGTGAGCCGGAAT 12046  
 Db 22875 GGGCGATGCGACACAGGGGACACATGCTGAACACCCGCCACTTCGCCACGTTAAT 22816  
 Qy 12047 GGTATGCCACCGGGGTACCGGAGTAGACAGCGTCTGCGGAGAGCTATTGCGCAAAACG 12106  
 Db 22815 GGTACGGCACTGGCGTACGGGAAGTCGATATTCTTCGCCACGGAATATTCGCAAGGGG 22756  
 Qy 12107 ATGCCCGCGCTTTTGGCGATTTTCGGGACCCGTTTAC-----TGTCCGTTCAGGAGAG 12160  
 Db 22755 ATCAACAGGCAATTTCCCAATTTTACCCCAACGCTTTACCCGTTATGACGAAAAATCCGGTG 22696  
 Qy 12161 ATGAGCAGACATATATCTCCGACGACAGCAAGACATTTCTGGTTGAGCGAGCCCTGAAG 12220  
 Db 22695 GTGATATGACGTCAGCGGACGCGAGCAAGAGATATCTGGTTACATCGAGCTTAAAG 22636  
 Qy 12221 GCATCCTGCTGCGAGTGTATACGGTCCGATGCGAGCAGCAGCCGATATCCCTT 12280  
 Db 22635 GACAAAGTTTACGAGTGTATGGGATGATGATTTCTATCTGCGCGGTACGCCCT 22576  
 Qy 12281 ACAGGCTCACTGAGTCTCGCCCGAGGTACGCTAGTTGAACGGAATGSA---GACTACC 12337  
 Db 22575 ATTGAGTGGATGAATCCCGCACCCCAAGTACGTTTGTACCCTGATGTTATCGGAGTGC 22516  
 Qy 12338 CGTGGTGTGGCGATGGCGGGAAGCGTACGTCAGTTTATGAAACGCTTACCAATG 12397  
 Db 22515 CTGCGTACTGTTTTCGGTGGCGGAATCCCGCAATACCGATATGAACGCGTTGCTACCG 22456  
 Qy 12398 ATCCTCAATGCCAACAGCAGCGGTACTCTCAGTGATGAATACCGTTTCCACCTGCTC 12457  
 Db 22455 ATCCAAGTGCAGCAAAAAGATCGCTTAAATCTGATGCGTTAGGATTTCCGCAAGACA 22396  
 Qy 12458 AGGTGAGTGTCAATTTATCCAGCGCTCCGTCGCGGACCAATCCATATCCGCGCTCT 12517  
 Db 22395 ATCTTGAGATTGCCATTTCGAGACGCTCCACAGCTTCTCGCTTATCCGGATACCC 22336  
 Qy 12518 TACCCGCAACGCTGTTTCGCCAACAGTTATGACGAGCAGCAGCAGATATTACCCCTGGGT 12577  
 Db 22335 TGCCCGCAACATTTTTCACGAGCTTCGACGAACAGCAGATGTTCTTCTGCTGACA- 22277  
 Qy 12578 TGCAACAGAGCAGTGCACATCACTTGTGTTTCTCTGTGAGGGGCAATGCGTTGTTGGGT 12637  
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 REFERENCE Song, Y., Tong, Z., Wang, L., Han, Y., Zhang, J., Pei, D., Wang, J., Zhou, D., Han, Y., Pang, X., Zhai, J., Chen, P., Qin, H., Wang, J., Li, S., Guo, Z., Ye, C., Du, Z., Lin, W., Wang, J., Yu, J., Yang, H., Wang, J., Huang, P. and Yang, R.  
 Submitted (24-APR-2003) The Institute of Microbiology and Epidemiology, Academy of Military Medical Sciences, No. 20, Dongdajie Street, Fengtai District, Beijing 100071, People's Republic of China  
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Db	88026	CACGGTAAACGCGTGGTGACCACTACATACATACGAGCCGAGACGCAACCCCTGACCGGC	87967	Qy	16523	AACCTGTTCCGATGTCGGGATTAATCCCGTCACTGCTGTTTACACAGACGCGCGGATC	16582
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DEFINITION Yersinia pestis strain CO92 complete genome; segment 12/20.  
ACCESSION AJ414152 AL590842  
VERSION AJ414152.1 GI:15980308

KEYWORDS  
SOURCE Yersinia pestis CO92  
ORGANISM Yersinia pestis CO92  
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
Enterobacteriaceae; Yersinia.

REFERENCE  
AUTHORS Parkhill,J., Wren,B.W., Thomson,N.R., Titball,R.W., Holden,M.T.G.,  
Prentice,M.B., Sebahia,M., James,K.D., Church,C., Mungall,K.L.,  
Baker,S., Basham,D., Bentley,S.D., Brooks,K., Cerdeno-Tarraga,A.M.,  
Chillingworth,I., Cronin,A., Davies,R.M., Davis,P., Dougan,G.,  
Fellwell,T., Hamlin,N., Holroyd,S., Jagsels,K., Leather,S.,  
Karllyshev,A.V., Moule,S., Oyston,P.C.F., Quail,M., Rutherford,K.,  
Simmonds,M., Skelton,J.J., Stevens,K., Whitehead,S. and Barrall,B.G.  
Genome sequence of Yersinia pestis, the causative agent of plague  
Nature 413 (6855), 523-527 (2001)

TITLE Nature 413 (6855), 523-527 (2001)  
JOURNAL  
MEDLINE  
PUBMED 11586360  
2 (bases 1 to 313050)

REFERENCE  
AUTHORS Parkhill,J.  
TITLE Direct Submission  
JOURNAL Submitted (04-OCT-2001) Submitted on behalf of the Yersinia  
sequencing team, Sanger Centre, Wellcome Trust Genome Campus,  
Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk

COMMENT Notes:  
Details of Y. pestis sequencing at the Sanger Centre are available  
on the World Wide Web.  
(URL, http://www.sanger.ac.uk/Projects/Y\_pestis/).

FEATURES  
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Microbiology, Horticulture Research International, Wellesbourne,  
Warwick, CV35 9EF, UNITED KINGDOM

## FEATURES

## source

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		Query Match 7.2%; Score 1367.8; DB 1; Length 38457;	DB	11143	AAAAAACAAGAACCTGCACCCTTGGATTTTCGCTCCAGAAATGAGAAATAAGAAATATATAT	11202
		Best Local Similarity 52.5%; Pred. No. 3.9e-268;	QY	3591	TTTACTCTGGGGATTAATCAGCTTTCAAAAAGGGGTTCCGTATATAGCATTCCTGTGTAATAG	3650
		Matches 3955; Conservative 0; Mismatches 3062; Indels 510; Gaps 24;	DB	11203	ACCAAGATAAAATTTTCGTCCTTAATACCCATTTACAGTATTCCTCAATTAATTTGA	11262
			QY	3651	ATGAAGAAAGTTAAATGATGGGATCACAATAGGATTTGATGATGATGATGATGATGATGATG	3698
			DB	11263	CGACAGAGCAAAATCACCAACGGTATACACACTCCGCTTATGGGAGGTTAAACCAAAATCCGT	11322
			QY	3699	GGGGGGATATTAATCAACAGTAAACTTCACTCTGATGTAATATGATCTCGGATATTC	3758
			DB	11323	CGATGCTATCAATGCCAATGCACACTTTAAATGATGGAGTTCCCGGATGATATATTC	11382
			QY	3759	TTCTTAAATTAATAAGTTATCCGCTATACAAGGCCACGGGCATGACCAACGGCGGAAA	3818
			DB	11383	TGTTAAAGCTGAATAAAGCGATTCGTTTGATTAAGCCACAGGCATATCTCCAGAGATA	11442
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			QY	3879	AAATCTTCTCGGTCCGTTACCTGATGCTCATCTATCAGCTTGATGTTGGCCGGTCACTGA	3938
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			QY	3939	TATGTCGAACGGAACCATCAGTGACCGAGGTTTCAGCGCGAACAACGGCTCTGTACCA	3998
			DB	11563	TATGTCGATTCAGATATCAGCAATATTTCCACTAAACAACCCAGTCATTTTACAA	11622
			QY	3999	CGCTGTTTCAACACCCCACCGCTGAACCGCCAGCTGTTTCTGAGATGATACCCCCCTCG	4058
			DB	11623	TGCTGTTCAATACACCGCTATTAATGSCCAAGAGTTTTCTGCTGATAATACCAAACTGG	11682
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			DB	11683	ATTTAAACCCCGGTGGAATCAAAAACCAATTTTATTTGGGAAATAAATAAAGCGCTTTCA	11742
			QY	4119	ACATCAGCGCCTCGGGGCTTTCCACGCTCTGGCAGTTGGCCAGCGGTGACAGCAGCGCTG	4178
			DB	11743	GAGTGAATGATCTGAATCTGTATACATTTAGAACTGGCTATGCGCGGAACAAATCCAG	11802



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KEYWORDS  
SOURCE unidentified  
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AUTHORS Morgan,J.A., Jarett,P. and Ellis,D.J.  
TITLE PESTICIDAL AGENTS  
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QY	7079	-----CGAAACATTAATAATGACACTTCGGTTATCGCAATTAAGTAAATAATACGCGTGGCG	7133	7766	GAGTGAACGACGCGGATTACAGGAGCCCTGCTGCGCGCTGGCGGCTTGGTCCCGCT	7825
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Db	23576	TTTCCAGAAATATAGCTGAAGAGCCAAATTTGGTATGATGTTTAAAGTATGGAAA	23517	22498	ACTCAAGGTTACTGGCAGACATTTGACCAACGCTCTATAACTTAAGCCATAACCTTGAC	22439
QY	7254	CCAGAGGCTTACCGAACCGCCCTCGAAGAGGGAGTCAATGTGTTATGACTTCTC--	7311	7945	CATTGAGCGCAGCGCTTTCCCTGCTGCTACGCCACGCGCTCCGAACCGTCCGCGCT	8004
Db	23516	CGCAAAATTTACAGAGCGCAATTAGGTGAAGGTTTATGCGACATTTAAGTTGCCCC	23457	22438	AATGACCGGTGAGCAGCTGTCATTTATCTCTATGACACGCGCCGAGATCCGTCATGTT	22379
QY	7312	-----	7311	8005	GCAGAGTCCGCTCGTCAACAGCGCGAGGCTGCTGACAGCTGCGGCGCGGCTGATGCC	8064
Db	23456	CCTACAATAAGAGAGCATGCTGATGAACGTTGTTTAAAGTCCATATTTGGAAATATTG	23397	22378	ACTCAGTCTGCCATCACTGCTTCAAGGCGGCGGATTTACTCTATGCAAGTATGCC	22319
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Db	23396	ATGGCAATTCGCCAGACAACTTATTAAGAGGAATGTTATCTGATATTTGAACACACAG	23337	22318	GATGTACCGTTTCCGGTATTCGGAATAATGCCAAGTGGGGGTAAACCACTGATACA	22259
QY	7312	-----	7311	8125	GTTCGCAACACACTGCTCGGTATTACCGAGCGTCAGATCGGAGGCGCTGGCCAACT	8184
Db	23336	TAACGCTCTTTGTTCCCTATGCTAAAGGATATTACATACGTGAAGGTGTCAGATTAGGG	23277	22258	ATTGGCAATACCTGCTCAGCATTTACTGAACGCGAGGATGAGAAGCTTTGGCTGAAT	22199
QY	7312	-----	7311	8185	GCTGAGACCCAGGCGAGTGAATGATACGCCAGGGCCCTTCGCCAGCAGGATTAAGTCT	8244
Db	23276	TTGGGTACAAAAAATATCTATGACAAATCTCGGAAATCTGCTTCTTTTATTTGATG	23217	22198	ACTGCAAACTCAAGGCGAGTTAGCCCTGCAAGTATTAAATGCAAGGATAAGGTAT	22139
QY	7312	-----	7311	8245	CGAAGAAATCGATCGGATATTGCGCCCTTGAGGAGAGCGCGCGCGCGCAGATCGG	8304
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QY	7312	-----	7311	8305	TTTTGAAAGTTTACAAAGTGTGTACAGCGGAGAGCTCAACACCGCGGAAAAACAGGCCAT	8364
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Db	23096	TAACACTGAACCCATGATTTCAACCGCGCAATGCAATCTATTTCTGGGATTTCT	23037	22018	GGATCTTTACCTCTTTCATCGCTTTGAGCACAGCGGCGCAGCCCTGCTCATATGCGCGC	21959
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Db	23036	ATTACAAACGCGCATGATGTTCCAGCGCTTATTGCAAGAGCAGATTTTACCGG-ATCG	22978	21958	CGCGCGGCGAGATCTGCTCCCAATATTACGGTTTGTGCTGGAGGTTCCCGTTTGG	21899
QY	7406	ACCGCTGGTGCAGTATGCTGAACCCCGCGGACGCTGGTAAACGCGGCTGTCAG	7465	8485	GGCACTATTTAAAGCCACCGCATCGGATCCAGGTGCTCTCGATGCCACCGCATATC	8544
Db	22977	ACAGCTGGTGGCTGATCT-AGACCCGACCGGATTTTCGTTTCAAGGTGAATGCG	22919	21898	GGCGCTTTTCAATGCGAGTGGTATCGAAATTTCTGCTGAGCAACAGTATTCG	21839
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QY	7586	TTTATGCTACCTCGACTGCTGATTTGCCCGGCTGATCGCGCTTACCGCTGCTCGAG	7645	8665	GGCGCGGAGGGGCTGAGCTGCAGAAACTTACCTTGAGACCCAGCAGACCCAGGCACA	8724
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AF046867 13162 bp DNA linear BCT 30-JUN-1998  
Photorhabdus luminescens insecticidal toxin complex proteins TcaA  
(tcaA), TcaB (tcaB), TcaC (tcaC), and TcaZ (tcaZ) genes, complete  
cds.

ACCESSION AF046867  
VERSION AF046867.1 GI:3265034  
KEYWORDS  
SOURCE Photorhabdus luminescens  
ORGANISM Photorhabdus luminescens  
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
Enterobacteriaceae; Photorhabdus.  
REFERENCE 1 (bases 1 to 13162)  
Bowen, D., Rocheleau, T.A., Blackburn, M., Andreev, O., Golubeva, E.,  
Bharthi, R. and ffrench-Constant, R.H.  
TITLE Insecticidal toxins from the bacterium Photorhabdus luminescens  
JOURNAL Science 280 (5372), 2129-2132 (1998)  
MEDLINE 98306208  
PUBMED 9641921  
REFERENCE 2 (bases 1 to 13162)  
Bowen, D.J., Rocheleau, T.A., Blackburn, M., Andreev, O. and  
ffrench-Constant, R.H.  
AUTHORS  
TITLE Direct Submission  
JOURNAL Submitted (04-FEB-1998) Entomology, University of Wisconsin-

Madison, 1630 Linden Drive, Madison, WI 53706, USA  
Location/Qualifiers  
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Db	6616	CTTCTGGGCGCATATCAAGATCTTTGAAGCACACTGGTAATGGGTGCGGAAATCGCC---	6672	7672	TCMAACCAACAGCAGCCTGTTCTGTTACTGGATAACGCACCTCCCGCACCGGAAGATGGC	7731
Qy	9323	CCCCGGGTTGACGCGGCTCGCGGCTCTACACGGAATGAACGACGCGGCCAATTCCAA	9382	10382	TGTTTATCTCGTGTGTTGATTTATGTTGAGCTGAGCTGCGTGTCTGTAAGCGCCGCGCT	10441
Db	6673	-----GCTTATCACACGCTGTAATGACGAGGCCGGTTGTT	6711	7732	TGTTTATCATCTGTGCTTTGACCAACGCTGAGCGGATACCTTCACTTATACCGTGCCAAAT	7791
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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 06:14:03 ; Search time 8842 Seconds  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	1921	10.1	39005	US-10-753-901-6	Sequence 6, Appli
C 2	1921	10.1	39005	US-10-754-115-6	Sequence 6, Appli
C 3	1658.8	8.8	38258	US-10-365-319-1	Sequence 1, Appli
	1365	7.2	39005	US-10-753-901-6	Sequence 6, Appli
	1365	7.2	39005	US-10-754-115-6	Sequence 6, Appli
	1364.6	7.2	7569	US-10-753-901-13	Sequence 13, Appl
	1364.6	7.2	7569	US-10-754-115-13	Sequence 13, Appl
C 8	1260.8	6.7	38258	US-10-365-319-1	Sequence 1, Appli
	1108.8	5.9	4431	US-09-817-514A-3	Sequence 3, Appli
	1108.8	5.9	4431	US-10-754-115-22	Sequence 22, Appl
	1108.8	5.9	4434	US-10-609-113-42	Sequence 42, Appl
	1046.4	5.5	4425	US-10-706-424-9	Sequence 9, Appli

13	1046.4	5.5	4425	17	US-10-609-113-43	Sequence 43, Appl
14	1046.4	5.5	4425	18	US-10-754-115-44	Sequence 44, Appl
15	969.8	5.1	4458	15	US-10-242-056-31	Sequence 31, Appl
16	969.8	5.1	4458	15	US-10-262-794A-31	Sequence 31, Appl
17	968.2	5.1	4458	18	US-10-754-115-56	Sequence 56, Appl
18	967.2	5.1	7508	18	US-10-754-115-54	Sequence 54, Appl
19	924.2	4.9	7614	18	US-10-753-901-19	Sequence 19, Appl
20	924.2	4.9	7614	18	US-10-754-115-19	Sequence 19, Appl
21	903.4	4.8	6055	15	US-10-262-794A-25	Sequence 25, Appl
22	848.8	4.5	7551	9	US-09-817-514A-1	Sequence 1, Appli
23	848.8	4.5	7551	15	US-10-242-056-46	Sequence 46, Appl
24	848.8	4.5	7551	15	US-10-435-835-1	Sequence 1, Appli
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29	825.8	4.4	4535	18	US-10-754-115-52	Sequence 52, Appl
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33	797	4.2	4482	17	US-10-609-113-20	Sequence 20, Appl
34	796	4.2	4479	18	US-10-753-901-17	Sequence 17, Appl
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36	781.2	4.1	7512	9	US-09-817-514A-7	Sequence 7, Appli
37	781.2	4.1	7515	15	US-10-242-056-11	Sequence 11, Appl
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ALIGNMENTS

RESULT 1  
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; Sequence 6, Application US/10753901  
; Publication No. US20040194164A1  
; GENERAL INFORMATION:  
; APPLICANT: Bintrim, Scott  
; APPLICANT: Mitchell, Jon  
; APPLICANT: Larrinua, Ignacio  
; APPLICANT: Appel-Birkhold, Patricia  
; APPLICANT: Schafer, Barry  
; APPLICANT: Bevan, Scott  
; APPLICANT: Young, Scott  
; APPLICANT: Guo, Lining  
; TITLE OF INVENTION: Xenorhabdus TC Proteins and Genes for Pest Control  
; FILE REFERENCE: DAS-105X  
; CURRENT APPLICATION NUMBER: US/10/753,901  
; CURRENT FILING DATE: 2004-01-07  
; PRIOR APPLICATION NUMBER: US 60/441,717  
; PRIOR FILING DATE: 2003-01-21  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 6  
; LENGTH: 39005  
; TYPE: DNA  
; ORGANISM: Xenorhabdus nematophilus  
US-10-753-901-6

Query Match 10.1%; Score 1921; DB 18; Length 39005;  
Best Local Similarity 49.6%; Pred. No. 0;  
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Db	28264	CCGATGATTTCAATAGTGCAGCGCCCTCTATTACTTGGGAATTTCTATTATACCCCG	28205	QY	8438	ATGCTGCCCAATATTATCCGGCTGGCGTCCGGGCTCCGCTATGCGGCACCTATTATAA	8497
QY	7358	ATGATGTTGTTCCAGCGGTTGTTGACGAAACAGCACTTCCCGGAAGCCACCCCTGCTG	7417	Db	27124	TTAGTCCAAAACGTTGCTGGTTTAGCTTGTGGCGGAGTCTGTTGGGGGGGAGCAGCTG	27065
Db	28204	ATGATGCTTCCAGCGTTGCTACAGGAAAAACAAATTCAGCAAGCCACACAATGGATA	28145	QY	8498	GCCACCGCATCGGCATCCAGGTGCTCTCCGATGCCACCGCATATACAGCGGACAAAAATC	8557
QY	7418	CAGTATGCTGGAAACCGCGGCGCAGTGGTAAACGGGTGCTGAGAAATTACACTGG	7477	Db	27064	GCTTCCGCTCCGTGATGCTGCTTCTGCCACAGCTTCCCAATATTTCCGAGACAAAAATC	27005
Db	28144	AACTACGCTTACAAATCCCGCGGCTATATCGTTAAACGAGAAATTCGCCCTCGATCTGG	28085	QY	8558	AGCCAGTCGGAAGTGTACCGCGCTCGCGGGAGGATGGGAATTCAGCGGTGATGTGCG	8617
QY	7478	AATGTCGCTCGCTGGAGGAGACACCGGCTGGAAACGACTCGCGCTGGACTCCATTGAC	7537				

Db 27004 AGCCGTTTCGGAAGCCTACCGCGCGCGTTCAGGAGTGGGAAATTCACGCGTGAATAATGCT 26945  
Qy 8618 CAGTCTGACGTGGCGCAGATTGATGCCAGCTGCGCGGCATGCGCAGTGGCGCGGAAAGG 8677  
Db 26944 GACGGTGAAGTCAACAATGATGCGCAGTTGGAAGCCTGAAATCCGCGCGAAGCA 26885  
Qy 8678 GCTGAGCTGCAGAAATCTTACCTTTGAGACCCAGCAGACCCAGGACACAGGGCGCAGTTGGCA 8737  
Db 26884 GCACAGATGCAAGTGAATATCAGAGAGACCCAGCAGGCCATATCTCAGGCTCAGTTAGAG 26825  
Qy 8738 TTCCTGCAGAGTAAGTTCAACAATACGCTCTGTACAGCTGGCTGCGGGCGAGTTGTCC 8797  
Db 26824 CTGTTACAGCGTAATTCACAAACAAGCGCTTACAGTTGATGCGCGCAAGCTGAGT 26765  
Qy 8798 GCCATTATTACCAAGTCTATGACCTGCGCAGTATCCCGCTGCCCTGATGGCGCAACAGGCC 8857  
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Qy 8858 TGGCAGTGGGATAAATTCGAGA---CTAGGTGCTTTATCCAGCCGGGGGCTTGGATGGG 8914  
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Qy 8915 GCAATGCCGTCTGCTGGCGGGAAACCTGTGATGCTGATCTGCGCGCAGATGGAGCAG 8974  
Db 26644 ACGACTGCGGGTTTGATGGCGGGTGAACGTTGCTGTGAATCTGGCAGAAATGGAANA 26585  
Qy 8975 GCCTGGCTGACGGGGATGACGGGCAATAGAGGTGACCGGACGGCTCTGCTGTCGGAG 9034  
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Qy 9035 GTCTATACCAAGCTCGGGAGATGCGGCAATCTCTGCGCGCAACAGGTGGTGGAACTG 9094  
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Qy 9335 AGCGGCTGGGGTCTCACACGGAATGAACGACAGCGGCCAAATTCCAACTGGATTTCAT 9394  
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Qy 9395 GACCGGCTTACCTGCGGTTTGAAGGACTTCAGATTGATGACACAGGAGCCCTGACACTG 9454  
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Qy	4844	GTGGTTAAACCGACGCGACCATGCGGGAGGTCTGTACCCGCACTTGAGACCGGAGAA	4903
Db	31189	TGGATTAAATGGGTGGGCAATCCCGCTCTGACACCGTGGATGTGTGCGCCAGCAGACA	31130
Qy	4904	CTGTCTGTACAGCCCTGTGTCGCGCGGCGCTGTCAAGAAATGAGCAGGATGTGACCGCGCC	4963
Db	31129	CTCACGGCCACAGACTGGCTCTCGGTATGGGCTGGACATCATGTATGTGTAAACGAGGCC	31070
Qy	4964	TTGGCGAGGTGAGGGGGCGGTGAACAAGGACAACAGACGCGTGTTCACCTCTCTGGGAAGAG	5023
Db	31069	ATGGTTTCCCGCGGTGAACACAGCTTCAAGTGTGGCAGGATATCAACACCGGTGTGCAG	31010
Qy	5024	GTGACCCAGCTGAGCAGTGGCTGGACATGAGTGAACCTGTCCATTAGCCCATCCGGT	5083
Db	31009	TGGATAGATGTGCATCAGCACTGTCAACAGATGCCGTGGTATTCGTACGCTGGTGAAT	30950
Qy	5084	CTGGCTAGCCTGATTGCCCTGGAAGTACATCAATGTGTCCGATGACAGTGACACCGTTGTAC	5143
Db	30949	ATCCGTTACGTGACTGATTAAACAAG-----CCGAGTCGAATCTGCCCTCTCTGG	30899
Qy	5144	AGCCAGTGGCAGTGTGATCCGTCTGTCAGCGCGGGGTGAAAAGCAGCCAGACTCG	5203
Db	30898	GATGAGTGGCAGACACTGGCAGAAAAATATGGAAGCCGACTCAGTACACAACAGGCTCAG	30839
Qy	5204	GCCTGCACCATTTATCTGGAGGAGGGACACAGACGCGCCTTTGTGCGTATATCTCGGT	5263
Db	30838	ACGCTGGCGATTATACCGCGAGCGCTGAGTAGCGTGTGTGCAATTGGTTTCTGGCG	30779
Qy	5264	AATCTGGCAACCAATGTGTATC-----CGGCGCGATGACCTCTTCGGGTATCTGCTG	5317
Db	30778	AATATCAGCCAGAGGGGTGTCCCTGCCACAGCGGGATGACCTGTACAGCTATTTCCTG	30719
Qy	5318	CTGATTAATCAGGTGTGACCAAGGTAAACACACCGGCATTTGCGGAGGCCATTCGCGGC	5377
Db	30718	ATTGATAATCAGGTCTCTTCTGCATATAAAACACACCGCACTGCGCAGAGGCCATTGCGGT	30659
Qy	5378	ATACGGGTGATATCAACCGGGCCCTTAACGGAATAGACTCAGCGCCATGGCAGAGGTG	5437
Db	30658	ATTTCAGCTCTACATCAACCGGGCGCTGATCGGATAGAGCTTAATGCCGTGCCGATGTG	30599
Qy	5438	AGGGGGCGTCAGTTTTTCACTGACTGGGATACGTTCAACAACGTTTACAGCACTTGGCG	5497
Db	30598	TCAACCGCGCAGTTTTTACCAGCTGG---ACGGTGAATTAACCGTTTACAGCACTTGGGC	30542
Qy	5498	GGCGTCTCAGAGCTGGTTACTATCCGGAAAACTACTCGACCCGACGGTCCGTATCGGG	5557
Db	30541	GGGGTGTGCGGGTGGTTATTATTCGGAAAAATTACATTGACCCAAACCCAGCGTATCGGG	30482
Qy	5558	CACACCGGATGATGACACCCCTGCTGCTGCTGTGAGCCAGCAGTATCAACCCGAT	5617
Db	30481	CAGACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	30422
Qy	5618	ACCGTGGAGGATGCCCTTTAAACCTATCTGACACACGTTTGGAGCAGATTGCCAATCTGAAC	5677
Db	30421	ACAGTGAGGATGCCCTTTAAACCTTACCTGACCCGCTTTGAACCGGTGGCGGATCTGAAA	30362
Qy	5678	ACTGTACGGGATATCACGTAACCGCAGCATGACGAGGGGACTACATGTTATGGGT	5737
Db	30361	GTGTGTGAGCGCTTATCACGACACGTCACACAGCAACACCGGACTGACCTGGTTGTGCGC	30302
Qy	5738	CGCAGCATCACAGATCAGACTTAATGTTACTGTCGCGCAGCGCCAAACACAGCAAAATCCAA	5797
Db	30301	CAAAACGGGAGAACCTGCGGAAATACTACTGCGGTAACTGGATATATCACGGATGCAG	30242
Qy	5798	GACTCAATGATCCCGGAATGCTCGACCGGATGGACAAAAATTAATCTCGGGAATGAAT	5857

Db	30241	GCGGGTGAATCGCCCAATGCCTGGAAAGAGTGGACGAAGATTGATACAGCGTCAAC	30182
Qy	5858	CGGTGTCAAGATCTTGTGTGCTCGGTGTTTTTCAACAGTCCGCTTTATGTCTCGGTC	5917
Db	30181	CCCTACAGGATGCAATCGTCCGCTCATATTTCAGGGAACGTTTGACACCTTATCTGGTA	30122
Qy	5918	GAGAGAATCAGTCTCTGATACGAGGCGAGAGACACACACACGACGAGCAGACTAC	5977
Db	30121	GAAGAAAGAGAAATGCGAAAAATGCTGATCCGGTGGAAACC---TATGACCGTTTT	30065
Qy	5978	AGCTGAAACTGTCTGCTCGGCTACGACGGTACATGAGTTCGCCGTGTCTGTCGAC	6037
Db	30064	ACTCTGAATCTGGGTTTCTGCTCATGTGCGATGAGTGGAGTCCGCTTGTCTTACGAT	30005
Qy	6038	ATTACCGGCAACATCG-----	6053
Db	30004	ATCAACAACGAGTGGAGCGGTCACTGACAAAAAACCTGACACTGAACGGCTGGCGCTG	29945
Qy	6054	-----CATTTCCGAAACGAGGCGCATGTGACCTGTAATCCCTGACTGAGCAG	6106
Db	29944	GCGCATCAGGCTTTCAGGGCAGGACACTCTGCTGGTGTGTCTTACAAAAACCGGAAG	29885
Qy	6107	CTCTATTGCGCGTTTACTCTCCGTCAACAGCAAGCCGGAATTTGATAACGCTCAGCTGATT	6166
Db	29884	AGTTACTCGGATTTTGGCGCAGCAATAAATAATGTGCGAGGCATGACATTTACGGGAT	29825
Qy	6167	TCGTGGATAATGATANGACGCTAAATGTCTCATGATATAGGAGATTTTAAAGAGGTC	6226
Db	29824	GGCTCTTCAAAAAGATGAGAAACACAGCACTCAGCCGTACAGCCAACTGAAAAATACC	29765
Qy	6227	AGTCAGAAATTAATACGAGCACTGAGAAATTTATTAATAATGTTTTTTCAGACCCCTTC	6286
Db	29764	TTTGATATCATCTACTCAAGGCAACGACTTGTGTAAGAAAGCCAGCTATCGTTCGGG	29705
Qy	6287	GCTAATTTTTCAGTGCAACGAGTTTAAATGTATGATGTTTATCCACAGCGATTTCTCA	6346
Db	29704	CAGGATTTTGAAGTGCCTGCCTCGTTGAATATGGGTCTGCCATCGGTGATGATGCTG	29645
Qy	6347	CTCCTTAATCTTAAACTACAAGTACTGTTTTTACTAATGAAGATTCC-----TCTCTT	6400
Db	29644	ACGGTATGAGGAACGGGAATATCCGCAGATAACCCAGTAAATATCTCCACGCGATAACCTT	29585
Qy	6401	TTGACGCCAGAGCTTCATATTACAGCAATGTTTCGTGTTTGTAGTAGTCTGCTGCATC	6460
Db	29584	GCTATTACGCTACATAACCCCGTTTCACTGTCAAGATATGATGGCAGTGCAATGTCATC	29525
Qy	6461	GCCACTCAATCTACCA-----TAGAAAAATTCGTTTCAGCAGGAGATAGAATTTGAGAAA	6515
Db	29524	AGAAACAAACAAATCAGCGCCATGAAACTGACGGGGTGGATGGAAAGTCCCAGTACGGC	29465
Qy	6516	TTAATTTTTCAGCGCCAGCGCGCGGATTTGACCGATTTTGTGGAGTGGATGTTTT	6575
Db	29464	AATGCAATTTTATCATCGCAATACCCGTTAAACATTAATGGCGGTTACTCTGATCTGGGGG	29405
Qy	6576	CTAATTTCAAAAGTATACCAAGTTCGAAA-----AGAAAGCAGTTGCTGTCACTGTA	6625
Db	29404	CGATCACCGTTTATTAATAAAGAAACTATATGCACTCAGTTCACGCCCACTTGATG	29345
Qy	6626	AAATCTTATTCGCTCACTGGCGTTAGTGGTCTCTGTGTAGTTATTTATGATTCATCAAT	6685
Db	29344	AACGCAAGTTACACTAGGCGTTTGATTCTTAACACCAAGTTGAAAAATAATATTATGCCAGA	29285
Qy	6686	AAATACTTCAGCGGAATTTTGTACAGATAAATGATAACCGCTTTAATTAGCGGCAGTACA	6745
Db	29284	TTGTTCGAGTTTCCATTTTCTCCAAACACAAATTTTAAACACCGTTTTTCAGGTTGTAGC	29225
Qy	6746	TCAAAAGTTAATTACGTGCTCTATTGGCTCTCAAGATTTTGGAGTGTAAAGTCCGCTC	6805
Db	29224	AATAAACCAGTGATTTTAAAAAAGTCAGTTATGTGTGATGTTAATAATTTCTCAGGGC	29165
Qy	6806	ATCGCGCACTTCAGATATATGAATTAATCGATGATATCATCTGACATCCGCGGTAAAT	6865
Db	29164	TTCCAGATATTATAGTTCTTATCAATCATCCGCTGGCTGGATATTGATACAGGCATTAAC	29105



Db	26944	GACGGTGAAGTCAAAACAATGGATGCCAGTTGGAAAAGCCGTGAATAATCCCGCCGGAAGCA	26885
Qy	8678	GCTGAGCTGCAGAAAACCTTACCTTTGAGACCCACAGACCAGGCACAGGCGGAGTTGGCA	8737
Db	26884	GCAAGATGCAGGTGGAATATACAGGAGACCCACAGGCCCATACTCAGGCTCAGTTAGAG	26825
Qy	8738	TTCTCGCAGAGTAAGTTCAACAATACGGCTCTGTACAGCTGGCTGCGGGGCGAGTTGTCC	8797
Db	26824	CTGTTACAGCGTAATTCACAAACAAGCGCTTTACAGTTGGATGCGCGCAAGCTGAGT	26765
Qy	8798	GCCATTTATTACAGTTCTATGACCTGGCAGTATCCCGCTGCCTGATGCGCGCAACAGGCC	8857
Db	26764	GCTATCTATTACAGTTCTTTGACCTGACCCAGTCTCTCTGCTGATGCGCACAGGAAGCG	26705
Qy	8858	TGCGAGTGGATAAATTCGAGA---CTAGTCTGTTTATCCAGCGGGGGGCTGGATGGGG	8914
Db	26704	CTCGCGCGGAGCTGACCGACAACGGTGTGTACCTTTATCCGGGTGGGGCTGGAACGGT	26645
Qy	8915	GCAAAATGCCGGTCTGCTGGCGGGGAAACCTGATGCTGAATCTGCGCGCAGATGGAGCAG	8974
Db	26644	ACGACTGCGGGTTTGATGGCGGTGAAACGTTGCTGCTGAATCTGCAGAAATGGAAAAA	26585
Qy	8975	GCCTGCGTACGCGGGGATGACGCGGCAATAGAGGTGACGCGACGGTCTGCCTGTGCGAG	9034
Db	26584	GTCTGCGTGAGCGTGATGAGCGGGCACTGGAAAGTACCCGTACCGTCTCGTTGGCACAG	26525
Qy	9035	GTCTATACAGCCTCGCGGAGGATGCGGCAATCTCTCTGCGCGCAACAAGTGTGTGAACATG	9094
Db	26524	TTCTATCAGCGCTTATCATCAGAA---CAACTTTAAATCTGACCGGAAAAAATCTACGCAATT	26468
Qy	9095	GTCAAGTAAAGGTTCCGGCAGTGGGTACGAAAGCAACGGATTTACAGATGGATCAACAG	9154
Db	26467	CTCGGTGAAGGGAAGCGCAACGTAGGAGCTTCGCGCAATGAATTTAAACTCAGTAACCGT	26408
Qy	9155	CAACTCGAGGCCACCTCGAACTGGCTGACCTCGGTATCGGCACAAAGATTACCCGGTCTCC	9214
Db	26407	CAGATAGAAGCCTCAGTGGGATTTGCTGATTTGAAATTTTCAGCGACTACCCCGAAAGC	26348
Qy	9215	CTTGGCACCATGAGGCGCATCAAAACAATAAGCGTCAACGGTCCCGCGCTGTGCGCCCC	9274
Db	26347	CTTGGCAATACCCGTCAAGTTGAAACAGGTGAGTGTCAACCTTGC CGCGCTGTGTTGGCGC	26288
Qy	9275	TATCAGAGCTCGTGGGTTCTCAGCTACGGCGGAAGTATGTCATGCTCCCGGGGTTCG	9334
Db	26287	TATGAAGATATTCGGCGGTGCTGAATTCGGGGGAGCATGTCATGCCACCGGTTGC	26228
Qy	9335	AGCGCGTGGCGGTCTCACACGGAATGAACGACAGCGGCCAATTTCCAACCTGGATTTCAT	9394
Db	26227	AGTGCTATTGCTCTCTCCACGGCGTGAATGACAGTGGTCAATTTATGCTGGATTTCAAC	26168
Qy	9395	GACCCGGTTACCTGCGGTTTGAAGACTTCAGTTGATGACACAGGACCCCTGACACTG	9454
Db	26167	GATTCGCGTTATCTGCGGTTTGAAGGTATTTCCGTGAATGACACGCGCGCTGACGTTG	26108
Qy	9455	AGCTCCCGGATGCTGACGCAAAACAACAGGCGATGCTCTCCTCAGTCTGACGCGCATCATC	9514
Db	26107	AGTTTCCGGATCGGACTGATCGGCAGAAAGCCCTCTGAGAGCCCTGAGCGGATATCAT	26048
Qy	9515	CTGCATATCCGTTACACCATTTATCAGCTGATAGGTATCAACATAGCGGAGGCCCGCCGAAC	9574
Db	26047	CTGCATATCCGCTATACCATTTGCTTTTAATTAACAATTTGTATAGGCGGCTCTCGA-	25989
Qy	9575	GAGGGCTCGGAGAGACTGAGCATGCAAAATCATCAAGACATGGCCATTTACTGCCCCCA	9634
Db	25988	GGGAGCGTGTTTAAGGAGTTTATTCAGGGTTTCAACACCTTTGAAACTTGAATACCGT	25929
Qy	9635	CGTTGCTTCCGGGGCGGTGCGGTCAACGGGCTCAAGGCTGATATCGCGGCGGAGGCG	9694
Db	25928	CATTGCCCTCTGGGGCGGATCACTAAAGGAATGGAGAGACACTCAATGCCGCTCGGAG	25869
Qy	9695	CGGATGTCGGCGACCCCTGAGTATTTCCCTTTCGCGGTAGCCCCGCTCGGGGTACGCC	9754
Db			
Db	25868	CGGAAGGGGAGCGTCATTTTCACTGCCCTTCCCGATCTCTGTGGGCGTGGTCTGGTGC	25809
Qy	9755	CACTGGGGCACATTAATTAACAGCCGTCGGGNAACGGCCCTTTTGGCATTTGGCTGGG	9814
Db	25808	CGGTGCTATCACTGAATTAACAGCAGTACTGCCCGCAATGGGTCAATTCGGGATGGGTGGC	25749
Qy	9815	GTATCGGCGGTGCTGCTGCCAGCGTACGCGCAACGGAGCACCTACTCTACGATGATA	9874
Db	25748	AATGTGGGTTGGTTTATCAGCTGCGTACCGCCAGGGCGTTCCGCACTATACGGGAC	25689
Qy	9875	CTGATGAATTCACCGTCCGACGCTGAGGTGCTGTGCCGCACTCAACGGTGTGGCA	9934
Db	25688	AAAGTGAATCTCGGCGGATGGGAAGTGTGAGTATTTGTCCGGACAGCAAGGCG	25629
Qy	9935	CCCAAGAAGCAGGCGGCACTCTACTACTGGGATATAAACCCAGCGGGAAGTTCACAG	9994
Db	25628	AAACAGAGCAACGCCCACTCTGTGTGGGACGGTCTTGACACAGCCGCATCTG	25569
Qy	9995	TTTCAAGTTTACCGTTTCACTGACGAGGTGAGTCTCAGCCGCTTGAGCGTTGGCTGCCG	10054
Db	25568	TTTACCGCTATCAGTCCCGCTGGCAGAAAAAATCGTTCTTTAGAACACTGGCACCAC	25509
Qy	10055	CCGA-----CGAGACAGAAACCGAATTTTGGGTGTTATATACCCCTGACGACAGGTG	10108
Db	25508	AGCAGAGACGTGAGGAAGAGACGTCTTTTGGGTACTTTTACGCGATGGTTTAGTGC	25449
Qy	10109	CTCTGCTGGCCGAAATGCGCAGGCTCGCATCAGCAACCCACAGCCCCAACACAGACCG	10168
Db	25448	ACCTATTTCGGTAAGCATCCATGACGTAATTTGCTGACCGCAGGATGAACAGAAATTG	25389
Qy	10169	CGGTTTGGCTGATGAGTCTCGGTATCACTTACCGGCAACAGATGTTATACCAATACC	10228
Db	25388	CCCGTGGCTGATGAGGAAACCGTCAGCATACCGGGGAATATTTACTATCACTATC	25329
Qy	10229	GTGCGAAGATGATGACGGTTGTGACGAGCGGAGCGGACCGCAACCGCGGCGCGG	10288
Db	25328	GGGCAAGACGATCTTGACTGTGATGACATGAACCTTCTCAGCATTCAGGTGTTACCG	25269
Qy	10289	CCCAAGTTATCCGTGGCGGTCTGGTATGGTAAACCGTCAGCGGCTCGACGCTACCGG	10348
Db	25268	CCGAGCGTTATCGCCAAAGTCAGCTATGGCAATCTCAGCGGGAACCGCTTTTTCG	25209
Qy	10349	CGCTGTGTGC---GACACCATCAATGATAGTGGCTGTGTTATCTGTGTTTGAATATG	10405
Db	25208	CGGTAATCAGGTATTCCTGCTGATATGATCTGCTGTTTCTCTGTTTGAATAG	25149
Qy	10406	GTGAGCTAGCTCGGTGCTGTGAAGCGCCGCGCTGGCAACAACAGAA-----	10456
Db	25148	GTGAGCGCTCATCTTCGCTGAACCTGTACCCGAAATTCATGTGTGAGAAAAAATGTGT	25089
Qy	10457	-----GTGGGAGTGGCTGTGTGCTGCTCAGAGTTGTTTTCGGGTATGAGT	10501
Db	25088	CTGAAAAAATGTGCTGAAAAATGGCGTTGCTGTCGGACAGTTTCTCCCGCTATGAAT	25029
Qy	10502	TTGGTTTTAACTCGCGACTCCCGCTGTGCGCTCAGGTGTTGATGTTTCCATTAACCTAG	10561
Db	25028	ATGGGTTTGAATTCGAACCCCTGCTGTGTGTGCGCAAGTCTGATGTTTCACTAGTGA	24969
Qy	10562	GTGTTCTGCGGGGAGTTCGGAGCGAATGATGCGCCAGCATGATTTCTCGCTGTGTC	10621
Db	24968	AAGCGTGGCAGGGGAAAAAGTTGCAGAGAAAAACACCGCGCTGGTTCCCGCTCTATTTC	24909
Qy	10622	TGGACTACAGGAAAGTCTTCACTCAGTCTGCTCGAGAACGTGCACAGGTGGCTTATG	10681
Db	24908	TGGATTATGACCTGAACAACAAGGTTCTTCTGCAACCGCCGCGCAGACTGGCCCATG	24849
Qy	10682	AGTCGGAAGGAGCTCTTGTGCTTTCGCGCACTGGCATTTGGGTGGCAAACTTTTACC	10741
Db	24848	AAACGGAAGTACGCGAGTATGATGTCGCCGCTGGAAATGATATCAAGCTGTTAATC	24789
Qy	10742	CGCCGACATTTGTCGCAATGGCAGACGCTGACGATATATGGCAAGTTGATTTGCTCAAC	10801
Db	24788	ATGGCGTGAATCTGAACCTGGCAGTCCATGCCGAGTTAGAAAAAATGAACACGTTGCAGC	24729

Qy 10802 CCTATCAGCTTGTAGACCTTAACGGCGAAGGTGTGGGTATCTCTGTATCAGGACA --- 10858  
Db 24728 CATAACCAATTTGGTTGATTTATATGGAAGAGAAATTTCCGGCGTACTTTATCAGGATACTC 24669  
Qy 10859 GCGGTGCTGCTGCTAGCGGTGAAACCGGTACGCCA ---GTCCGGGATGATCCGGATGCTG 10915  
Db 24668 AGAAGCCTGTGTGTACCGGTCTCCGTACGGGTATACATGCGCGAAGGAACGAATCCGG 24609  
Qy 10916 TGACCTGGGGGGGCTGCGGCCCTGCGCAATGCGCGTTTGCAATAACAGCGGATCC 10975  
Db 24608 TTACCTATGAGGAGCCAAACCACTGCCATATTCGGGCACACAGGAAGCGCATGT 24549  
Qy 10976 TGGCGGATCTTAATGGGGATGGTCCGCTGAGTGGGTGTTTACCGCCCCCGGTGTGCGG 11035  
Db 24548 TGTGGACATCAATGTGTGACGGGCTCTGGATGGGTGAATACGGCATCAGGGTTACGGG 24489  
Qy 11036 GGATGTATATCGCACCCCGCGCGACTGTTGCAATTTACCCCCCTGTACGCTTGC 11095  
Db 24488 GCTACCAACACATGTCACCGGAAGGTGAATGGACACCCCTTTATTTCCATTTATCCGCTGTG 24429  
Qy 11096 CCGTAGAATATGCGCATCCAAAAGCAGTGTGCGCGATATCTGGGGGCTGGGTTTACCG 11155  
Db 24428 CAATGGAAATTTCCATCCGAGGCAAACTGGCTGATTTATGGGGCTTGGGCTGCTG 24369  
Qy 11156 ACATGGTGTATCGGGCCGCGCAGTGTTCGCTCTATTCGGGCAAAACGATGGTTGGA 11215  
Db 24368 ACTTAGCGCTTATCGGGCCAAATAGTGTGCTGTCTGTCGTCGTCGTCGTCGTCGTCG 24309  
Qy 11216 ATAAAGGGGAGACGCTGAGCAAAACGGAAGACTCTCTGCGGTCCCGGGGTGTAAC 11275  
Db 24308 ATCCGCTCAGGATGTGATTCATTTGTGATATGTCACATGTCGCTGTCGCTGTCGCTG 24249  
Qy 11276 CAGTACCTCTGCGGTTCAGTGATATGCTGCGCAGTGTGACGACGACATTTGACGGAG 11335  
Db 24248 AGCTCATCTTGTGCGCAATTCAGTGATATGACAGCTCCGGGCAATCATCTGTGTGAAG 24189  
Qy 11336 TGGTGTAAATGGAGTACGTTACTTGGCCAAACCTTGGGCGACGCTGCTTTCGGTCAGCCG 11395  
Db 24188 TAACGGCAGATAGCGTGGCTGCTGCGGCAACCTGGGCGATGGAATTTTGTGAGCCTC 24129  
Qy 11396 TGAATATTCGGGTTTTAGCCAGTCACTGACTAGCTTTTAACTTACCTGTGACAGATATGCTG 11455  
Db 24128 TGATGATGACAGGCTTCAGATTTAGCGGGGAAAGCTTTTAAACCCCGACAGACTGTATATG 24069  
Qy 11456 CCGATACCGAGGTTCCGGTACACGACCTGATTTATGCGATGAGTACGCTTACTCA 11515  
Db 24068 TAGACATAGATGGCTCAGGACCAACCGATTTTATGCGCGCAATACTTACCCTTGAAC 24009  
Qy 11516 TTTATTTCAACACAGTGGTAATTTATTTGCGGAGCGGCATACGCTGCTCTTGGCCGAAAG 11575  
Db 24008 TCTATGCCAATGAAGCGCAATCATTTTGTGAACTCAGCGTATTTGATCTGCCGATG 23949  
Qy 11576 GTGCGGTATGATCGACCTGTGAGTCTGCAAGTGGCGGATATCCAGGGGCTGGGGTGC 11635  
Db 23948 GGGTACGCTTTTGATGATACTTGTGCGTTTCAAAATAGCGGATACACAAGGATTAGGGACTG 23889  
Qy 11636 CTAGCCTGTTACTGACGCTCCCATGTCGCGCTCATCTGCGGTGTCGATTTTATCGG 11695  
Db 23888 CCAGCATTTATTTGACGATCCCCCATATGAGGTGACAGCTGGCGATTTGGATATGACCA 23829  
Qy 11696 CAGACAAACCTGTGTGTTGAATGGCATGAACAAATATGCGGGGCGCGCATGCACTGC 11755  
Db 23828 TATTCAGCCTTGTGCTGCTGATGCTGCTGATACATATGGAAGCAAGAACCAAGCTGT 23769  
Qy 11756 ACTATCGAGTTCGGTCACTGCTGCTGCTGATGAGAAAGCGGCACTGCGCGCAGGCA 11815  
Db 23768 ATTATCGAGCTCTGCCAGTCTCTGGTGGATGAGAAATACAGGCTTCTGAATCCGGGA 23709  
Qy 11816 GTTCCCCTGCTGCTACCTGCCATTTACATTTGATGATACCTGTGCGGTTCGGTGTGAG 11875  
Db 23708 TGACGGTGGTCAGCTACTTACCGTTCCCGGTGCAATGTGTTGTGCGCACGGAAGTGTCTG 23649

Qy 11876 ATGAGATCAACCGGTAAACCGTCTGGTCAGCGACGCTGCTTTATTCGCCACGGCGTCTGGAGC 11935  
Db 23648 ATGAAATTTTCGGGTAAACCGATTCACGAGCATTTATCACTACTACTGTGCTGCTGGATG 23589  
Qy 11936 GGCAGGAACCGAGTTTCGGGGTGTGGTTTGTGAGATCAGGATACGATACCTTGG 11995  
Db 23588 GTCTGAACCGGAGTTTCGGTGTGGTGTGGCGGTGACACAACTGATTTGATTTACGGG 23529  
Qy 11996 CAAAG-----CCAGGGTACCGGCACGAACTGAGTATGCTTCTGTGAGCCGGAACCTGGT 12049  
Db 23528 CGAGTCGACACAGGGGACACATGCTGAAACCCGACACCTTCGCGCACGGTTAAATGGT 23469  
Qy 12050 ATGCCACCGGGGTACCGGCAGTAGACAGGCTGTGCGGAGACGTATTGCGCAAAAACGATG 12109  
Db 23468 ACGGCATGCGGTACGGAAGTCAATATCTTCTGCCACGAAATATTGCGAGGGGATC 23409  
Qy 12110 CCGCGCTTTTGGCCGATTTCCGACCCGCTTAC-----TGTCGGTTTCAGGAGAGGATG 12163  
Db 23408 AACAGGATTTTCCCATTTTACCCACGCTTTTACCGTTTATGACGAAATTCGGTGGT 23349  
Qy 12164 AGCAGACATATCTCCGACGACAGCAAGACATTTCTGGTTGACGAGCGCTTGAAGGCA 12223  
Db 23348 ATATGACGGTCAACCGGACGACAGGAATACTGTTTACATCGAGCTTAAAGGAC 23289  
Qy 12224 TCCTGCTGCGAGTGTATACGGTCCGATGGCAGCAGCAGCGCGATATCCCTTTACA 12283  
Db 23288 AAGCTTACGAGTGTATGGGATGATGATTTCTATCTGCGCGGTACGCTTATT 23229  
Qy 12284 GCGTACTGATCTCCCGCAGGTACGGCTAGTTGAGCGAATGGA-----GACTACCCGG 12340  
Db 23228 CAGTGGATGAATCCCGACCCCAAGTACGTTTGTACCGGTGATGGATATCGAGCGTGCCTG 23169  
Qy 12341 TGTGTGGCGATGGCGGAAAGCGTACGTCAGTCAGTTATTAAGCGGTACCAATGATC 12400  
Db 23168 CGGTACTGTTTCGGTGGCGAATCCCGCAATACCGATATGAACGGGTGCTACCGATC 23109  
Qy 12401 CTCATTCACACAGCAGCGGTACTCTCAGTGATGAATACGTTTCCCACTCGGTGAG 12460  
Db 23108 CACAGTGCAGCAAAAGATCGCTTAAATCTGATGCTGATGATTTCCGACGACAATC 23049  
Qy 12461 TCAGTGTCAATTTACAGACCGCTCGCTCGGCGCAATCCATATCCCGGCTCTTAC 12520  
Db 23048 TTGAGATGCTTATCGAGACGCTCCACGCTCAGTTCTCGCTTATCCGGATACCCCTGC 22989  
Qy 12521 CGCGCAGCTGTTTCGCCAACAGTTATGACGAGCAGCAGATATTAACGCTCGGGTGC 12580  
Db 22988 CCGAAACATTTTACACGAGGTTTGAAGCAGCAGATGTTCTCTGCTGAC-----AC 22932  
Qy 12581 AACAGAGAGTGACATCACTCTTGTTCATCTGTCTGAGGGGCATTTGTTGTTGGGTTGG 12640  
Db 22931 GCCAGGTTCTTCTTATCATCTGAATCATGATGATATACGTGATCACAGGGCTTA 22872  
Qy 12641 CGAGGGTTCGGGAGAGTATTTACGTACTCTGCGGCAAGCTGCGGAGGGGGTGC 12700  
Db 22871 TGGATACCTCACGAGTGACGACGATTTTATCAAGCCGATAAAGTCCCGACGCTGGAT 22812  
Qy 12701 TGACGCTGGAACACCTTGTGGCGCCGAAAGCTGCTCGGATAGTACAGTCTCGGTACGC 12760  
Db 22811 TTTCCCTTGAATGGTTTTCTGCCACAGGTGACAGGATTTGTTGTCCTGATGCCCGAG 22752  
Qy 12761 TGGCGGTTCAGCAGCAAGTCTGGTATCTGGATTTCAAGAGCTTGGCCACGCTCGCTGCTC 12820  
Db 22751 CCGATTTCTGGAC-----ATCAGCGTGTAGCATATACCGGTCCAGAGAACAAC 22701  
Qy 12821 CGGCACTCCCCCAAGGTAGCTTTTATCGAAACGGCGGTGCTGGATGAGGGTATGCTCA 12880  
Db 22700 CCGCTATTCCTCGCTGGTGACATACATTTGAAACCGCAGAGTTTGTATGAACGATCGTTGG 22641  
Qy 12881 GTTCACTGGCTGCTACATTTGTGGATGAACATCT-----CGAGCAAGCCGCTTACCG 12932  
Db 22640 CCGCTTTTGAAGAGGTGATGATGAGCAGAGCTGACAAACAGCTGAATGATCGCGGCT 22581  
Qy 12933 GCAATCCGATACCTTTTCCCTCGAGCGAGGGAAGCAGAACAGGCATTTGTGGACCCAGTG 12992

Db 22580 GGAATACGCAAAAGTCCCTTCAGTGAAAGA--CAGATTTCCATGCTCGGTGGGACA 22523  
QY 12993 TCAGGGATATGTTACCTATCCGGCGGAGAGCAATTTCTGGCTACCGGTATCCCTTTTCGGGA 13052  
Db 22522 AAAGGAATTTACAGAAATATCCGGTGCAGACGGATTTCTATCGGCCATTTGGTCAACGGGA 22463  
QY 13053 CAGTATGTTGACCGGCCCGGAGTTACCGTGCAGCGCTGACCGTACGATGCGTCAACGCA 13112  
Db 22462 AACCAAGCTTACAGGTAAACGACAGTCACGTGGGATAGCCATTACTGTGTTATACCCGC 22403  
QY 13113 GTGGCAGGATGCGCGAGGATTTGCACACAGCGGACTATGACTGGCGCTTCCTGACGCC 13172  
Db 22402 AACAGAGGATGCGCTGSCCTGCGTATGCAAGCGCATTAGCAATATCGATTTATGTTGC 22343  
QY 13173 CGTCCGGTGACGGAACCCCAATGATATTCGAGTCCGTCCTCACTCTCGATGCTCTGGCCG 13232  
Db 22342 GGAATACACACAGATGTCATGATACTATCACACGTCGACGCTTTGATGCACTGGGGAG 22283  
QY 13233 GGTGACCACTCGGATTTCTGGGGCAGGAGATGTTATGCCACCGTTACAGTATGC 13292  
Db 22282 GGTAAACAGCTTCCGTTCTGGGGGACTGAAACCGGTGAAACAGGATATACCCCTGC 22223  
QY 13293 CACGTTGTCCGATCCGAGCGCGCAGCGCTCTGGCGTTGACGGCGCCCTACCACT 13352  
Db 22222 -----GGAAATGAACTGTCCCTTTATTTGTCCCAACAGGT 22184  
QY 13353 AGCACAGTGTCTGGTATGTCACGACAGTTGGGAGATGACGAACAATGAGAAATGCC 13412  
Db 22183 GGAATGATGCTCTGGCATTGAAACCCGGTATACCTGTTGAGGGCTGATGTTTATGCCCG 22124  
QY 13413 CCGCAGTGGTCTGCTGCTACCGATCGCTATGACAGTATACCGGACAGAGTCCG 13472  
Db 22123 TCTGAGCTGATGGTTCAGGCCAGCTTTCTAATGATGGGAGCTTTATGGAGAGTGAA 22064  
QY 13473 CCAACAGGTGACATTCAGTACCGGTTTGGCGTGAGTTGCAATCGCAACCGCGAGCG 13532  
Db 22063 ACCGGTGGATCATCACTGAAGAT----- 22039  
QY 13533 CGAGGGAACGCTGGCAACGAGGACGCGACGCAAACTGGTGACGCCAGTGACGGATT 13592  
Db 22038 ----- 22039  
QY 13593 GCCGGTCACTGTAGCAACGAATTTCCGCTGGCGGTCAACGGAGCGGAGTATGACAA 13652  
Db 22038 -----GGTATCTCCTGTGCTGCTTTTCGCGCTGGCAACAAA 21998  
QY 13653 TAAAGTCTGCTGTTTCGGGTTTATCAGCGTATTTTCTGGACAGTTGGCAATATGTCAG 13712  
Db 21997 TAACCTGCGCTGCCATGCCAAGCAAGTCAATTCACAGAACCCATGTAATGAG 21938  
QY 13713 TGATGACAGTCCCGCAGCACTGTATGCGGACACGCACTTTTACATCCGACGCAACG 13772  
Db 21937 TGTGATCACGACCGCTATGATCCGATCCGAAACCAAACT----- 21896  
QY 13773 GGAATGGCAGTTTATACGGCAAAAGGTGAACGGCGACAGTCTGTATACCCCGTGT 13832  
Db 21895 -----ACGTCAAAAGCTTTACGTTTGTAGTGAAGTTT 21866  
QY 13833 TGTGGTCAGTGAAGACGAGAAATGATACCGTTGGGCTTAAACGACGCGATCTCTGACTGGGAAG 13892  
Db 21865 TG-----GGCGAACCTTACAAACGCCGTACGCCATGAAGTGGTG 21825  
QY 13893 GAGGGGGACGAGTATGATCGCTGCCCTGACAGCGCTGCCCTGTATGGAGACAAAG 13952  
Db 21824 AAGCTTGGGTACGTGATGATGAGTATGGAGCC----- 21796  
QY 13953 ATGAAATACATATCAGTTGCGCGGTTGTCTGACAGGTGTTATGTTTGGGGCTT 14012  
Db 21795 ATTGTGGCTGAAATCATGGCGGCTGAAACGGCGATGACAGATTTCCGTTGGGAGTT 21736  
QY 14013 TCCCATTTGGCGTTTACCCCTGCGTTTACCACGCGGACAGATCACTCAATGGCAACAAACCCAG 14072

Db 21735 TCCGAGCTACAGAAATATGACGGAAGGCAAGCCCTCGGTAAGTATCAAC----- 21684  
QY 14073 GCCGAACAGAAAGGCCCGATCGTTGGCCCTCTCGGACGAGAAACCCGGGAAAGAAAG 14132  
Db 21683 -----CGTATTTCTGAATAGTTGGCAGTAC-GTCAGTGTATGACAGTGCCTCCGAGG 21633  
QY 14133 TGGGACGACAAACGACAGACTGACATGAACAAGGTGGCTATACATCTGCTGAAGAAGACTG 14192  
Db 21632 ATATATATCCGATACCCATTACTATGATCCGTTGGGCGGTGAATATCAGGTATCACGG 21573  
QY 14193 GTGTCTGCGCGTACGCTGCCCTGATGCTCAAGCGCACTGGTCAGCGCTGACGACACAC 14252  
Db 21572 CCAAGCGCGGTTTCTGTCATCTTATTCACCTCCCTGGTTTGTGGTGAATGAAGATGAAA 21513  
QY 14253 GTTACACCCCTCAGCGGCAACTTTCAGTCTGTGAAACCCGCGCTTTTCCGAGTACC 14312  
Db 21512 ATGAC----- 21508  
QY 14313 GCTATCGGTACAGACGACCTCGGAGGCCAACCCGGGTTTTGTTGCCGNACTGTTCGCG 14372  
Db 21507 ----- 21508  
QY 14373 CGCGCTGACAGAGCGGAGAGCTGGCAGCGTATGCTGACAGGACAGAGTGAATGG 14432  
Db 21507 -----ACTGCCGTGAATGACAGCAT-----AAGCT 21480  
QY 14433 CAGGCTTGGGGCGGCGCTATCAGCGGCTACGCGAAGAGAGAAATAAAGCGGATTTA 14492  
Db 21479 CAGTATGCTGCTTCACTGAACAGACATCACTCCATTTAGGAATGAA----- 21433  
QY 14493 GCCGTTAAGAAAGTGACGCTGTTTCCGATTAATAATTAACAGGAGATCACTAGCA 14552  
Db 21432 -----TCATGAAGA 21424  
QY 14553 CATCTTTGTCAGTAGCACCCCGTGGTCTGCAACACCGCGCTGTTGGTGC 14612  
Db 21423 ATTTGTTCAACAGCAATACGCCATCCGTACCGTACTGACAAACCGTGTGACAGTAC 21364  
QY 14613 GGGAGCTGCACTATACCGCCATTCGCGATACACCGAGAGAGACGCGAGCGTATCACCT 14672  
Db 21363 GCGAAATAGCTGCTGATCGGACCCCGATACACCTCAGGTAACCGATGAACGATCACCG 21304  
QY 14673 GCCATCAGACCATGAGCGCGCAGCTGTCTCAAAAGCCCGACCGGCTTACGCGG 14732  
Db 21303 GTTATCATATGATGCTCAAGGATCTCTGACTCAGAGTATGATCCGCAATTTATGAAC 21244  
QY 14733 CCGGTCTGACA-----AATTTACGTACCTGAATAGCC 14765  
Db 21243 GCCAGCAGACAGAGTGACAAGACGCCATTACACCCAATCTTATCTTGTGTCATCAC 21184  
QY 14766 TGACCGGACAGTACTGCAAGCGGTACGCGCGATGCGGTACGTGCTGGAACTGAGCG 14825  
Db 21183 TCAGTAAGAAGGCAATTTGGCTACGCAAGTGTGGATCGCGAAACCGGTGTCGCTGCATG 21124  
QY 14826 ATGCGCGCGGCGGCGTTCCTGCGCTCACCGGCGCTGGGACGGAAGCGGCTCACCC 14885  
Db 21123 ATGTTCCGCGGCTCCCGTTTGTAGCTGTCAGCGCAATGG-----CGTTAGCC 21076  
QY 14886 GCACCTGGCAATATGAAGACGATACCTCGCGGCGCGCGCTGAGCATCACCGAGCAGG 14945  
Db 21075 GAACTTTTCACTATGAAGTGAATACCTTCGCGGACGATGCTAACGATTAACGAGCAGG 21016  
QY 14946 TTACCGGTGAAGCGGCCCAATTAACGAAACGCTTCTGTCGTCGCTGGCAATACGATGCGG 15005  
Db 21015 TAAAGGAGAGAACGCTGTATCAAGGAGCATGATCTGCTGTCAGGAATACGCGCGCAG 20956  
QY 15006 AGAAGATTTCTCAATCTGCTGCGAGTGTGTCAGTCACTTACCATACCGCGGACTGCTGC 15065  
Db 20955 AAAAGGCAATATCTGCGCGGCGAGTGGTGGTTCATTTATGATCCACCGGAATGAATC 20896  
QY 15066 AGACGACAGCATCGCCCTGAGCGGCTGCCCTCGCGCTACGCGGAGATTTGCTGCCCG 15125  
Db 20895 AAACCAACAGCATATCGTTAAACAGCATACCCCTTGTTCATCACACAGCAATTTACTGAAG 20836







Db	10978	TACGTCATAATCCCGCGGTATATCGTTAAACGAGAAATCGCCCTCGATCTGGAAC	11037
Qy	7481	GTCCGTCCGTGGAGGAGACACGGCTGGAACGACTCGCGCTGACTCCATTGACCC	7540
Db	11038	TGCCGCGCGTGGAAAG--ACACTCCTGGAATGCCAATCCGTGGATGCCATTGATCCG	11095
Qy	7541	GATGCAATAGCCAGTAGACCCCATCAATTAACAAGGTCCCACTTTATGTGTAACCTC	7600
Db	11096	GATGCCGTGCACATATGACCCGACACACTATAAGTTGCCACCTTTATGCGCCTGTTG	11155
Qy	7601	GACCTGCTGATGCCCGCGGTGATGCGCCTACCGGTGCTCGAGCGGACACCCCTTAAC	7660
Db	11156	GATCAACTTATCTGCGCGCGATATGGCTATTCGGAACTGACCCCGATGGTTGAAT	11215
Qy	7661	GAGCCCGGATGTGATGCTCAGGCTTGAACCTTCTGCGGACAGAGCCCTATATTTCC	7720
Db	11216	GAAGCCAAAGATGTGATGTGCGGTGTTTGGAAATGCTGGGTGATGAGCGGAGGATTAC	11275
Qy	7721	TTTGAGCCGACTGGTCCGGGTTGACCTCGGTGAGCAGCCAGCGAGGTGACGCGACGC	7780
Db	11276	GGCAGCAACAGTGGGCGGACCGTCTCTTTTCGTGGCGGGAACACACTGTGCAAGCG	11335
Qy	7781	GATTACAGAGGCCCTGTGTCGCGGTGCGCGGTGCTGTCGCCCTCCCGAGACACGAGCG	7840
Db	11336	GGCTATCAACAGACCTTACCGCGCTAGACAAACGAGAGGTTGCACTCAACCCCGCAAC	11395
Qy	7841	GCGAATTCCTGAGGCACTGTTCTCCCGCAGCAGAACGAGTGTCAAAGCTACTGG	7900
Db	11396	GCTAACTCGTGTGTGG--TTTGGTCTGCGCGAATAAACCAGGAATCAACCGATTACTGG	11454
Qy	7901	CAAACTTGGCACAACGGGCTCCATACTTCGCGCAACAACTCTCAATTGACGCCAGCCG	7960
Db	11455	CAAAACC--TGGGTTTGGCCTTGGTTAACTTCGCGCAATACTCTTCCA--TGACGGGCAACCG	11512
Qy	7961	CTTTCCCTGTCCTTAACGCCACGCGGTCCGAACCGTCCGCTCCGCTGCAGAGTGCCGTCGT	8020
Db	11513	TTATCGTGGCAATTAACGGAGCC--TACGATCCGAAAGCGTGTCTCACCATATGGTA	11570
Qy	8021	AACAGCGCAGAGGTGCTGCAGCACTGCCGCGCGGTGATGCGGTTTACAGTTTCCCG	8080
Db	11571	CAGCCTTCTCAGGCGGTGATGCAGTGTCTGCCCGCACATGTGCTTATACCGCTTCCCG	11630
Qy	8081	GTCAATGTCGAGAAACGCCCGGGGATGTGAGCGCTGCTGACCGGGTTGGCAACACACTG	8140
Db	11631	GTGATGCTGAGCGGCGCCCAATCTGGTAGCCCAATTAACCACTTCCGCACTCTCTG	11690
Qy	8141	CTCGGTATTAACGAGCGTCAAGATGCGGAGCGCTGGCCAAATCTGTGCAGACCCAGGCG	8200
Db	11691	CTCAGTATGCGAGCATGATGATGCGGATGAATCAACACGTTGCTACTACAGCAGGCT	11750
Qy	8201	AGTGAACTGATACCCAGGCGCTTCCGACAGGATAACGTCCTCGAGGAAATCGATGCG	8260
Db	11751	ATGGAATGGCGACACAGAGCATCCGTATTCAGCAACGAACTGCTCGATGAAGTGGATGCT	11810
Qy	8261	GATATTGCCCGCTTGAGGAGAGCGCGCGCGCGCGCAGATGCGTTTGAACGTTACAA	8320
Db	11811	GATATTGCTGATTTGCGAGAGCGCGCGCAGTGCGCAAAATCGTCTGGAANAATACCAG	11870
Qy	8321	GTGTTGTACAGCGCGGACGTCACACCGCGCAAAAACAGCCCATGCACTTTGTAACCTCAGT	8380
Db	11871	CAGCTGTATGACGAGGATATCAACACCGAGAACAGCGTGGATGTCACTGTTTGATGCG	11930
Qy	8381	TCGTCCGTGCTGCGGCATCAACCGCGCGCTCTTTTGGCCGAGGCGCGCGGATATG	8440
Db	11931	CGCGAGGTGAGTCTTGGCCGGGCGGCGCTCTCAGTAGCAAGGGTGGCTGACTTA	11990
Qy	8441	CTGCCCAATATTACCGGCTGGCGGTCCCGGCTATCGGCGCACTTAITTAAGGCC	8500
Db	11991	GTTTCAAAACGTGTTCGTTTCGTTTGTGGCGGCGAGTGTGGGGGCGACACTCGCGTCT	12050
Qy	8501	ACGCCATCGGCATCCAGGTGCTCTCGATGCGCACCGGCATATCAGCGGACAAAATCAGC	8560
Db	12051	TCCGCTCCGTGATGTGCTTTCTGCGCAGAGCTTCCCAATATTTCCGACAGCAAAATCAGC	12110
Qy	8561	CAGTCGGAAGTGTACCGCGGTGCGCGGAGGAGTGGAAATCCAGCGTGATAGTCGCGCAG	8620
Db	12111	CGTTGGAAAGCCTACCGCGCGCGCGTCAAGAGTGGGAAATTCAGCGTGATATATGCTGAC	12170
Qy	8621	TCTGAGCTGGCGCAGATTGATGCCAGCTGGCGGCATGGCAGTGGCGGAAGGGCT	8680
Db	12171	GGTGAAGTCAAAACAATGATGCCAGCTGGAAAGCTGAAATACGCGCGAGCAGCA	12230
Qy	8681	GAGCTGCAGAAAACCTTACCTTGAGACCCAGCAGACCCAGGCAACGCGCATTTGGCATTC	8740
Db	12231	CAGATGCAGGTGGAATATCAGGAGACCCAGCAGGCCCTACTCAGGCTCAGTTAGAGCTG	12290
Qy	8741	CTGCAGAGTAAGTTCAACAATACGGCTCTGTACAGCTGCTGCGGGCAGGTTGTCCGCC	8800
Db	12291	TTACAGCGTAAATTCAAAACAAGCGCTTTACGTTGATGCGCGCAAGCTGATGCT	12350
Qy	8801	ATTATTACAGTTCTATGACCTGGCAGTATCCCGCTGCTCTGATGSCGCAACAGGCTCTG	8860
Db	12351	ATCTATTACAGTTCTTTGACCTGACCCAGTCTTCTGCTGATGGCACAGGAAGCGCTG	12410
Qy	8861	CAGTGGGATAAATTCGAGA--CTAGGTGCTTTATCCAGCCGCGGCGCTTGGATGGGGCA	8917
Db	12411	CGCGCGAGCTGACCGACAAACGCTGTACCTTTATCCGGGCTGGGCTTGGAAACGCTACG	12470
Qy	8918	AATGCGGCTCTGCTGGCGGGGAAACCTGATGCTGTAATCTGGCGCAGATGGAGCAGGCC	8977
Db	12471	ACTGCGGGTTTATGCGGGTGAACGTTGCTGCTGTAATCTGGCAGAAATGGAAGATC	12530
Qy	8978	TGGCTGACGCGGGGATGAGCGGCAATAGAGGTGAGCGGACGCTTGCCTGTCGAGGTC	9037
Db	12531	TGGCTGGAGCTGATGAGCGGCACTGGAAGTGACCCGTACCGTCTGTTGGCACAGTTTC	12590
Qy	9038	TATACAGCCTCGCGAGGATCGGCAATCTCTGCGCCGACAAGGTGTGGAACCTGCTG	9097
Db	12591	TATCAGGCTTATCATCAGACAAC--TTTAATCTGACCGAATACTCACGAAATTCCTG	12647
Qy	9098	AGTAACGTTCCGGGAGTCCGGTACGAAACGAAACGAACTACAGTGGATCAACAGCAA	9157
Db	12648	CGTGAAGGAAAGGCAACGTAGAGCTTCCGGCAATGAATTAATACTCAGTACCGCCAG	12707
Qy	9158	CTCAGGCGCACCTCTGAACTGCTGACCTCGGTATCGGCAACGATTTACCCGCTCTCCCTT	9217
Db	12708	ATAGAAGCTCTAGTCGATGTTGTTGAAATTTTTCAGCGATACCCCGGAAAGCTTT	12767
Qy	9218	GGCACCATGAGCGGATCAAAACAATAAGCGTACGCTCCCGCGCTGTGTCGGCCCTAT	9277
Db	12768	GGCAATACCCGTCAGTTGAAACAAGTGTGTACCTTCCCGCGCTGTTGTTGCTCGTAT	12827
Qy	9278	CAGGACGTCGTCGCTTCTCAGCTACGCGGAGTATGTTGTCATGCCCCGGGTTGCAGC	9337
Db	12828	GAAATATCCGGGCGTGTGAATACGCGCGAGCATGTCATGCGCGGTTGCAGT	12887
Qy	9338	GCGCTGGCGGTCTCACCGAATGAACACAGCGGCAATTCCTCACTGATTTCAATGAC	9397
Db	12888	GCTATTGCTCTCTCCACCGCGTGAATGACAGTGGTCAATTTATGCTGATTTCAACGAT	12947
Qy	9398	CGCGTTTACTCGCTTTGAAGCACTTCCAGTTGATGACACAGGGAACCTGACACTGAGC	9457
Db	12948	TCCCGTTATCTCGCTTTGAAGGTATTTCCGTGAATGAACGCGTAGCCTGACGTTGAGT	13007
Qy	9458	TTCCCGGATGCTGAGCGCAACAAACAGCGGATGCTCTCAGTCTGAGCGACATCATCTG	9517
Db	13008	TTCCCGGATGCGAGTATCGACAGAAAGCGCTGCTGGAGAGCTGAGCGATATCATCTG	13067
Qy	9518	CATATCCGTTACACCATTTACGCTGATAGGTATCAACATAGCGAGGCCCCCGAACGAG	9577
Db	13068	CATATCCGCTATACCATTCGTTCTTAAATTAACAATTTGATAGCAGGCTCCTGAGG-G	13126
Qy	9578	GGCTGCGAGGAGACTGAGCATGCAAAATCATCAAGACATGGCCATTACTGCCCCCAGCT	9637
Db	13127	AGCCTGTTTAAGAGGTTTATATGCGGGTTCAACACCTTTTGAACCTTGAATACCGCTCAT	13186

Qy	9638	TGCTTCCGGGGCGGTGCGGTCA	CGGGCTCAAGGGTGATATCGCGGGAGGCGCGG	9697
Db	13187	TGCCCCCTCTGGGGCGGATCACTAAAGAGAAATGGGAGAACACTCAATGCCGTTCGGAGCGG	13246	
Qy	9698	ATGGTCGGCGACCCCTGAGTATTTCCTTCGCCGTTAGCCCCGGTGGGGTTACGCCCCCA	9757	
Db	13247	AAGG-GGAGGGTCATTTTCACTGCCCCCTGCCGATCTGTCTCGGGCGTGGTCTGTGTGCGG	13305	
Qy	9758	CTGGGCACTTAATTATCACAGCCGGTCGGGGAACGGCCCCCTTTTGGCAATTGGCTGGGGTA	9817	
Db	13306	TGCTATCACTGAATTAACAGCAGTACTGCTGGCAATGGGTCAATTCGGGATGGGTGGCAAT	13365	
Qy	9818	TCGGCGGTGCTGCTGTCTAGCGTGTGTAACGGCAACGGAGACCTTACCTACGATGATCTG	9877	
Db	13366	GTGGGGTTGGTTTATACAGCTCGGTACCGCACCGCAAGGGGTTCCGCACTATACGGGACAAG	13425	
Qy	9878	ATGAATTCACCGTCCGGACGGTAGGTGCTGGTCCGGCACTCACGCTCTCGCACCC	9937	
Db	13426	ATGAGTATCTCGGGCCGGATGGGGAAGTGTGAGTATTGTGCCGGACAGCAAGGGCAAC	13485	
Qy	9938	AAGAAGCACGGCAGGCACTCACTACTGGGATAAACCCAGGCGGAAGCTTCAACGTTTC	9997	
Db	13486	CAGAGCAACGCACCGCAACTCACTGTTGGGACGGTTCAGACAGCGGCTACTGTTA	13545	
Qy	9998	AGGTTTACGGTTCACGTACGGAGGGTAGTCTCAGCGCGCTTGAGCGTTGGCTGCCGCCG	10057	
Db	13546	CCCGCTATCAGTCCCCGCTGGCAGAAAAAATCGTTCGTTAGAACACTGGCAGCACAGC	13605	
Qy	10058	A-----CGAGACAGAAACGGAAATTTTGGGTGTTATATACCCTTGACCGACAGTGGCTC	10111	
Db	13606	AGAGCGTAGGGAAGAGACGTCTTTTGGGTACTTTTACTCGCGGATGGTTTAGTGACCC	13665	
Qy	10112	TGCTGGCGCCAAATGGCAGGCTCGCATCAGCAACCCACAGCCCAACACAGACGGCGG	10171	
Db	13666	TATTCGGTAGCANCATCATGACAGTATGCTGACCCGAGATGAACACAGATTTGCC	13725	
Qy	10172	TTTGGCTGATGGAGTCCCTCGGTATCACTTACCGCGGAACAGATGATTACCAATACCCTG	10231	
Db	13726	GCTGGCTGATGGAGGAACCGTCAGCATACCGGGGAACATATTTACTATCACTATCGG	13785	
Qy	10232	CGGAAGATGATGAGTCTGTGACGAGGCGGAGCGGACGCGCACCGCAGCGCGCGCGCC	10291	
Db	13786	CAGAACACATCTTGACTGTGATGACATGAACCTTGCTCAGCATTCAGGTGTTACGCCCC	13845	
Qy	10292	AAGCTTATCCGGTGGCGGTCTGGTATGTTAAACCGTCAGCGCGCTCGGACGCTACCGGCGC	10351	
Db	13846	ACGGTTATCCGT-GCAAGTCCACTATGGCANACTACGCGGGAACCGCTTTTTCGCGG	13904	
Qy	10352	TGCTGTGCAACCATCAATGGATA---GCTGGCTGTTTATCCTGGTGTGTTGATTATGGTG	10408	
Db	13905	TAAATCAGGTATCCCTGTTGATTAATGACTGTGTTGTTTTCATCTGGTATTTGATTACGGTG	13964	
Qy	10409	AGCGTAGCTCGGTGC-----TGCTGGAAGCCGCGCTGGC	10444	
Db	13965	AGCGCTTATCTTGCTGTAACCTCCGTACCCGAATTCAAATGTGTCAGAAACAAATGTGCTG	14024	
Qy	10445	AAACACAGGAAGTGGGGAGTGGCTGTGTCGTCAGATTGTTTTTTCGGGTATCAGTTTG	10504	
Db	14025	AAACAAATGTCTGAAATAATGGCGTTGTCGTCGAGCAGTTTTCTCCGCTATGAATATG	14084	
Qy	10505	GTTTTAACTTCGGAATCCCGTCTGTCGCAAGTTCGATGTTTTCATCAGCTGAAG	14144	
Db	14085	GGTTTGAATTCGAACCCCGTCTGTTGTCGCAAGTTCGATGTTTTCATCAGCTGAAG	14144	
Qy	10565	TTCTGGCGGGAGTTCGGAGCGAATGATGCGCCAGCATTTGATTTCTCGCTGTGCTGG	10624	
Db	14145	CGCTGGCAGGGGAAAAAGGTTGCAAGAGAAACACCGCGCGTGGTTTCCCGTCTTATTTCTGG	14204	
Qy	10625	ACTACAGGGAAGTCTCTCACTCAGTCTGCTCGAGAACGTGCACAGGTGCTTATAGT	10684	
Db	14205	ATTATGACCTGAACAAACAGGTTTCCTTGCTGCAACCGCCCGCAGACTGGCCCATGAA	14264	
Qy	10685	CGACCGGACGCTCTTGCTGCTTCCCGGCACTGGCAATGGGGTGGCAACCTTTTACCCCGC	10744	

14265	CGGACGGTACGCCAGTGATGATGTCCCCGCTGGAAATGGAATTATCAACGTGTAAATCATG	14324
10745	CGACATTTGCGCATGGCAGACGCGTGACGATATGGCGAAGTTAGTTGCTTCTCAACCCCT	10804
14325	GGTGAATCTGAACCTGGCAGTCCATGCCCGAGTTAGAAAATAAGAACGCTTGACGCCAT	14384
10805	ATCAGCTTTGTAGACCTTTAACCGCGAAGGTGTGTGGGTATC-CTGTATCAGGACA---GC	10860
14385	ACCAATTGGTTGATTTATATGAGAAGGAATTTCCGCGCTTACTTTATCAGGATACTCAG	14444
10861	GGTGGCTGGTGTAACGGTGAACCGGTACGCCA---GTCGGGGGATGATCCGGATGCTGTG	10917
14445	AAAGCCTGGTGTAACGGTCTCCGGTACGGGATATCACTGCCAAGGAACGAATGCGGTT	14504
10918	ACCTGGGGGGCGCTGCGGCCCTGCCGACAATGCCCGCTTTGATACACAGCGGCATCCTG	10977
14505	ACCTATGAGGAGCGGAACCACTGCCACATATTTCCGGCAACAACAGAAAGCGGATGTTG	14564
10978	GCGGATCTTAATGGGGATGGTCCGGTGGAGTGGGTCTTACCGCCCCCGGTGTGGCGGGG	11037
14565	TTGGACATCAATGGTGAACGGGCGTCTGGATTTGGGTGATTAACGCAATCAGGTTACGGGGC	14624
11038	ATGTAATGATCGACCCCGCGCGACACTGGTTGCAATTCACCCCTGTACAGCTTGTGCC	11097
14625	TACCACACCATGTACACCGAAGTGAATGACACACCCCTTTATTCATTCACCGTGTGCCA	14684
11098	GTAGTAATGCGCATCCAAAGACAGTGTCTCGCGATATCCTGGGGCTGGGTTAACCGAC	11157
14685	ATGGAATATTTCCATCCGACGCAAAACATGGTGTGATTAATGATGGGCTGGGCTGCCTGAC	14744
11158	ATGGTCTTATCGGGCCGGCAGTGTTCGCCCTCTATTCCGGCAAAACAGATGGTTGGAAT	11217
14745	TTAGCGCTTATCGGCGCAATAGTGTACGTGCTGTGTCAATTAATCCGGCAGATGGGAT	14804
11218	AAAGGGGAGACGTCGACGAAAACGGAAGACACTCACTCTCCGCTCCCGGGGGTTGACCCA	11277
14805	CGCGCTCAGGATGTTATTCAATTTGCAATAAGCCACTCGCGTTCCTCCGCAAAAATAAG	14864
11278	CGTACCCCTCGTGGCGTTTCACTGATATAGCTGGCAGTGGACAGCAGACATTTGACGGAGTG	11337
14865	CGTCATCTGTGCGCAATCAGTGTATGACAGGCTCCGGGCAATCAATCTCTGGTGGAAATT	14924
11338	CGTGTAAATGGAGTACGTTACTTGGCCAAACCTTGGGACAGCTCGTTCGTTCCGTCAGCCGGTG	11397
14925	ACGGCAATAGCGTCGCTACTTGGCGGAACCTTGGGCAATGGAATAATTTGGTGAACCTCTG	14984
11398	AATATTCGCGTTTTAGCCAGTCAGTGACTACGTTTAACTTAACTTAACTTAACTTAACTTAACTT	11457
14985	ATGATAACAGG-CTTCCAAATTTACGGGAAACGTTTTAACTTAACTTAACTTAACTTAACTTAACTT	15043
11458	GATACCGAGGTTCCGGTACCA-CGGACCTGATTTATGCGATGAGTGACCGGTTAGTTCAT	11516
15044	GACCTAAATGGCTCAGGCACCAACCGGATTTTATTTATGCGCGCAATTACTTAACTTAACTTAACTT	15103
11517	TTATTTCAACAGAGTGGTAAATTTATTTCCGCGAGCGCATACGCTGCTCTTTCGCGAAGG	11576
15104	CTATGCCAATGAAACGGCAATCATTTCTGCTGAACCTCAGCGTATTTGATCTGCGGATGG	15163
11577	TGTGCGCTATGATGCACCTGCACTGCAAGTGGCGGATATCCAGGGGCTGGGGGTGCC	11636
15164	GGTACGTTTTGATGATCTTTGTCGGTTACAAATAGCGGATACACAAGGATTTAGGGACTGC	15223
11637	TAGCCTGTTACTGACGGTCCCCCATGTCCGCGCTCATCACTGGGTGTGCCATTTATCGGC	11696
15224	CAGCATTTATTTGACGATCCCCCATATGAAGGTGCAGCACTTGGCGGATTTGGATATGACCAT	15283
11697	AGACAAAACCTGGTTTGAATGGCATGAACAACAATATGGGGGCGCGCATCAGCTGCA	11756
15284	ATTTAAGCCTTGGCTGCTGAATGCCGTCAATTAACAATATTTGGGAACAAGAACCAACGCTGTA	15343
11757	CTATCGCATGTCGGTGCAGTTCTCGGTGCGATGAGAAAGCCGAGGCACCTGCGCGCAGGCAG	11816



QY	13953	ATGAAATACACTATCAGGTTGGCGGTTGTCTGTCAGAGGTGTATGGTTTGGGGGCTT	14012	Db	18171	AAAAAGCAATAATTTTGGCGGCGAGTGGTTCATATGATCCACCGGAATGAATC	18230
Db	17331	ATCAAGCGCC-----	17341	QY	15066	AGACGACAGCATCGCCCTGAGCGGCGTCCGCTCGCGTCAGCGGCGAGTTCCTGCCCG	15125
QY	14013	TCCCATTTGGCGTTACACCGTCGGTTACACCGGSCAGATACTCAATGGCAACAACGCCAG	14072	Db	18231	AAACCAACAGCATATTTGTTAAACAGCATACCTTTGTCCATCACACAGCAATTAGTGAAG	18290
Db	17342	-----CCTGAAACGGGGATTACAATTTCCCGTTGGGCAATTTCCCGGACG--T	17389	QY	15126	ACGCGCGGGGGCCAACTGGATGGGTGAGGATGCCTCGGCGTGGAAATGACTCTCTGGATG	15185
QY	14073	GCCGAACAGGAAGGCGGATGCGTTGGCCCTCTCTGCGCAGAGAAACCCGGGAAGAAAG	14132	Db	18291	ATGACAGCGAAGCCGATTGGCAGGTTATGGAATTTGGCTGGAATAACCGCTGGCGC	18350
Db	17390	ACAGATATTAAACGGGAAGGCAAGCCCTCGGTTACGTTTCAA-----	17435	QY	15186	GGGAGACGTTTTCACCCAGAACCCACGCTGATGCGACCGGCGCGCTCTGAGCATCACCG	15245
QY	14133	TGGAGCAGCAACGACAGACTGACATGAACAAGTGGCTATACATGCTGAAGAAGACTG	14192	Db	18351	CGAAAGCTTCACTTCTGTGACACCAACGATGCTACCGGACGATTAATTAACAGTACAG	18410
Db	17436	-----ACCGTATTCTCGAAATAATTTGGGCAACTGTCAAGTTGACCAAAAAAT	17485	QY	15246	ATGCAAAAGGTAATCTGACGCGTGTGGCATATGATGCTGGCTGGCTGCTATCGGCGAGTT	15305
QY	14193	GCTGCTGCGGTGACGCTGCGCTGATGCTCAGCGCACTGGTCAGCGCTGCAGCACACC	14252	Db	18411	ATGCTCCGGAACAAGCAACGATATCGCTATGATGTGCGCGTCTGCTTCAAGGCGAGTT	18470
Db	17486	GCCGGCAGGATATGTAATGCCGATACCCATTACTATGATCCGTTGGGGCGTGAAATCAG	17545	QY	15306	GGTTGACGCTGAAGGACGGCACCGGACAGGTATCTGTGGCCTCCCTGACGTACTCGGCCG	15365
QY	14253	GTTACCAACCTCCAGCGGCAACTTGGCCAGTCGTGAACCCGCGCGCTTTCCGCGAGTACC	14312	Db	18471	GGTTGGCGCTGAAGGGGAACAAGAACAGTTATCTGGAATCCCTGACCTATTCGGCTG	18530
Db	17546	GTTATCAGCCCAAGGCGGTTGGTCGATCCTTATTCACCTCCCTGTT-----	17594	QY	15366	CCGGGAAAAAGTTGCTGTAAGAACACGCAACGGCGTGTGTAACCTCGTATATTTACGAGC	15425
QY	14313	GCTATCGGTACAGAGACCTCGGAGGCCAACCCGCGGTTTTGTTGTCGGAACGTTCCGC	14372	Db	18531	CCAGCGAAGCTTACCGGAGGAACATGTTAAACGGGATAGTACTACATATACCTATGAAC	18590
Db	17595	-----	17594	QY	15426	CGGAACACAGCGCTGACGGGGATTAAACCGAAGCTCGCTGCGGACAGTTGCCGGAG	15485
QY	14373	CGCGCTACAGAGACGGGAGAGCTGGCAGCGTATGCTACAGGACCAGATGAATGG	14432	Db	18591	CGGAGACGCAACAGGTTATTGGCATAAACAGAACGTCCTTCCGCTCATGCCGCTGGGG	18650
Db	17595	-----TGTTGGTAATGAAGTTGAAATGACACTCCCGG-----	17627	QY	15486	CAAAAGTGTGACGAGACCTGCGCTATACGTATGACCCGCTGAGCAACGTTACTCAGCGTCA	15545
QY	14433	CAGCGCTCGGGCGCGCTATCAGCGGCTACGCACGAACAGAAAAATAAGCGATTTA	14492	Db	18651	AGAAATTTTACAAACCTTGGTTATGAATATGATCTGTGCGAATATGCTCGAATCAA	18710
Db	17628	--TGAATGACAGCATAAAGCTCAGTGATGCTGTTACTGAAACAGATCACTCCATTTA	17685	QY	15546	ATAACGATCGGAAGAGACCCGCTTCTGCGCTAACACAGAAAGTGTACCGGAATACTCGT	15605
QY	14493	GCGGTTAAGAAAGTGACGGTGTGTTGCGGATTAATTAATTAACAGGAGATCAATGAGCA	14552	Db	18711	CTAATGATGCTGAAATTAACCGCTTTTGGCGCAACCCAGAAAAATTGTACCGAAAACTTT	18770
Db	17686	GGAATGAA-----TCATGAAGA	17702	QY	15606	ACATCTACGACGCTGTACCAAGCTGGTCAGCGCCACAGGGCGTGAGATGGCCAAATGCCG	15665
QY	14553	CATCCTTGTTCACTAGCACCCGCTCGGTGCGGTGCTCGAACACCGGCGCTGTTGGTGC	14612	Db	18771	ACACCTATGACAGCTGTACCAAGCTGGTTTCCGTCCTCTCGGCGTGAATGGCGAATATTG	18830
Db	17703	ATTTCGTTTACAGCAATACCCCATCCGTCACCGTACTTGGCAACCCGTGTCACACAGTAC	17762	QY	15666	GCCAGCAGGCAACACTTACCATCGCTACAGCCCGCTTCTCTACAGACAGCTCTGCGCT	15725
QY	14613	GGGAGCTGCACTACTACCGCCATCCGATACACCGGAGGAGACGGACGCGGTATCACCT	14672	Db	18831	GCGGCAAAAAAACCAAGTTAC-----CATCCCCCTCTGATTTGATTAACAATCTT	18881
Db	17763	GCGAATAGCTGGTATCGGCAACCCGATACACTCAGGTAAACGATGAACGATCACCG	17822	QY	15726	ACACCAATTACCGGCACTACCGTTATGACCGTGTGGCAACCTGACGAGATCGGCC	15785
QY	14673	GCCATCAGCAGATGACGCGGAGCTTGTCAAAAGCGCCGACCCGCGTTTACAGCGG	14732	Db	18882	ATACGAATTACTCTCGCACTTACGACTATGATCGTGGGGAATCTGACCAGAAATCGCATA	18941
Db	17823	GTTATCAATATGATGCTCAAGGATCTCTGACTCAGAGTATTTGATCCGCGATTTTATGAAC	17882	QY	15786	ACAGTCCCTCGCCAGCAACAATTAATATACGACAGATACAGGTTAGTACCGGAGCA	15845
QY	14733	CCGGTCTGACA-----AATTCAGTACTGAAATAGCC	14765	Db	18942	A-----TTCCAGATCACCGGTAATACTATAACAAGAACATGACCGTTTCAGATCACAGCA	18997
Db	17883	GCCAGCAGACAGCGAGTGACAAGAAGCCATTACCCCAATCTATTCTCTGTCATCAC	17942	QY	15846	ATAGGCGGTACTGACAGCTTGGCGGAAGTGCCTGACAGTGTGATATGCTGTCAGTG	15905
QY	14766	TGACGGGACAGTACTGACAGGCTCAGCGCCATGCGGTACGTCTGCGTGAATCAGG	14825	Db	18998	ACGGGCTGTACTGGAAGAGCTGGCCCAAGATCCCACTCAGGTGGATATGTTGTTTACCC	19057
Db	17943	TCAGTAAGAAGGCAATTGCGTACGAAGTGTGATGCCGGAACCCGTGTGCGCCCTGATG	18002	QY	15906	CAGGAGGTCAACAGAAAGCACTCGCAGCGGGGCAAGCACTGTGTGTGGAGCCCACTGCGGAG	15965
QY	14826	ATCGCGCGGGCGGCTTTCTGGCCGTCAACCGGGGTGGGACGGAAGACCGGTCACCC	14885	Db	19058	CCGGGGGCGCATCAGACCCCGCTTGTTCGCGGTGAGGATCTTTTCTGACACCCCGGTGACG	19117
Db	18003	ATGTTGCGGGCGTCCGTTTATGCTGTGACGCCAATGG-----CGTTAGCC	18050	QY	15966	AACTGAAAAGGTGACACCGGTGGTGGTGGGGGGGCGGACGACGAGGAAAGCTATC	16025
QY	14886	GCACTGGCAATATGAAGAGCATACCTCGCGGGCGCGCTGAGCATCACCGAGG	14945	Db	19118	AAATGCAACAAGTGAATTTGGTCAATAGGGAATAACGACGCGCTGATCAGGAATTTTACC	19177
Db	18051	GAACGTTTCAATGATGAAGTGATAACCTTCGGGACGATTTGCTTAACGATTTACCGAGCAG	18110	QY	16026	GGTATGATCGGCGAGTCAGCGTATTATCAAAACCGGACGCGGCAAACTGGCAACAACG	16085
QY	14946	TTACCGGTGAAGCGCCCAATTAACGGAACGCTTCGTGACGTGCGCAATACGGATGCCG	15005	Db	19178	GTTATGATCAGACAGTACGCGTGTCAATTAAGACTCATATTTCAGAAAGACGGTAAACAGTG	19237
Db	18111	TAAAGAGAGAACCCCTGTATCAGGAGCGATTTGATTTGGTCAGGAATACCGCGGAG	18170	QY	16086	TTCAGACACAGCGGGTGTGTACCTCGCGGGGTGGAGTTACGTATCATGCGCAAAATGGCG	16145
QY	15006	AGAAGATTCTCAATCTGGCTGGCCAGTGTGTGTCAGTCAATTACGATACCGCGGACTGGTGC	15065				

Db 19238 AGCAATACAGCGAACAATTATATTTCCAGAGCTGGATGCGCACGACATATAGCGGCA 19297  
Qy 16146 TGACGGAAAAGAAAGCTGCAGGTTATACGGTGGCGAGGCTGGCGGGGCAAGTGC 16205  
Db 19298 ATACATTAAGAGAGTTTTCAGGTCATCACTGCGTGAAGCGGTGACGCAAGTGC 19357  
Qy 16206 GCGTATTGCACTGGGAGATCGGAAGCGGATGACCTCGATGAGGACTCGGTGCTTACA 16265  
Db 19358 GGGTGTGCAATTGGGAAACAGGCAACCGCGGATATCAGCAATGATCAGTGGCTTACA 19417  
Qy 16266 GTTACGATAACCTGGTGGGAGCAGCAGCTGGAGCT-GGACAGAGAGGTTTACCTTATC 16324  
Db 19418 GTTATGGCAACCTGATTGGCAGTAGCGGGCTGGAATTGGGACAGTCAAGCGGACAGATCAT 19477  
Qy 16325 AGTGAGGAGAGTTCTACCGTATGGCGGAACGGCTGTCTGACGGCGGGAAGTGAAGTT 16384  
Db 19478 AGTCAGGAAGAATTTACCCCTATGGGGGAACCGCCG-TGTGGGCAACCCGAAATCAGTCA 19536  
Qy 16385 GAGGCTGACTACAAAATATCCGATCTCAGGCAAGGAGCGTGACCGCAGCGGGCTGGAT 16444  
Db 19537 GAAGCTGATTACACAGCGGCGTTATTTCTGGCAAGAGCGGGATGCAACAGGTTGTAT 19596  
Qy 16445 TATTACGGTTATCGGTATTACACGCCATGGCAGGCGCTGGCTCTCCACGACCCGGCA 16504  
Db 19597 TACTACGGCTATCGTTATTATCAATCGTGACAGGCGGATGGTTGAGTGTAGATCCTGCC 19656  
Qy 16505 GGCACGGTGGACGGGCTGAACCTGTTCCGATGGTGGGAATATCCCGTCAGCGTGT 16564  
Db 19657 GGTGAGCGCGATGGTCTCAATTTGTTCCGAATGTGAGGAATTAACCCCATCGTTTCT 19716  
Qy 16565 GACAGCAACGGGGGATC 16582  
Db 19717 GATCTGATGGTCTTC 19734

## RESULT 4

US-10-753-901-6  
; Sequence 6, Application US/10753901  
; Publication No. US20040194164A1  
; GENERAL INFORMATION:  
; APPLICANT: BINTRIM, Scott  
; APPLICANT: MITCHELL, Jon  
; APPLICANT: LARRINUA, Ignacio  
; APPLICANT: APEL-BIRKHOID, Patricia  
; APPLICANT: SCHAFER, Barry  
; APPLICANT: BEVAN, Scott  
; APPLICANT: YOUNG, Scott  
; APPLICANT: GUO, Lining  
; TITLE OF INVENTION: Xenorhabdus TC Proteins and Genes for Pest Control  
; FILE REFERENCE: DAS-105X  
; CURRENT APPLICATION NUMBER: US/10/753,901  
; PRIOR FILING DATE: 2004-01-07  
; PRIOR APPLICATION NUMBER: US 60/441,717  
; PRIOR FILING DATE: 2003-01-21  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6  
; LENGTH: 39005  
; TYPE: DNA  
; ORGANISM: Xenorhabdus nematophilus  
US-10-753-901-6

Query Match 7.2%; Score 1365; DB 18; Length 39005;  
Best Local Similarity 52.4%; Pred. No. 0;  
Matches 3947; Conservative 0; Mismatches 3070; Indels 510; Gaps 23;  
Qy 2511 TGACGGATTATTCTCGCGTTCTGTTCCGAGGTCAAAAATCACTGGCGCAGCGCTGT 2570  
Db 10773 TGACAAATCTTCGTTTATGCTCTTCAGCGAATTCGTATAGGACAAGTGGNACTCTGA 10832  
Qy 2571 CATGGGAGAGGTCTCTATCTGTACAGTCAGCGCAGCAGCAAGAAAGAAACCGGC 2630  
Db 10833 CGTGGCGAAGAACAGACTTTTATATCAACAGGCTCATCAGGAATCAAAACAGAAATAAAC 10892

Qy 2631 TCACCGAATCCCGTATTCTGGCCCGGGCGAATCCCTACTCTGTAATGCGGTTCCGCTGG 2690  
Db 10893 TTGAAGAACTGGCGCATTTTGTCCCGTGTAAATCCCACTGGCTAATACCACTTAAC 10952  
Qy 2691 GAATACGGCAGCAGCGGCTGCGCAGCTATGATGACTGGTTGGCTCCCGCGCAGACG 2750  
Db 10953 ATATTACACCGTCAACCCCTAAACAATGTTACACAGTTGGTTTATGGCGGTGCCACC 11012  
Qy 2751 GTTTCGCCCGCCCGGCTCGGTGGCTCCATGTTCTACCGCGGCGTATCTGACGAGC 2810  
Db 11013 GTTTTGTAAACCGGGATCAATTGCTTCCATATTTTACCAGCGGCTTATTTAAACAGAA 11072  
Qy 2811 TCTACCGTGAAGGAGACCTGTCATCCGACACCTCGCTGTTCGGCTGGACATCCGCG 2870  
Db 11073 TATATCGGGAAGCGAAGATTTTCATCTCTGCAATTTCTCAATATCACCTGAATAAACGAC 11132  
Qy 2871 GTCCCGACCTGGCGGCGCTGGCCCTTAGCCAGAATAATATGACACGAGCTCTCCACCC 2930  
Db 11133 GCCCGGACATTCCTTCACTGGGACCTGACACAGAAATATGATGATGAGAAATTTCCACAT 11192  
Qy 2931 TGAGCCTGTCCAATGAGCTACTGTATCGCGGTATCGGGGACGCGGAAGGCTTTGACGAG 2990  
Db 11193 TATCCTTATCTAATGAATTTACTGCTGCATAATATTTCAGACGTTAGAGAAAACTGACTATA 11252  
Qy 2991 ACAGCGTCAAGGAGCTGCTCGCGGGTATCGCTGACCGGCGCTGACCCCTATCACTGGG 3050  
Db 11253 ACGGTGTATGAATAATGTTGTCCATTACCGGCAACCGGCGATGACACCTATCATCTGC 11312  
Qy 3051 CGTACGAGCGCGCCGCAAGCAATTTCTGGTCAGGACCCGACGCTGATGGGGTTTCAGCC 3110  
Db 11313 CGTATGAGTCAGCCGCTCAGGCAATTTATTCAGAGATAAAACCTCACCAGATTAGCC 11372  
Qy 3111 GTAATCCGGATGTGGCGAGCTTATGAGCCCTGCTCCATGTGGCATTTGAAGCGGATA 3170  
Db 11373 GTAATACAGACGTAGCGGAATTAATGGACCCCAACATCGCTACTGGCTATTAAGACTGATA 11432  
Qy 3171 TTTTACCGGAGCTGTATCAGATACCTGCGCGAAGAAATACGACACAGCTTACGAGCAC 3230  
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Qy 3231 TCTGGAGTAAGAAATTTGGTGATATGCCCTCCCTCACTGTATTATCTTATGATGCACTTG 3290  
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Qy 3291 CAACATTTTATGATCTTGATTTAGATGAGCTAACTTCGTGTTATGTCATTTAAGCGTGGACT 3350  
Db 11553 CTCGCTACTACGATTTTGTCTTATGATGAACCTCAGTTTATTTGTCAATCTCTCTCTCGGTA 11612  
Qy 3351 TTTTCAAAATCCAAACATGAATACTACATTAATAGTCAATTAAGTGTGTAACCTCTGAATG 3410  
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Qy 3411 AAAGCAGCTGTTTAAATACTATACATCAFTATTTAAGAACGCTAGCGGAGACTCACAGC 3470  
Db 11673 ATGATACGCAACCGGCAAGATTGATTAAGCGAACCCGCAAGATTTCTACGATTACATTT 11732  
Qy 3471 AGATTAAACCTGAGCTTATACCTTATGGGATGGAACATATCTTTATTAATTTTACGGCTGG 3530  
Db 11733 TAAACTATGACAGAACTTAATTCCAATCAAGAAAAATGAATACAAATATATATTTTCACTGTAA 11792  
Qy 3531 TGTCAACGATATCAGAGGATAGTTTTCAAACTAGGGTCTGTTAGGTTCTTAACAGTAGCAATC 3590  
Db 11793 AAAAAACAGAACTGACCACTTGGATTTTCTGCTCCAGATGGAGATAAAGAAATATATAT 11852  
Qy 3591 TTTTACTTGGGGATTATCAGCTTCAAAAAGGGGTTTCGCTATAGCATTTCTCTGTGAATAAG 3650  
Db 11853 ACCAAGATAAAAAATTTTGGTCCCAATGCTAATACCACTTACAGTATTTCCCAATTAATTCGA 11912  
Qy 3651 ATGAAGGAAGTAAATGATGGATCACAATAGGATTTAGTAGGAA-----AG 3698  
Db 11913 CGACAGAGCAATTCACCAACGGTATAACATCCGCTTATGGCGAGTTAAACCAATCCGT 11972





Db 14121 CCATCAATGATATGCGCAGGAAAATATCAGACCTGTTATTACAAAGTCTCGCTTTGTATTATAC 14180  
Qy 5910 TCTGGGTGGAAGAGATCAGTCTGCTGATACGAGGCGAGAGACGACGAAACACCCAGC 5969  
Db 14181 TGTGGCTGGAACAAAAGAGCTGAAAATGAAAGTGAAGATGCGAAGATGATACACTG 14240  
Qy 5970 AGAGCTACAGCTGAAATGTCGTTCCGGCGCTACGACGGTACATCGAGTTCGCCGGTGT 6029  
Db 14241 AT---TATATATTAAACGTGCACATATTCGTTATGATGCGAGCTGAGCTACCGTTTA 14297  
Qy 6030 CGTTCGACATACCGGCAACATCGCATTTCCGG-----AAACGAGGCGCATGCAATG 6082  
Db 14298 ATTTTAATGTGACTGATAAAATAGAAAACCTGATCAATAAAGCCAGCATTTGGTATGT 14357  
Qy 6083 ACCTGTAATCCCTGACTGAGAGCTCTATTGCGCGTTTACTCCGTACCCAGCAAGCC- 6141  
Db 14358 ATTTGTTCTTCTGATTAAGAAAAGACGTCAATATTGTTTATTTTCCATGAGAAAAAGACA 14417  
Qy 6142 -----GGACTTTGATAACGCTCAGCTGATTTCTGTGGATAATGATATGACGC 6188  
Db 14418 ATTTATCTTTTATAGTCTTCCTGCAAGAGAGGATGACCAATAACCTGATATGACAT 14477  
Qy 6189 TAAATGTCATCTCAGATA-----TAGGGATTTTAAAGAGCGTCAGTCACGAATTTA 6239  
Db 14478 TATCCATCTTCACAGAAAATGATTTAGAGCCATTTGTTAAGAGCACATTTATCAGAATTTG 14537  
Qy 6240 ATACGAGCACTG---AGAAATTTAATAATGTTTTTTCAGACCCCTTCGCTAATATT 6296  
Db 14538 ATACCAGGACAGAAATCAAGTCAACAATCAATTTGCTACAGATTAATTTGGCGGAATATA 14597  
Qy 6297 TTCTCAGTCAACAGCTTTAAATTTGA---TGATGTTATCACAGCGATTTCTCACTCCTTA 6353  
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Qy 6354 ATTTCTAAAACTACAAGTACTGTTTTTACTAATAAGAGATTCCTCTCTTTTGAOCCAGAGC 6413  
Db 14658 CGTATATATCACAGGAAATGGTCATATTAAATTTAAGTTCAATCTTCAATGGAATTA 14717  
Qy 6414 TTCTATATTACAGCAATGTTCTGTTGTTGTAGTA-----CTG 6452  
Db 14718 ATTTTCTCAAAGGCAATATATATAAATGATGAGGTAAATACCTGTTATCGATGGTAGAAG 14777  
Qy 6453 CTGGCATCGCACTCAATCTACCATAGAAAAATTCGTTTCAGGCGGAGTAGAATTTGAGG 6512  
Db 14778 ATGAAACGGTTATTTTATTTGATATGATAGACATGATGAATGCTTTGGAAAGAGAAG 14837  
Qy 6513 AAATTAAT-----TTTTATGAGGCGCAGGCGCGCGGAGTTGACCG 6555  
Db 14838 AAGTTTTTTCATTTATGGAACCTTTGGATTTTATTTATTTCCATCGATCTTAAAAATGCCGAAT 14897  
Qy 6556 ATTTGTTGGAGTGGATGTTCTTAATTTCAAAGTATACCGGTC-GGAAAAGAGCAGTTG 6614  
Db 14898 ATTTTATAGTGTAAATGTCATTAAGAACCAAGGAAAAAATTCCTAGAAAAATCAGAAATTTG 14957  
Qy 6615 GTCTCACTGTAAATCTTATTCGTCACCTGGCGCTTAGTGGTT-----CTGTTGAGTTATT 6669  
Db 14958 GAGTTGGTATAATTTATGATATGAATCAAAATGATCTGAAATTCAACTTGATCTAAACA 15017  
Qy 6670 TATTGATTCATCAATAATAATACTTCAGCGGAAATTTTGTGAGATA-----AAATGATAACCGC 6726  
Db 15018 TAGTATTAGATTGGAAAGATAACACAGGAGTATGGCATACTATATGTGAATCATTTACTA 15077  
Qy 6727 TTTTAAATAGCGGAGTACATCAAAAGTTAATTAACGTGCTGCTATTGGCTCTCAAGATTT 6786  
Db 15078 ATGATGTTTCAATTAATAACATGGGAATATTTGGGCACTGTTCTTTCGGGAGATC 15137  
Qy 6787 TTGGAGTGTAAAGTTCGTCATTCGCGCACTTCAGATATATGAAATTAATCGATGATATCAT 6846  
Db 15138 CATGTGTGATTTATTTTCAATAGCACAGATATAAAATTTGCTTCTATCTATGATCGAAC 15197  
Qy 6847 ACTGACATCGGCGTAAATGGGACTGAAATTAATTAATCTTGGCCCTT----- 6890  
Db 15198 AGATCCAAGATAAAAAATAGTTAGTTTTTTTATTAATAAATAGTCTGATATTCTTAGTGGAGT 15257

Qy 6891 -----CCGCTGAATGGTATAATGATAAGCTGAGTCTGCAATCCGGAATAAT 6937  
Db 15258 TAAATGCTGAAGACCATGTTGGCATCTAAACCTTTCAACGAATCTGACCCCTATGTTATATG 15317  
Qy 6938 CTTTTTCAACACCAAAATCGCTGAGTTTTTA----- 6965  
Db 15318 ATTTTAAATCAAGTAAAGTTGATATTGAAGGCTATCATATTCTCTGTTGAGCGAGTTTA 15377  
Qy 6966 -----CCGTTAAATACCAAGTGAATTTGTTGAA----- 6991  
Db 15378 TTATTAAAGCAACCCGACGCGGTATACGATATTGTTATTGAATCGCAATTCATATAA 15437  
Qy 6992 ----- 6991  
Db 15438 AACTAAATTCAAAGATACAAGTAAAGTTATATCATCTGATAAATGCCATCAGGCACAC 15497  
Qy 6992 ----- 6991  
Db 15498 AATATATGAGATTGGCCCTTACAGAACCCGGTTAAATACTTTATTTTCCAGAAAATTAG 15557  
Qy 6992 ----- 6991  
Db 15558 CTGAAAAGAGCAATATTGGTATTGTAATGTTTTTAAGTATGGAACGCAAAATTTACCAG 15617  
Qy 6992 -----GATGAGTTTTCAGTGACGTTTACGTTTACCGCTGTCGATCA----- 7032  
Db 15618 AGCCGCAATTAGGTGAAGGTTTTTATGCGACATTTTAAGTTGCCCTTCAATATAAGAGG 15677  
Qy 7033 -----GAATAACGTCGCTGCGCCGCGGAGCGGCATATTAACCGTCAATC----- 7079  
Db 15678 AGCATGGTGAATCGTTGGTTTAAAGATCCATATTGGGAATATTGATGCAATTTCTGCCA 15737  
Qy 7080 -----GAAACATTAATAATGACACTTC----- 7101  
Db 15738 GACAACCTTTATTACGAAGGAATGTTATCTGATATTGAAACCCAGTAACGCTCTTTGTTTC 15797  
Qy 7102 CGTTATCGCATTTACGTAAATAATACGTCGCGCGAGTATATTCTGTTTTCACCTCGCGGTA 7161  
Db 15798 CTTATGCTAAAGATATTAATACATACGTGAAGGTGTAGATTAGGGTTGGGTACAAAAA 15857  
Qy 7162 CGATGTGGCGCTTATTTCGCTCAACACCCCTCTTTGCGCCCAACTGTCGA----- 7212  
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Qy 7213 -----CCGGCGAATACCGGGATTGACCACTTC----- 7241  
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Qy 7242 TTTCCATGAGACCCAGAGGCTTTACCGAACCCGCTGGAAGAGGGAGTGTGTTGTTTA 7301  
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Qy 7422 ATGTCTGGAACCCGCGCGGACGCTGTTAAACGGGTGCTGCAGAAATTAACCTGGAATG 7481  
Db 16158 ATATCTGGAACCCGCGCGGATATTTCGTTACGGGTGAATGACAGGATTTACTGGAACG 16217  
Qy 7482 TCCGTCGCTGGAGGAGGACACCGGTGGAACGACTCGCGCTGGACTCCAATTGACCCCG 7541  
Db 16218 TCCGCGCAATTGGAGGAAGATACGTCCTGGAATGCCAATCCGCTGGATTCCGTCGATCCTG 16277  
Qy 7542 ATGCAATAGCCAGTACGACCCCATGCTATTACAAGTCCGCACTTTATGTCGTACTCTG 7601  
Db 16278 ACGCCGTTGCCAGCATGATCCGACTATATAAGTGGCTACCTTTTATGAAAAATGCTGG 16337



Qy 7602 ACCTGCTGATTTGCCCGCGGTGATGCCCTTACCGCTGCTCGAGCGGACACCCCTTAAACG 7661  
Db 16338 ATTTGTTGATTAACCGCGAGATAGCGCTTATGCCAGCTTGAACGTGATACCTTAAACG 16397  
Qy 7662 AGCCCGGATGTGTAGTCCAGCCCTGAACCTTCTGGGCGAGGAGCCCTATATTTCTT 7721  
Db 16398 AAGCTAAATGTGTATGTACAGCGCTCACTTTATTTGGGTGATGAGCCCTTATTTTCAT 16457  
Qy 7722 TTGACGCGCATGCTCGCGGTGACCTTGGGTGACGACGCGAGGCTGACGCGACGCG 7781  
Db 16458 TGGATACGATTTGTTCAGAGCCCGCTTGAAGAAGCTGCGAGCAACATGCGGCATC 16517  
Qy 7782 ATTAACGAGGCGCTGCTGCGCGGTGCGCGGTGTTGGTGGCGCTTCCGAGACACGAGCG 7841  
Db 16518 ATTATCAATATAATGCTGCAACTGCGTCAAGCGCTGATTAACCCACGAAACGTACGG 16577  
Qy 7842 CGAATTCCTGACGGCACTGTTCTCCGCGAGACGAGGCTCAAAAGGCTACTGCG 7901  
Db 16578 CAAATTCGTTAAACCGCATGTTCTCTCCCTCAAAATTAATAAAAACTGCAAGGTTACTGCG 16637  
Qy 7902 AAACCTTTGGCACAGCGCTCCATAAATCTGGGCCCAACACCTCTCCATTTGACGGCCAGCGCG 7961  
Db 16638 AGACATTTGACGCAACGCTCTATTAATCTTACGCAATACCTGACATCGAGGTGAGCCAC 16697  
Qy 7962 TTTCCCTGTGCTTACGCCACGCGCTCGAAACCGTCCGCCCTGACAGAGTCCGTCGTCA 8021  
Db 16698 TGTCAATATCTCTATGCGCAAGCGCGCAGATCGTCCATGTTACTCAGTGTGCCATCA 16757  
Qy 8022 ACAGCGCGAGGCTGCTGACGACTGCGCGCGCGGTGATGCCGCTTACAGTTTCCCGG 8081  
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Qy 8322 TGTGTACGAGCGGACGTCAACACCGCGGAAACAGGCGCATGGAATTTGACCTCAGTT 8381  
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Qy 8382 GTCCTGCTGTGCGCATCAACCGCGCGCTCTTTTGGCGAGGCGCGCGCGATGCG 8441  
Db 17118 CATCGGTCTTGAGCACCAGCGGCAACGCTGCAATATGGCGCGCGCGCGAGATCG 17177  
Qy 8442 TGCCCAATATTTACGGCTGCGCGTCCGCTGCTGAGGCTGCTGAGGCTGCTTAAAGCCA 8501  
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Qy 8502 CCGCCATCGGCATCAGGTGCTCTCGATGCGCACCGCATATCAGCGGACAAATCAGCC 8561  
Db 17238 GTGCGATTGTTATCGAAATTTCTGCGTCAGCAACACGATTTGCGCGAGACAAATCAGCC 17297  
Qy 8562 AGTCGAAGTGTACCGCGCTGCGCGGAGGAGTGGAAATCCAGCGGTGATGCGCGAGT 8621  
Db 17298 AATCAGAAATATACCGTGGCGCTGCGCAAGAGTGGAAATTTAGCGCAATATGCGGAAG 17357  
Qy 8622 CTGACGTGGCGCAGATTGATCCCGAGCTGGCGGCGCATGGCAGTGGCGGAGGCGCTG 8681  
Db 17358 CTGAGATAAAACAAATGATGCTCAATTAAGGACGCTGGCTGTACGTCGTGAAGCGGAG 17417  
Qy 8682 AGCTGCAGAAACTTACCTTGAGACCCAGCAGACCCAGGCGACGCGCAGTTGCGATTCC 8741

Db 17418 TATTACAAAAAACTATCTGAAACTCAGCAGGCACAAACTCAGGCGCAGTTAGCCTTTC 17477  
Qy 8742 TGCAGAGTAAAGTCAACAATACGGCTCTGTACAGCTGGCTCGGCGGCGAGGTTCTCCGCCA 8801  
Db 17478 TGCAAAAGTAAATTCAGTAATGACAGCGCTATACAACTGGCTCCGTTGAAGGTTGTCCGCTA 17537  
Qy 8802 TTTTATTACCAAGTTCTATGACCTGGCAGTATCCCGCTGCTGATGGGCGCAACAGCCTGGC 8861  
Db 17538 TTTTATTACGTTTTTATGATTTGGCGGTCTCACTCTGTTTAAATGGCAGCAAACTTATC 17597  
Qy 8862 AGTGGGA---TAAATTCGAGACTAGTGTGTTTTATCCAGCCGGGGGCTGTAGTGGGGCAA 8918  
Db 17598 AGTATGAATTTGAATAATGCGGACGACACTTTATTAACCCAGGTGCTGCTGATGGGACTT 17657  
Qy 8919 ATCCCGGTCTGCTGGCGCGGGAACCTCTGATGCTGAATCTGGCGCAGATGGCAGAGCCT 8978  
Db 17658 ATCCGGGTTTATTAGCGGGTGAACCTCTGATGCTGAATTTAGCACAGATGGAAAAAGCT 17717  
Qy 8979 GCGTACGCGGGGATGACGCGGCAATAGAGGTGACGCGGACGCTCTGCTCTCGGAGGTCT 9038  
Db 17718 ATTTGGAAAGATGAACGGGCACTGAGGTACACGAGACCGTTTCTCTGCTGAAGTGT 17777  
Qy 9039 ATACCAAGCTTCGCGGAGGATGCGGCAATTTCTCTGGCGCGCAAGGTTGGTGGAACTGTGCA 9098  
Db 17778 ATGCTGCTCTGACAGAAAAAT---AGTTTCAATTTTAAAGATAAAGTGAAGTTAGTCA 17834  
Qy 9099 GTAAAGCTTCGGGCGCTGGGTACGAAAGCAACCGATTTACAGATGGATCAACAGCAAC 9158  
Db 17835 ATCAGGTGAAGGCACTGACGAGCAACCGTTTAAACGTTTGAACGTCGAAAGGACACAAC 17894  
Qy 9159 TCGAGGCGCACTCGAACTGGCTGAGCTCGGTATCGGCAACGATTTACCCGCTCTCCCTTG 9218  
Db 17895 TCGAAGCGCGCTCAATTTATCGGATCTGAATTTGCTACCGATTTATCTGACGGTTTATG 17954  
Qy 9219 GCACCATGAGGCGCATCAAAATAAGCGTCAAGCTTCCGCGCGCTGGTTCGCGCCCTATC 9278  
Db 17955 GTAAATACGCGCTATCAAAATAATCAGTGTGACATTTACCTGCGCTTTTAAAGGCTTATC 18014  
Qy 9279 AGGACGCTCGTGGGTCTCAGCTACGCGGGAAGTATGGTCATGCCCGGGTTGCAAG 9338  
Db 18015 AGGATGTTGGGCAATTAAGTTATGGCGGAGCAACAATGATGCCACGTGGCTGCAAG 18074  
Qy 9339 CGCTGCGGTCTCACAAGGAAATGAACGACAGCGGCAATTTCCAACTGGATTTCAATGACC 9398  
Db 18075 CGATTGGATCTCAGATGGCATGAATGACAGTGGTCAATTCAGATGGATTTCAATGATG 18134  
Qy 9399 CGGTTACCTGCGTTTGAAGGACTTCCAGTTGATGACACAGGGAACCTGACACTGAGCT 9458  
Db 18135 CCAAGTACCTGCGCTTTGAAGGGCTTCTGTGGCGGATACAGGCACATTAACCTCAGTT 18194  
Qy 9459 TCCCGGATGCTACGCGCAACACAGCGGATGCTCTCAGTCTGAGCGGACATCATCTGCG 9518  
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Db 18255 ATATCCGTTACACCATTTGTTCTTGAT 18281

RESULT 5  
US-10-754-115-6  
; Sequence 6, Application US/10754115  
; Publication NO. US20040208907A1  
; GENERAL INFORMATION:  
; APPLICANT: Hey, Timothy  
; APPLICANT: Schleper, Ananda  
; APPLICANT: Bevan, Scott  
; APPLICANT: Bintrim, Scott  
; APPLICANT: Mitchell, Jon  
; APPLICANT: Li, Ze Sheng  
; APPLICANT: Ni, Weiting  
; APPLICANT: Zhu, Baolong

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; APPLICANT: Merlo, Don
; APPLICANT: Apel-Birkhold, Patricia
; APPLICANT: Meade, Thomas
; TITLE OF INVENTION: Mixing and Matching TC Proteins for Pest Control
; FILE REFERENCE: DAS-104XC1
; CURRENT APPLICATION NUMBER: US/10/754,115
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/441,723
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 39005
; TYPE: DNA
; ORGANISM: Xenorhabdus nematophilus
; US-10-754-115-6

Query Match          7.2%; Score 1365; DB 18; Length 39005;
Best Local Similarity 52.4%; Pred. No. 0;
Matches 3947; Conservative 0; Mismatches 3070; Indels 510; Gaps 23;

QY 2511 TGACGGATTATTCTCGCGTTCGTTCCGAGGTCAAAAATCACTGGCGACGCTGT 2570
DB 10773 TGACAAACATTTCTGTTATGCTTTTCAGCGAATTCGTATAGACAAGTGGAACTCTGA 10832

QY 2571 CATGGGAGAGGTCTGCTATCTGTACAGTCAGGCGGACGACGACGACGAGAAACCGGC 2630
DB 10833 CGTGGCGAGAAACAGAGCTTTTATATACACAGGCTCATCAGGAAATCAAAACAGATAAAC 10892

QY 2631 TCACCGAATCCGTTATTCGCGCGGCGGAATCCCTACTGTGTGAATGCGGTTCGCGCTGG 2690
DB 10893 TTGAGAACTGGGCAATTTGTCTCGGTGCTAATCCAACTGGCTAATACCACTAACCTTA 10952

QY 2691 GAATACGGCAGGCGCGCAGTCGCGAGTCATGATGATGATGATGATGATGATGATGATG 2750
DB 10953 ATATTACACGCTCAACCTCAACAAATAGTTACAAAGTGTGTTTATGGCGGTGCCACG 11012

QY 2751 GTTTCCGCGCGCGCGCTCGGTGGCTCCATGTTCTCACGGCGCGGTCTCTGACCGAGC 2810
DB 11013 GTTTTGTAAACCGGGATCAATTTGCTTCCATATTTTACACGAGCGGTATTTTAAACAG 11072

QY 2811 TGTAACGCTGAGGCGAAGGACTGTCATCCGAGACCTCGCTGTTCGCGCTGGACATCCGGC 2870
DB 11073 TATATCGGGAAGCGAAGATTTTTCATCTGACAACTTCAATATCACTGAAATAAGGAC 11132

QY 2871 GTCCGACCTGGCGGCGCTGGCCCTTAGCCAGAAATATATGAGACGAGCTCTCCACCC 2930
DB 11133 GCCCGACATTTGCTTCACTGGCACTGACACAGAAATATATGATGAAAGAAATTTCCACAT 11192

QY 2931 TGAGCCTGTCATGAGCTACTGTATCGCGGTATCGGCGGACGCGGAGGCTTGACGACG 2990
DB 11193 TATCCTTATCTAATGAATTAATGCTGCTAATATATGAGCTTAGAATAACTGACTATA 11252

QY 2991 ACAGCGTCAGGAGCTGCTCGCGGGTATCGCCTGACCGGCGCTGACCCCTATCACTGGG 3050
DB 11253 ACGGTGAATGAATAATGTTGTCACCTTACCGGCAAAACCGGATGACACCCCTATCACTGC 11312

QY 3051 CGTACGAGGCGCGCGCGCAAGCCATTTCTGGTGAGGACCGGACGCTGATGGGCTTAGCC 3110
DB 11313 CGTATGAGTCAGCCCGTCAGGCAATTTTATTTGCAAGATAAAACCTCACCGCAATTTAGCC 11372

QY 3111 GTAATCCGGATGTGGCGAGCTTATGACCTGCTCCATGCTGGCCATTTGAAGCCGATA 3170
DB 11373 GTAATACAGCTAGCGGAATTAATGACCAACATCGTACTGCTGCTATTAAGCTGATA 11432

QY 3171 TTTTCCCGGAGCTGATCAGATATCGCCGAAGAAATTAACACAGACAGTTACGAAGCAC 3230
DB 11433 TATCGCTGAATTTGATCAAACTCTGTAGAAGAAATTTACACGGAATAATTTCAACAGAAC 11492

QY 3231 TCTGGAGTAAGAAATTTGGTGATGCTGCTCCCTCCTCACTGTTATCTTATGATGACCTTG 3290
DB 11493 TGATGAAGAAATAATTTCCGTACAGATGATGATGATGATGATGATGATGATGATGATGATG 11552

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QY 3291 CAACATTTTATGATCTTGTATACGATGAGCTAACTTCGTTATTGTCTATTAAGGCTGGACT 3350
DB 11553 CTGCGTACTACGATTTGTCTTATGATGAACCTCAGTTTATTTGTCAATCTCTCTTCGGTA 11612

QY 3351 TTTTCAATCCAAACAAATGAATACATTAATAGTCAATTAAGTGTCTGTAATCTGTAATG 3410
DB 11613 AGMAAATACAAATCAACAGTATAAGATGAGCAACTGATAACATTTGTCTCAATGACGGGA 11672

QY 3411 AAAGCAGCTGTTTAAATAACTATACATCATTTATTAAGAACCTAGGCGGAGACTCACAGC 3470
DB 11673 ATGATACGGCAACCGCAAGATTGATTAAAGCGAACCCGCAAGATTTCTTACGATTCACAT 11732

QY 3471 AGATTTAACCCCTGAGCTTATACCTTATGGGATGGAACATATCTTTATTAATTTACGCGTGG 3530
DB 11733 TAACTATGCGAAGTAATTCATCAAGAAATGAATACAAATATTAATTTTCACTGTAA 11792

QY 3531 TGTCAACGATATCAGAGGATGTTTCAAACTAGGTCGTTAGGTTCTTAACAGTAGCAATC 3590
DB 11793 AAAAAACAGAACCTGACCCTTGGATTTTCGTCCAGAATGGAGATAAAGAAATATATAT 11852

QY 3591 TTTTACTCTGGGATTTATCAGCTTCAAAAAGGGTTTCGCTATAGCATTCCTCTGTAATAG 3650
DB 11853 ACCAAGATAAAATTTCTGTCGCCATTTGCTAATACCATTAAGTATTTCCCATTAATTTGA 11912

QY 3651 ATGAAGGAAAGTTAAATGATGGGATCAATAGGATTCAGTAGGAA-----AG 3698
DB 11913 CGACAGAGCAATCAACACGGTATAACACTCCGCTTATGGCGAGTTAAACCAATCCGT 11972

QY 3699 GGGGGGGATATTTACTCAACAGTAAACTTCACTCTGTAATGAATATGATCCTCGGATATTCA 3758
DB 11973 CGGATGCTATCAATGCCAATGCATCTTTAAATGATGAGGTTCCCGCGTGATATATTTCC 12032

QY 3759 TTTCTAAATTAATAAGTTATCCGCTATACAGGCCACGGGATGACCAAGCGGAAA 3818
DB 12033 TGTAAAGCTGAATAAGCGATTCGTTTGTATAAAGCCACAGGCATATCTCCAGAAGATA 12092

QY 3819 TATATCAATCAACCAATTTCTTAATAACGGTCTCAACATTCACCATTCGCGTCTGAGTA 3878
DB 12093 TCTGCGAAGTATAGAAAGTATTTATGATGACTTAAACCATTTGACAGCAATGTTGGGTA 12152

QY 3879 AAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3938
DB 12153 AGCTGTTTATGTTCAATATATATATGAGCACTATAATATTTAGCTGACGATGCGCTGG 12212

QY 3939 TATTTGCGAACCGAACCTACGTGACACGAGGCTTCAGCGGGAACCCGCTGTTTCAACA 3998
DB 12213 TATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 12272

QY 3999 CGCTGTTCAACACCCCGCTGAAACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4058
DB 12273 TACTGTTCAATACACCGCTTATTAATGGCAAGAGTTCCTGCTGATAATACCAACCTGG 12332

QY 4059 ACTTACGCTGCTGAAGACCGGAGGATGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 4118
DB 12333 ATTTAACCCCGCTGAAATCAAAAAACCAATTTTATTTGGGAATAATGAACGCTGCTTCA 12392

QY 4119 ACATCAGCGCTCGGCGCTTTCACCGCTGCTGCGAGTTGGCGAGCGGTGACACGAGCGCTG 4178
DB 12393 GAGTGAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 12452

QY 4179 GGTTTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4238
DB 12453 AATTTATGTTTCCATCGGAACCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 12512

QY 4239 TCCACGACCTATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4298
DB 12513 TTTATCATCTGACGAGTGAATTAATCCATGTTGTTGCGGTTTCTTCCCTATGTAACA 12572

QY 4299 TGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4349
DB 12573 CGMAAATGCGCTTTTCTGATACAGCAATTAACGCAATTAATCAGCTTTCTGTTCCAAT 12632

QY 4350 CCACCACTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4409

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12633 GCACCCAGTGGCTGACAAACAGAAATGGTCTGTGACGTGATGTTTCTGATGACACGG 12692 Db  
4410 CGCAGTACGTAACCTGCTGACCCCGACCAATGAGAACCTGCTCGCTTCCCTGGCAACG 4469 Qy  
12693 ATAATTACAGCACTGCTTACGCGCGGATATGAAAACCTTATCAGACACTAAGTAATG 12752 Db  
4470 GACTGTCCGGCCGCTGAGCTGTTCCGGAACCGTCCCGCGGATGGCGCTCCCTTTATTG 4529 Qy  
12753 GATTATCAACACTTCTACCTCGGTGATGACGAATGATCCGTGACGTGCCCCGCTGATTG 12812 Db  
4530 CCGCGGCATGACGCTGGAACCCACGATACGGCAAGGCGATGCTGACTTGGCGGAC 4589 Qy  
12813 CTGCGAGCTTCAATGGAATGAGCAAGCAAGCAGACAGCAAACTAATTTGCTGTGATTAAATC 12872 Db  
4590 AGTTGAGCCAGAGGGCTGACGCTGACGGAATTTATCTTTTGGTGATGAATGCCGCC 4649 Qy  
12873 AGATAAACACCAAGGACTGACATTCGATGATTTTCATGATTTATGCGGGTAAACCGTGATC 12932 Db  
4650 CAAATGACGAGCGCGGCGCAGATGCGAGGTTCTGCCAAGCCCTGTGGCAACTGGCAC 4709 Qy  
12933 GCTCAGAGATGAACACGACAAACATGTTGCTTTTGTGAGTACTGGGCAACTTCTC 12992 Db  
4710 TGATATCCGACACCGGCTCAGCACGCGGAGCTGACGCTGCTGGTCAGCCAGCCGG 4769 Qy  
12993 TGATTGTGCGCAATATTGGACTCAGCGAAACGAACTGACCCCTGTTGGTGACAAAACCGG 13052 Db  
4770 GACGCTCCGACAGAGTGGACCATCTGCCCATGACCTGCGCGGCTTCGGCAATTA 4829 Qy  
13053 AGAAATCCAAATCAGAAACACACGACTGCAACATGATCTCCCACTTTGCAAGCGGTGA 13112 Db  
4830 CGGTTTTTCATGCCGTGTTAAACGACGCGGACGCAATGCGGGAGGCTCTGACCGCAC 4889 Qy  
13113 CCGCTTCCATGTGTCATGATGTTGTGGAAGCTACGCGACAGAAATCTTTAACAGCAT 13172 Db  
4890 TTGAGACCGGAGAACTGCTGACGCCCTGCTGCGCGGCGCCTGTACAGAAATGAGCAGG 4949 Qy  
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4950 ATGTGACCGGCGCTTGGCGAGGTGAGGGGGCGGTGAAACAGGACAAACAGCGTGTCA 5009 Qy  
13233 TTGTGACACAGCAATTCACACAGACCGGTTTGGGAGTGAATACC-----TTTA 13280 Db  
5010 CCTCTCGGGAAGGTGACACAGCTGACGAGTGGCTGGGACATGAGTGACACCTGTC 5069 Qy  
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5070 TTACGCCATCCGGTCTGGCTAGCCTGATGCCCCTGAAGTACATCAATGTGTCGATGACA 5129 Qy  
13341 TTACCCCGGATGGTGTGCTGCACTCATATAAATTTAAATATATCGGTGAACCAACCC 13400 Db  
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13401 CGATGCCAACATTTGATGATTTGGCAAGCCCGCAGTACTTTGTTGACGGCGGACTGAACA 13460 Db  
5190 GCAGCAGAGCTCGGCGCTCAGATTTATCTGAGGAGGGGACACAGCGCCCTTTGTG 5249 Qy  
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5250 CGTATTATCTCGGTAATCTGGCACCGCAACATGGTATCCGGCGCGATGACCTCTTCGGGT 5309 Qy  
13521 CTTACTACATCAAAATAGTGCACTCAACAGATTAAGCCGGATGAGTTGTACAGCT 13580 Db  
5310 ATCTGCTGGTAATAATCAGGTGTACCGCAAGGTAAAAACACCGCAATTTGGGAGGCCA 5369 Qy  
13581 ATCTGCTGATTGATAACCAAGTTCTGCCCAAGTGAACCAACCGGTGGCAGAGGCCA 13640 Db  
5370 TCGCGGCATACGCTGTATATCAACCGGCCCTTAACGGAATAGAACTCAGCGCCATGG 5429 Qy  
13641 TTGCCAGCATTCAGTTTATATGTAACCGGGCTTGAATTAATGTGGAAGAAAAGTATCAA 13700 Db  
5430 CAGAGGTGAGGGGCGTCAGTTTTTCTGACTGGGATACGTTTCAACAAACGTTTACAGCA 5489 Qy

13701 AGCCAGTGAACCCCGTCAGTTCTTCTGCGACTGGGAAACCTACAACTCGACGGTATAGCA 13760 Db  
5490 CCTGGGGGGCGCTCTCAGAGCTGGTTTACTATCCGGAACACTACCTCGACCCGCGTCC 5549 Qy  
13761 CCTGGGGCGCGCTATCTGAACCTGGCCTATTTATCCGGAACATATATCGACCCCGCATTC 13820 Db  
5550 GTATCCGGGAGACCGCGCATGATGGACACCCCTGCTGCAGTCTGTGACGACGAGCAGTATCA 5609 Qy  
13821 GTATTGGTCAGACAGGTATGATGAACAACTGTTACAGCAACTTTCCCAAGTCAGTTAA 13880 Db  
5610 ACCCGCATCCGTTGGAGGATGCTTTAAACCTATCTGACCACTGTTTGGAGCAGATTGCCA 5669 Qy  
13881 ATATCATATCCGTTGAAGATAGCTTTAAAAATTTATCTGACCGCATTTGAAGATGTGCTA 13940 Db  
5670 ATCTGAACACTGTGACGGGATATCAGATAACCCAGCATGACGCGAGGAGCTACATGGT 5729 Qy  
13941 ACTTGCAGTGATTTAGCGGATATCATGACAGTATCAATGTCAATGAGGAGTCACTTATT 14000 Db  
5730 ATGTGGTCCGACATCAGCATCAGACTAACTGGTACTTGGCGCAGCGCCAAACACAGCA 5789 Qy  
14001 TAATTGGTTATAGCCAGACAGAACCCAGATATATTATTGGCGCAATGTGATCACAAA 14060 Db  
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14121 CCATCAATGATGGCAGGAAATATCAGACCTGTTATTACAAGTCTGCTTTGTTATTTAC 14180 Db  
5910 TCTGGGTCGAAGAGAACTAGTCTGTGATACGAGGACAGAGACAGCAACCAACGCGAGC 5969 Qy  
14181 TGTGGCTGGAACAAAGAGCTGAAAAATGAAGTGAAGTGCAGATAGATATCACTG 14240 Db  
5970 AGAGCTACAGCTGAAACTGTGTTCCGGCGTACGACGGTACATGAGTTCCCGGTGT 6029 Qy  
14241 AT---TATATATTAAACTGTACATATTCGTTATGATGCGAGCTGAGCTACCGGTTA 14297 Db  
6030 CGTTCCACATACCAGCAACATCGCATTTCCGG-----AAACGAGGCGATCATGTG 6082 Qy  
14298 ATTTTAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 14357 Db  
6083 ACCTGTAATCCCTGCTGACGAGCTCTATTGGCGCTTACTCCGTCACACGACAGCC- 6141 Qy  
14358 ATTGTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 14417 Db  
6142 -----GGACTTTGATAACCTCAGCTGATTTCTGTGGATAATGATATGACGC 6188 Qy  
14418 ATTATTCTTTTAAATAGTCTTCTGCAAGAGAGGAGTACCAATTAACCTGATATGACAT 14477 Db  
6189 TAAATGTCATCTCAGATA-----TAGGGATTTTAAAGCGCTCAGTCACGAAATTTA 6239 Qy  
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14598 AGGAATCTATAACCAAAAAATAAATAGCCAGTTTACCGGAATATTTTGTGATCTCT 14657 Db  
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6414 TTCATATTACAGCAATGTTTCTGTTTGTGTTAGTA-----CTG 6452 Qy  
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6453 CTGGCATCGCACTCAATCTACCATAGAAAAATTCGTTACGCGGAGGATAGAAATTTGAGG 6512 Qy  
14778 ATCAACCGTTATTTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 14837 Db

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Db	14838	AGGTTTTCAATATGGAACCTTGGATTTTATATTTCCATCGATCTAAAAATGCCGAAT	14897
QY	6556	ATTGTGGAGTGGATGTTTCTAATTCAAAGTATACCAAGTCC- GGAAAAGAACGAGTTG	6614
Db	14898	ATTTAGAGTGTAAATGTCATCTAAGAACCAAGGAAAATTTCTAGAAAATCAGAAATTG	14957
QY	6615	GTGTCACTGAAATCTTATTCGCTCACTGGCGTTAGTGGTT-----CTGTTGAGTTATT	6669
Db	14958	GAGTTGGTATAAATTATGATTATGAATCAAAATGATGCTGAAATTCAAAACCTTGATCTAAACA	15017
QY	6670	TATTTGATTCATCAATAAATACCTTCAGCGAAATTTTGTACAGATA---AAATGATAACCG	6726
Db	15018	TAGTATTAGATTGGAAAGATAACACAGGAGTATGGCATACTATATGTGAATCAATTACTA	15077
QY	6727	TTTTAATTAGCGGCAGTACATCAAAAGTTAATTACGTGCTGTCTATTTGGCTCTCAAGATTT	6786
Db	15078	ATGATGTTTCAATCAATTAATAACATGGGAAATATTGGGCACGTTCCTTCGCGAGGATC	15137
QY	6787	TTGGAGTGAAGTCCGTCTATGCGGCACCTTCAGATATATGAATTAATTCAGATATCAT	6846
Db	15138	CATGTGTGTATTATGTTCAATAGCCACAGATATAAAAATTTGCTTCATCTATGATCGAATC	15197
QY	6847	ACTGACATCCGCGTAAATGGGACTGAAATTAATCCTCGCCTT-----	6890
Db	15198	AGATCCAGATAAAAACATTAGTTTTTTTATTAATAATGGCTCTGATATTTAGTGGAGT	15257
QY	6891	-----CCGCTGAATGGTATATATGATGAAGCTGAGTCTGCAATCCGCGGAATAAT	6937
Db	15258	TAAATGCTGAAGACCATGTGCATCTAAACCTTTCACAGAACTCGACCTATGTTATATG	15317
QY	6938	CTTTTCAACCAAAATCGCTGAGTTTTA-----	6965
Db	15318	ATTTTAATCAAGTAAAGTTGATATTGAAGGCTATGATATTCCTCTGCTGAGCGAGTTTA	15377
QY	6966	-----CCGTTAATACAGTATATTTGTTGAA-----	6991
Db	15378	TTATTAAAGNACCGGAGCGGGTTTAAACGATATTGTTATTGAATCGCCAAATTCATATA	15437
QY	6992	-----	6991
Db	15438	AACTAAAAATCCAAAGATACAAGTAACTTATATCACTGCAATAAATGCCATCAGGCACAC	15497
QY	6992	-----	6991
Db	15498	AATATATGCAGATTGGCCCTTACAGAACCGGTTAAATACTTTATTTCCAGAAAAATTAG	15557
QY	6992	-----	6991
Db	15558	CTGAAAAGCCAAATATTGTTATGATAATGTTTAAAGTATGGAACGCAAAATTTACCAG	15617
QY	6992	-----GATGAGTTTGAGGTGACGTTTACGTTTACCGCTGTCGATCA-----	7032
Db	15618	AGCGGCAATTAGGTGAAGGTTTTATGCGACATTTAAGTTGCCCTACCAATAAGAGG	15677
QY	7033	-----GAATTAACGTGTGCTGGCGGCCGCGAGCCGCAATATAACCGTCAATC-----	7079
Db	15678	AGCATGGTGATGAACGTTGGTTTTAAGATCCATATTGGGAATATTGATGGCAATTTCTGCCA	15737
QY	7080	-----GAAACATTAATAATGACACTTC	7101
Db	15738	GACAACTTATTACGAAGGAAATGTTATCTGATATTGAAACCAACAGTAACGCTCTTTGTTTC	15797
QY	7102	CGTTATCGCATTAACGTAATAAATACGGTGGCGCGCAGTATATTTCGTTTCACTGCGGGTAA	7161
Db	15798	CCTATGCTAAAGGATATTACATACGTGAAGGTGTCAAGATTAGGGTTGGGTACAAAANA	15857
QY	7162	CGATGTGGCGCTTATTTCGCCCTCAACCCCTCTTTTCGCCGCGCAACTGGTCTGA-----	7212
Db	15858	TTATCTATGACAAATCCTGGGAATCTGCTTTCTTTTATTTTGTATGAGACGAAAAATCAAT	15917
QY	7213	-----CCGGCGGAATACCGGAGTTGACACATTC-----	7241
Db	15918	TTATATTCAATTAATGATGCCGATCATGATTCGGGAATGACACAAACAGGGGATAGTAAAAA	15977
QY	7242	TTTCCATGGAGACCCAGAGGCTTACCGAACCCGCCCTTGAAGAGGGAGTGTGTGTTTTA	7301
Db	15978	ATATCAAAAAATATAAAGGTTTTATTTCATGTCTGTTGTCATGAAAAATAACACTGAACCCA	16037
QY	7302	TGGACTTCTCCGAGGCAATGCCCTCTATTTCCTGGAGAGTGTTCATTATACAGCCGATGA	7361
Db	16038	TGGATTTCAACGCGCCCATGCAATCTATTTCCTGGGAATTTGTTTATTAACGCCCATGA	16097
QY	7362	TGCTGTTCAGCGGTTGTTTGCAGGAACAGCACTTCCCGGAAGCCACCCGCTGGCTCACT	7421
Db	16098	TGGTATTTCCAGCGCTTATTGCAAGAGCAGAAATTTTACCGAATCGACACGCTGGCTCGCT	16157
QY	7422	ATGCTCTGGAACCCGCGCCGACAGTGTAAACGGGGTCTGCAGAAATTAACCTTGGAAATG	7481
Db	16158	ATATCTGGAACCCGCGCGGATATTTCGGTTTCAGGGTGAATGCGAGATTATTACTGGAACG	16217
QY	7482	TCGCTCCGCTGGAGGAGACACGGCTGGAACAGACTCGCGCTGAGTCTCAATTCAGCCCG	7541
Db	16218	TCGCGCCATTGGAGGAAGATACGCTCTGGAATGCCAATCCGCTGGATTCCGTCGATCCCTG	16277
QY	7542	ATGCAATAGCCCACTACGACCCATGCTATTACAAGTGCACCACCTTTATGTCTGACTCTCG	7601
Db	16278	ACGCGTTGCCAGCATGATCCGATGCACTATAAAGTGGCTACCTTTATGAAATGCTGCG	16337
QY	7602	ACCTGTGATTCCGCGCTGATGCGCTACCGCTGCTCGAGCGGGAACACCTTTAAACG	7661
Db	16338	ATTTGTTGATTACCCGCGGAGATAGCGCTATCGCCAGCTTGAACGTGATACCTTAAACG	16397
QY	7662	AGCCCGGATGTGTACGTCAGGCCCTGAACTTCTGGCGACAGGCCCTATATTTCCT	7721
Db	16398	AAAGCTAAAAATGTGGTATGTACAGGGGCTCACTTTATGGGTGATGAGCCCTTTATTTTCAT	16457
QY	7722	TTGACGCCGACTGTGTGGCGTTGACCCCTGGGTGAGCAGCCAGCAGAGTGACGCGACGCG	7781
Db	16458	TGGATAACGATTGGTCAGAGCCACCGCTGGAAGAGAGCTGCCAGCCAAACAAATGCGGCATC	16517
QY	7782	ATTACAGAGAGCCCTGTGTGGCCGTGCGCGGTTGGTGGTCCGCTCCCGAGACAGGACGG	7841
Db	16518	ATTATCAACATAAAATGCTGCAACTGCGTCAGCGGCTGCAATTAACCCACGAAACGTACGG	16577
QY	7842	CGAATTCCTTGACGCACTGTTCTCCCGCAGCAGAAACGAGGTGCTCAAGGCTACTGCG	7901
Db	16578	CAAAATTCGTTAAACCGCATTTGTTCTCCCTCAAAATTAATAAAAACTGCAAGGTTACTGCG	16637
QY	7902	AAACCTTTGGCACAGCGGCTCCATAACCTGCGCCACAACCTCTCCATTGACGCGCAGCCGC	7961
Db	16638	AGACATTTGCGCAACGCCCTCTATTAATTAACGCCCATTAACCTGACATCGACGCTCAGCCAC	16697
QY	7962	TTTCCCTGTCCGTCTACGCCACCGCTCGAAACCGTCCGCCCTGCGAGAGTGCCTGCTCA	8021
Db	16698	TGTCTATTCTCTCTATGCGCCGCGCAGATCCGCTCCATGTTACTCACTGTGCTGCCATCA	16757
QY	8022	ACAGCGCGCAGGCTGCTGACGCACTGCGCGCCGCGGTGATGCGCTTTACAGTTTCCCG	8081
Db	16758	CTGCTTCAACAGCGCGCGGATTTACCTCATGCAAGTATGCGGATGATCCGCTTTTCCCG	16817
QY	8082	TCATGCTGAGAAACGCCCGGGGATGTGAGGCTGCTGACCGGTTTCGGCAACACACTGCG	8141
Db	16818	TGATTTCTGGAATAATGCCAAGTGGGGGTAAGCCAGTTGATACAAATTTGGCAATACCTGCG	16877
QY	8142	TCGGTATTACCGAGCGTACGAGTGGAGGCGCTGCGCAAACTGCTGCAAGACCCAGGCA	8201
Db	16878	TCAGCATTAATGAAACGCGAGGATGCAAGACCTTGGCTGAAATCTGCAAACTCAAGGCA	16937
QY	8202	GTGAAGTATAGCCAGGCGCTTCCGACAGAGATAACGCTCCGAGGAAATCGATGCGG	8261
Db	16938	GTGAGTTAGCCCTGCAAAAGTATTAATAATGCAAGTCAAGGTCAAGTGAATTTGATGCTG	16997
QY	8262	ATATTGCCGCCCTGGAGGAGAGCCCGCGCGCGCAGATGCGTTTTTGAACGTTTACAAAG	8321

Db 16998 ATAAATTGGCGCTTCAAGAAAGCGCTCATGGTGACAGTCTCGTTTTCAGAGTTTCAATA 17057  
 Qy 8322 TGTGTACGAGCGGAGTCAACACCGCGGAAACAGGCATGAGCTTGTACTCTAGTT 8381  
 Db 17058 CGCTGTACGAGCAAGATGTTAACGCTGGTGAAGAAACAGGATGATGATCTTTTACCTCTCTT 17117  
 Qy 8382 CGTCGCTGTCTCGGCTCAACACCGCGCTCTTTTGGCGAGCGCGCGCGATATGC 8441  
 Db 17118 CATCGGCTTGAGCACAGCGCACAGCCCTGCATATGGCGCGCGCGCGAGATCTCG 17177  
 Qy 8442 TGCCCAATATTACGGGCTGGCGCTCGGGGGCTCCCGCTATAGGGGCACTATTAAAGCCA 8501  
 Db 17178 TCCCAATATTACGGTCTGTGGGAGGTTCCCGTTTGGGGCGCTTTTCAATGCCA 17237  
 Qy 8502 CCGCATCGGCATCCAGGTGCTCCGATGCCACCGCCCATATCAGCGGACAAATCAGCC 8561  
 Db 17238 GTGGATGTGATCGAATTTCTCGCTCAGCAACACGATATGGCGGACAAATCAGCC 17297  
 Qy 8562 AGTCGGAAGTGTACCGCGCTGCGCGGAGGAGTGGAAATCCAGCGTGATAGTGCAGT 8621  
 Db 17298 AATCAGAAATATACCGTGGCGTGGCAAGAGTGGAAATTCAGCGCAATATGCGGAG 17357  
 Qy 8622 CTGACGTGGCGCAGATGATGCCAGCTGGCGGCGCATGGCAGTGGCGCGGAGGGCTG 8681  
 Db 17358 CTGAGATAAAACAAATTCATGCTCAATAGCGAGCTGGCTGTACGTGCTGAAGCGCAG 17417  
 Qy 8682 AGCTGCAGAAACCTTACCTTGAGACCCAGCAGACCCAGGACAGCGCGAGTGGCATTC 8741  
 Db 17418 TATTACAAACAACTATCTGGAACCTCAGCAGGACAACTCAGCGCGCATGTAGCTTTC 17477  
 Qy 8742 TGCAGATGAAGTTCACAAATACGCTCTGTACAGCTGGCTGCGGGCAGGTTGTCGCCCA 8801  
 Db 17478 TGCAAGTAATTCAGTAATGCAGCGCTATACACTGGCTCCGTGGAGGTTGTCGCTA 17537  
 Qy 8802 TTTATTAACGATCTATGACTGGCAGTATCCCGCTGCTGATGGCGCAACAGCGCTGGC 8861  
 Db 17538 TTTATTAACGATCTATGACTGGCAGTATCCCGCTGCTGATGGCGCAACAGCGCTGGC 8861  
 Qy 8862 AGTGGG- --TAATTCGAGACTAGTTCGTTTATCCAGCGCGGGGCTGATGGGGCAA 8918  
 Db 17598 AGTATGAATTAATTAATGCGGACGACACTTTTATTAACACGAGTGCCTGGCATGGGACTT 17657  
 Qy 8919 ATGCGGCTGCTGCGCGGGAACCTGATGCTGAATCTGGCGCAGATGGAGCAGCT 8978  
 Db 17658 ATGCGGCTTATAGCGGTTGAACCTGATGCTGAATTTAGCACATGGAAGAAAGCT 17717  
 Qy 8979 GGTGACGCGGGATGAGCGGCAATAGAGTGACGCGGAGCTGCTGCTGTCCGAGGTCT 9038  
 Db 17718 ATTTGGAAGAAAGATGAACGCGGCACTGGAGGTACACAGAACCGTTTCTGCTGAAGTGT 17777  
 Qy 9039 ATACGAGCTCGCGGAGGATCGGCATCTCTGCGCGACAGGTTGGTGGAACTGTGCA 9098  
 Db 17778 ATGCTGTCTGACAGAAAT- --AGTTTCATTTTAAAGATAAAGTGAAGTGAAGTGA 17834  
 Qy 9099 GTAACGCTTGGGAGTGGCGGTACGAAAGCAACGATTAACAGATGATCAACAGCAAC 9158  
 Db 17835 ATGAGGTGAAGGAGTGGCGGCAACAGCTTAACGTTTGAAGCTGGAAGGACACAC 17894  
 Qy 9159 TCGAGGCAACCTGAACTGCTGACCTCGGTATCGGCAACGATTAACCGGCTTCCCTTG 9218  
 Db 17895 TGCAAGCAGCGCTCAATATTACGATCTGAATATTGTACCGATTAATCTGACGGTTTAG 17954  
 Qy 9219 GCACATGAGGCGCATCAACAAATAGCTCAGCTCCGCGGCTGGTCCGCCCTATC 9278  
 Db 17955 GTAATACGCGCGTATCAACAAATCAGTGTGACATTAACCTGCGCTTTTAGGGCTTATC 18014  
 Qy 9279 AGGAGCTCGGCTGCTCAGCTACGCGGCAAGTATGGTATGCGCGGGTTGACGCG 9338  
 Db 18015 AGGATGTTGCGGCAATTAAGTTATGGCGGACACAAATGATGCCACGTGGCTGCAAG 18074  
 Qy 9339 CGCTGGCGGTCTCAGCGGAATGAACGACGCGGCAATTTCCAACTGGATTTCAATGACC 9398

Db 18075 CGATTGCGATCTCACATGGCATGAATGACAGTGGTCAATTTCCAGATGGATTTCAATGATG 18134  
 Qy 9399 CGGTTACCTGCGGTTTGAAGGACTTCCAGTTGATGACACAGGACCTGACACTGAGCT 9458  
 Db 18135 CCAAGTACCTGCGCATTTGAAGGGCTTCTCTGCGCGATACAGGCATTAACCCCTCAGTT 18194  
 Qy 9459 TCCCGATGCTGACGCGCAACCAACAGCGCATGCTCTCTCAGTCTGAGCGACATCATCTGCG 9518  
 Db 18195 TCCCGATGCTGAGTGAACAGCAAGCAAGCTTATTGCTCAGCCTGAGCGATATCATCTGCG 18254  
 Qy 9519 ATATCCGTTACACCATATATCAGCTGAT 9545  
 Db 18255 ATATCCGTTACACCATATTCGTTCTTGAT 18281

RESULT 6  
 US-10-753-901-13  
 ; Sequence 13, Application US/10753901  
 ; Publication No. US20040194164A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bintrim, Scott  
 ; APPLICANT: Mitchell, Jon  
 ; APPLICANT: Larrinua, Ignacio  
 ; APPLICANT: Apel-Birkhold, Patricia  
 ; APPLICANT: Schafer, Barry  
 ; APPLICANT: Bevan, Scott  
 ; APPLICANT: Young, Scott  
 ; APPLICANT: Guo, Lining  
 ; TITLE OF INVENTION: Xenorhabdus TC Proteins and Genes for Pest Control  
 ; FILE REFERENCE: DAS-105X  
 ; CURRENT APPLICATION NUMBER: US/10/753,901  
 ; PRIOR FILING DATE: 2004-01-07  
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 ; PRIOR FILING DATE: 2003-01-21  
 ; NUMBER OF SEQ ID NOS: 22  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 13  
 ; LENGTH: 7569  
 ; TYPE: DNA  
 ; ORGANISM: Xenorhabdus nematophilus  
 ; US-10-753-901-13

Query Match 7.2%; Score 1364.6; DB 18; Length 7569;  
 Best Local Similarity 52.5%; Pred. No. 0;  
 Matches 3943; Conservative 0; Mismatches 3064; Indels 510; Gaps 23;

Qy 2511 TGACGGATTTATCTCGCGTTCTGTTCCCGAGGTCAAAAATACATCGGCGACAGCTGT 2570  
 Db 65 TGACAAACATTTCTGTTTATGCTTTTCAGCGAATTTCTGTCATAGGACAAAGTGGAACTCTGA 124  
 Qy 2571 CATGGGAGAGGTCTGCTATCTGTACAGTCAGGCGGAGCAGCAACAGAAAGAAACCGGC 2630  
 Db 125 CGTGGCGAGAAACAGACTTTTATATCAACAGCGCTATCAGGAATCAAAACAGAAATAAC 184  
 Qy 2631 TCACCGAATCCCTATTTCTGGCGCGGCAATCCCTACTGTTGTAATCGCTTTCGCTGG 2690  
 Db 185 TTGAAGAACTGCGCATTTTGTCCGTTCTATCCACAACTGGCTATACCACTAACCTTA 244  
 Qy 2691 GAATAGCGGAGGAGCGGCGAGTCGAGCTATGATGATGCTGTTGGCTCCGCGGAGACC 2750  
 Db 245 ATATTACACCGTCAACCCCTAAACAAATAGTTTACAAAGTTGCTTTTATGGCGCTGCCACC 304  
 Qy 2751 GTTTCCCGCGCGGCTGGTGGCTCCATGTTCTCACCGGCGGCTATCTGACCCGAGC 2810  
 Db 305 GTTTGTGTAACCGGAGTCAATTTGCTTCCATATTTTCCACGCGGCTTATTTAACAGAA 364  
 Qy 2811 TGTAACGCTGAGGGAAGGACCTCACTCCGACACCTCGCTGTTCCGCTCGACATCCGGC 2870  
 Db 365 TATATCGGAGGAGGAAGATTTTCTCTGACAAATTTCTCAATATCACCTGAATAACGAC 424  
 Qy 2871 GTCCCACTGCGCGGCTGGCCCTTAGCCAGAAATATATGAGCAGAGCTCTTCCACC 2930  
 Db 425 GCCCGGACATTTGCTTCACTGGCACTGACACAGAAATAATATGGATGAAGAAATTTCCACAT 484

QY	2931	TGAGCCTGTCCATGAGCTACTGTATCGCGGTATCGGGCAGCGGAAGGCTTGACGAGC	2990	QY	3999	CGCTGTTCAACACCCACCGCTGAACGCGCAGCTGTTTTCTTCAGATGATACCCCCCTCG	4058
Db	485	TATCCTTATCTAATGAATTAATCTCTGCTGATAATTAATCAGACGTTGAGAAACACTGACTATA	544	Db	1565	TAATGTTCAATTAACACCGCTTAATTAATGCGCAAGAGTTTTCTGCTGATAATACAAACTCG	1624
QY	2991	ACAGCGTCAGGGAGCTGCTCGCGGGTATCGCCTGACCCGCGCTGACCCCTATCACTGGG	3050	QY	4059	ACTTAGCTCTGAAGCACCGGAGGATGCTTCCGCTCTCAGCGTACTGAAACCGCATTTTA	4118
Db	545	ACGGTGAATGAAATGTTGTCCACTTACCGGCAACCGGCATGACACCCCTATCATCTGC	604	Db	1625	ATTAAACCCCGGTGAATCAAAAACCAATTTTTATTGGGAATAATGAACGCTGCTTCA	1684
QY	3051	CGTACAGCGCGCCGCCAAGCCATTTCTGGTGACGACCGGCGCTGATGGGGTTCAGCC	3110	QY	4119	ACATCAGCGCCCTCGGGGCTTTCCACGCTCTGGCAGTTGGCCAGCGGTGACAGAGCGCTG	4178
Db	605	CGTATGAGTCAGCCCGCTCAGGCAATTTTATGCAAGATAAAACCTCACCGCATTTAGCC	664	Db	1685	GAGTGAATGATACGAACTGATATACATATATGAAGCTGGCTAATGGCGGAACAAATCCAG	1744
QY	3111	GTAAATCGGATGCGCGCAGCTTATGGACCTCGCTCCATGCTGGCCATTAAGCCGATA	3170	QY	4179	GGTTAGCTGCTCTGCTGACAAATATCGCGCACTCTACCGAGTGAATCTCCCTGGCTGACA	4238
Db	665	GTAAATCAGACGAGCGGAATTAATGGACCAACATCGCTCTGGCTATTAAGACTGATA	724	Db	1745	AAITTTATGTTCCATCGGAAACCTGTCTCTCTTTATCGCGTTGCTCTGCTGGCAGACA	1804
QY	3171	TTTTCACCGGAGCTGTATCAGATACTCGCCGAAGAAATTAACGACAGACAGTTACGAAGCAC	3230	QY	4239	TCACGACCATATCCGCTGGTGAGCTGTCAATGTGTGCTGCTCCCTCTCCCTTTTCAGCGGG	4298
Db	725	TATCGCTGNAITGTATCAATCTTGTAGAAGAAATTAACCGGAAATTTCAACAGAAC	784	Db	1805	TTTCATCACTGACAGTGAATTAATCAATGTTGTTGTCGTTCTCCCTATGTGAACA	1864
QY	3231	TCGTGAGTAAAGATTTTGTGATATGCCCTCCCTCTCACTGTATCTTATGATGCACTTG	3290	QY	4299	TGGCGCGCGCTCGCTGTCCGATATAGCTGACGCA-----GTTTCTGTACCAGA	4349
Db	785	TGATGAAGAAAAATTTCCGTACAGATGATGATGATTTTAAAGAGTTATGCTTCTTTGG	844	Db	1865	CGAAAAATGCCCCCTTTTCTGATACAGCAATTAACGCAATTAATCAGCTTTCTGTTCCAAT	1924
QY	3291	CAACATTTTATGATCTTGATGATGAGTAACTTTCGTTATTTGTTCAATTAAGCGTGGACT	3350	QY	4350	CCACACCTGGCTCAGCGGACAGGCTGGAAGCTCAGCGATGTTTCTGATGCTGACGA	4409
Db	845	CTCGCTACTACGATTTGTCTTATGATGAATCAGTTTATTTGTCATCTCTCTCGGTA	904	Db	1925	GCACCGAGTGGCTGACACACAGAAATGCTGTGATGATGTTTCTGATGACCAACCG	1984
QY	3351	TTTCAAAATCAAAATGAATACATCAATTAATAGTCAATTAAGTGTGCTAACTCTGAATG	3410	QY	4410	CGCAGTACGGTACCTGCTGACCCCGCAATTTAGAAACCTGCTGCTTCCCTGCGCAACG	4469
Db	905	AGAAATACAATCAACAGTATAAGATCAGCAACTGATACATTTGGTCAATGACGGGA	964	Db	1985	ATAATTTACAGCACTGCTCTTACGCGGATATTTGAAACCTTATCAGCACACTAAGTAATG	2044
QY	3411	AAAGCACTGTTTAAATACATACATTAATTTAAGAACGCTGAGCGGAGACTCAACG	3470	QY	4470	GACTGTGGGCGCTGAGCTGTTCCCGGAAAACGCTCCCGCGCATGGCGCTCCTTTATTG	4529
Db	965	ATGATACGGCAACCGCAAGATTTGATTAAGCGAACCCGCAAGATTTCTACGATTCACAT	1024	Db	2045	GATTATCAACACTTTCACTCGGTGATGACAACTGATCGTCAGCTGCGCGCTGATTTG	2104
QY	3471	AGATTAACCTGAGCTTATACCTTATGGGATGGAACATATCTTTAATATTTTACGCGTG	3530	QY	4530	CGCGCCCATGAGCTGGAAGCCACCGATACGCGGAAGCGATGCTGACTTGGCGGACCC	4589
Db	1025	TAACTATGAGAACTAAATTTCCAAATCAAGAAATGAATACAAATATAATTTTCAAGTAA	1084	Db	2105	CTGCAGCATTTCAATGATTTTCAAGACAGCAGCAAACTATTTGCTGTGATTAATC	2164
QY	3531	TGTCAACGATATCAGAGGATAGTTTCAAACTAGGGTCTGTTAGTCTTCAACAGTAGCAATC	3590	QY	4590	AGTTGAAGCAGAGGGGCTGACGCTGACGGAATTTATTTCTTTTGTGTGATGAATGCGCCC	4649
Db	1085	AAAAAACAGAACCTGACCACTTGGATTTTCGTCTCCAGAACTGGAGATAAGAATATATAT	1144	Db	2165	AGATAAAACCAACGAGCTGACATTCGATGATTTTCATGATTTTGGCGCTAACCGTGATC	2224
QY	3591	TTTACTCTGGGATATACGCTTCAAAAGGGGTTGCTTATAGCATTTCTGTTGAATAG	3650	QY	4650	CAATTAAGCAGCAGCGGGCGCAGATGGCAGGGTTCTGCCAACCTGTGCGCACTGGCAC	4709
Db	1145	ACCAAGATAAAATTTTCGTCCCAATTTGCTAATACCAATTAACGATTTCCCAATTAATGA	1204	Db	2225	GCTCAGAGAAATGAACCAAGCAATGGTGGCTTTTTTGTGATGATCTGGGGCAACTTCTC	2284
QY	3651	ATGAAGGAAGTTAAATGATGGGATCACAATAGGATTTGATGAGNAA-----G	3698	QY	4710	TGATCATCGCAGCACCGGCTCAGCACGCGGAGCTGACGCTGCTGCTGCTGAGCAGCCGG	4769
Db	1205	CGACAGCAAAATCAACAACGGTATTAACACTCCGCTTATGGGAGTTAAACCAATCCGT	1264	Db	2285	TGATTTGGGCAATATTGACTCAGCGAACAACGAATGACCTGTGTTGTCACAAACCGG	2344
QY	3699	GGGGGGGATATTAATCAACAGTAACTTCACTCTGATGAATATGATCTCTGGCATTTCA	3758	QY	4770	GACGCTTCGCAACAGGATGGCAACCATCTGCCCATGACCTGCCGGGCTTCGCGCATTA	4829
Db	1265	CGGATGCTCAATGCAATGCTACTTTAAATGATGAGTTCCCGGTGATATATCC	1324	Db	2345	AGAAATTTCAATCAGAAACCAACAGCACTGCAACATGATCTCCCACTTTTGAAGCGCTGA	2404
QY	3759	TTCTTAAATTAATAAGTTATCCGCTTATACGCGCAAGGGCATGACGCGCGGAAA	3818	QY	4830	CGCGTTTTCATCGCTGTTAAACCGCAGCGGACCATGCGGGGAGGTCTTGACCGCAC	4889
Db	1325	TGTTAAAGCTGAATAAAGCGATTCGTTTGTATTAAGCCACAGGCATATCTCCAGAAGATA	1384	Db	2405	CCGCTTCCATGCTGATCATCGCTTGTGAAGCTACGCGACAGAAATCTTTAAACAGCAT	2464
QY	3819	TATATCAAAATCACAATATTTTAAACGGTCTCACCATTTGACCATGCGGCTCTCAGTA	3878	QY	4890	TTGAGACCGGAGAACTGCTGCTCAGCCCTGCTGCGCCCGGCGCTGTGCAGAAATGAGCAG	4949
Db	1385	CTGGCAAGTATAGAAAGTATTTATGATGACTTAACCATTTGACCAATGTTGGGTA	1444	Db	2465	TGGAATAGGAGCGCTGACTGCGCAACAAATTTGGCGGTGGCGTTAAATTTTGTGCTCAGG	2524
QY	3879	AAATCTTCCTGGTCCGTTACCTGATCGCTCACTATCAGCTTGTATGTGGCCCGGTCACTGA	3938	QY	4950	ATGTGACCGGCGCTTGGCGCAGGTGAGGGGCGCGGTGAAACAGGACAAACAGCGTGTCA	5009
Db	1445	AGCTGTTTTATGTTCAATATTAATGACGACTATAATATTAAGCGTCAGCATGCGCTG	1504	Db	2525	TTGTGACACAAGCAATTTGCAACAGACCGGTTTGGAGTGAATACC-----TTTA	2572
QY	3939	TATTTGCAACGAAACCATCAGTGACCGGCTTACGCGCGGAAACCGGCTGTTTCAACA	3998	QY	5010	CCTCTCTGGGAAGGTGGACAGGCTGAGCAGTGGCTGGACATGAGTGAGACCTGTCCA	5069
Db	1505	TATTTGTCTATCAGATATCAGCCAATATTTCCACTAAACAACCAACCCGCTATTTTACAA	1564	Db	2573	CAAACTGGAGAACTATAGATGTCACTCTGCAATGGCTGGATGTGCTGTCTATTGGGTA	2632
QY				QY	5070	TTACGCCATCCGCTCTGGCTAGCTGATTTGCCCTGAAAGTACATCAATGTGTCGATGACA	5129





QY	6992	-----	6991
Db	4850	CTGAAAGACCAATATTGGTATTGATAATGTTTAAAGTATGGAAACGCAAAATTTTACCAG	4909
QY	6992	-----	7032
Db	4910	AGCCGCAATAGGTGAAGGTTTATGCGACATTTAAAGTTGCCCCCTACAAATAAGAGG	4969
QY	7033	-----	7079
Db	4970	AGCATGGTATGAACGTTGGTTTAAAGATCCATATTGGGAATATTGATGGCAATTTCTGCCA	5029
QY	7080	-----	7101
Db	5030	GACAACTTATTACGAAGGAATGTTATCTGATATTGAAACCCACGATGACGCTTTTGGTTC	5089
QY	7102	CGTTATCGCATTACGTTAAATAATACGCGTGGCGGAGTATATTCTGTTTCACTGCGGGTAA	7161
Db	5090	CCATGCTAAAGGATATTACATACGTGAAGGTGTCAGATTAGGGTTGGGTACAAAAA	5149
QY	7162	CGATGGGCGCTTATTGCGCTCMAACCCCTCTTTTGGCCCGCAACTGGTGA	7212
Db	5150	TTATCTATGACAAATCTCGGAATCTGCTTCTTTTATTGATGAGACGAAAAATCAAT	5209
QY	7213	-----	7241
Db	5210	TTATATTCAATTATGATGCGGATCATGATTCGGGAATGACAAACAGGGGATAGTAAAAA	5269
QY	7242	TTTCCATGGAGACCCAGAGCTTTACCGAAACCGCCCTCGGAAGGGGAGTGTGTTTAA	7301
Db	5270	ATATCAAAAATATAAAGGTTTATTTCATGTCGTTCATGAAAATAACACTGAAACCA	5329
QY	7302	TGGACTTCTCGGAGCAATGCCCTCTATTCTGGGAGCTGTTCTATTACAGCCGATGA	7361
Db	5330	TGGAATTCACCGCGGCAATCAATCTATTCTCGGGAATGTTCTATTACAGCCCAATGA	5389
QY	7362	TGCTGTTCCAGCGGTTGTTGCGAGAACAGCACTTCCGGAAGCCACCGCTGGCTGCAGT	7421
Db	5390	TGTTATTCAGCGCTTATTGCAAGACAGAAATTTTACCGAATCGACAGCTGGCTCGCT	5449
QY	7422	ATGCTGGAACCCGCGCGGACAGTGTGTAACCGGGTGTGCAAGAAATTACACTGGAATG	7481
Db	5450	ATATCTGGAACCCGCGCGGATATTGCGTTTCAGGGTGAATGAGGATTTATTCTGGAACG	5509
QY	7482	TCCGTCGCTGAGGAGGACACCGGCTGGAAACGACTCGCGCTGGACTCATTTGACCCCG	7541
Db	5510	TCCGCCCATTTGGAGGAAGATACGTCCTGGAATGSCCAATCCGCTGGATTCCGTCGATCCTG	5569
QY	7542	ATGCAATAGCCCAATACGACCCCATGCTATTACAAGGTCCCACTTTTATGTCTACTCTCG	7601
Db	5570	ACGCCGTTGCCAGCATGATCCGATGCACTATAAGTGGTACTCTTTATGAAAATGCTCG	5629
QY	7602	ACCTGCTGATTGCCCGGTGATGCGCCCTACCGGCTGCTCGAGCGGACACCTTTAAGC	7661
Db	5630	ATTGTTGATTACCCGCGGAGATAGCGCTATCGCCAGCTTGAACTGATACCTTAAACG	5689
QY	7662	AGGCCGGATGTTGGTACGTCAGGCCCTGAACTTCTGGCGACGAGCCCTATTATTCCT	7721
Db	5690	AAAGCTAAATGTGGTATGATACAGGGCGCTCACTTTATTGGGTGATGAGCCCTATTATTCAT	5749
QY	7722	TTGACCCGACTGGTCGGCGTTGAACCTTGGTGACGACGACGAGGTTGAGCGACGCG	7781
Db	5750	TGGATAAACGATTGGTCAGAGCCACGGCTGGAAGAGCTGCCAGCCAAACATGCGGCATC	5809
QY	7782	ATTACAGGAGGCCCTGCTGGCGGTGCGCGGTGGTGGCCCGCTCCCGGACACGAGCGG	7841
Db	5810	ATTATCAACATAAAATGCTGCAACTGCGTCAGCGCGCTGCAATTACCACGAAAGGTACGG	5869
QY	7842	CGAATTCCTGACGGCACTGTTCTCCCGCAGCAGAACAGGTGCTCAAGGCTACTGGC	7901
Db	5870	CAAAATTCGTTAACCGCATGTTCTCCCTCCCTCAAATTAATAAAAACTGCAAGGTTACTGGC	5929
QY	7902	AAACCTTTGSCACAGCGGCTCATAACTCGCGCACAACTCTCTCATTTAGCGGCCACGCCG	7961
Db	5930	AGACATTTGACGCAAGCCCTTATACTTACGCCATTAACCTGAAATTCGACGGTCAGCCAC	5989
QY	7962	TTTCCCTGTCCTTACGCCACGCGCTCGAAACCGTCCGCCCTCGAGAGTGGCGTGTCA	8021
Db	5990	TGTCATTATCTCTCTATGCCACGCCCGCAGATCCGTCCTATTTACTCAGTGTGCCATCA	6049
QY	8022	ACAGCGCGAGGTTGTCAGCACTGCGCGCCGCGGTGATGCGGCTTTACGTTTCCCGG	8081
Db	6050	CTGCTTCAAGCGCGCGGATTTTACCTCATGCAATGATGCCGATGATACCGTTTCCCG	6109
QY	8082	TCATGCTGAGAAACGCCCGGGGATGTTGAGCTGCTGACCGGTTTCGGCAACACACTGC	8141
Db	6110	TGATTTCTGAAAATGCCAAGTGGGGGTNAGCCAGTTGATACAAATTTGGCAATACCTGC	6169
QY	8142	TCGGTATTACCGAGCGTCAGGATGCGAGGCGCTGCCAAAACCTGTGACAGCCAGGGCA	8201
Db	6170	TCAGCATTTACTGAACGGCAGGATGCAGAAAGCTTGGCTCAAATCTGCAAACTCAAGGCA	6229
QY	8202	GTGAACTGATAGCCAGGCGCTTCCGACGACAGATAACGTCCTCGAGGAAATCGATCCG	8261
Db	6230	GTGAGTTAGCCCTGCAAAAGTATTAAATGACAGATAAGGTCAATGGCTGAAATTTGATGCTG	6289
QY	8262	ATATTGCCCGCTGAGGAGAGCCGCGCGGCGCGCAGATGCGTTTGAACGTTACAAAG	8321
Db	6290	ATAAATTTGGCGTTCAAGAAAGCGCTCATGTGTCAGTCTCGTTTGTGACAGTTTCAATA	6349
QY	8322	TGTTGTACAGCGGACGTCACACCGCGCAAAAAACAGCCCATGGAATTTGTACCTCAGTT	8381
Db	6350	CGCTGTACGACGAAGATGTTAACGCTGGTGAATAAACAAGCGATGGATCTTTACCTCTCTT	6409
QY	8382	CGTCCGTGTCGCGCATCAACCGCGCGCTCTTTTGGCCGAGGCGCGCGCATATGC	8441
Db	6410	CATCGCTCTTGACACCAAGCGGCACAGCCCTCATATGGCCCGCGCGCAGATCTCG	6469
QY	8442	TGCCCAATTTTACGGGCTGGCGCTCGGGGCTCCCGCTATGGGGCACTATTATAAGCCA	8501
Db	6470	TCCCAATATTACGGTTTGTGTGGAGGTTCCCGTTTGGGGGCTTTTCNATGCCA	6529
QY	8502	CGCCCATCGGCATCCAGGTGTCCTCCGATGCCACCGCATATCAGCGGCAAAATCAGCC	8561
Db	6530	GTGCGATTGGTATCGAAATTTCTGCGTCAGCAACAGTATTTCGCGCAGACAAATCAGCC	6589
QY	8562	AGTCGGAAGTGTACCGCGCTCCGCGGAGGAGTGGGAATCCAGCGTGATGTAGCGCAGT	8621
Db	6590	AATCAGAAATATACCGTCGCCGTGCGCAAGATGGGAAATTCAGCGCAATATATGCGGAAG	6649
QY	8622	CTGAGTGGCGCAGATTGATGCCCGCATGCGCGCCATGCGCAGTGGCCCGGAAGGGCTG	8681
Db	6650	CTGAGATAAAACAAATTTGATGCTCAATTAGCGACGCTGGCTGTACGTCTGGAAGCGCAG	6709
QY	8682	AGCTGAGAAAACTTACCTTGAGACCCAGCAGACCCAGGCAAGGGCGCATGTTGGCATTC	8741
Db	6710	TATTACAAAAAACTATCTGGAATCTCAGCAGGCAAACTCAGGCGCAGTTAGCCTTTC	6769
QY	8742	TGCAGATTAAGTTCAACATACGCTCTGTACAGCTGGCTGGCGGCGCAGGTTTTCGCCCA	8801
Db	6770	TGCAAGTAAATTCAGTAATCAGCGCTATACAACCTGGCTCCGTGGAAGGTTGTCTCGCTA	6829
QY	8802	TTTTATTACAGTTCTATGACCTGGCAGTATCCCGCTGCTGATGGCGCAACAGGCTGGC	8861
Db	6830	TTTTATTACAGTTTATGATTTGGCGGTCTCACTCTGTTTATGCGAGCAAACTTATC	6889
QY	8862	AGTGGGA---TAAATTCGAGACTAGTCTGTTTATCAGCCGGGGCTCGATGGGGGCAA	8918
Db	6890	AGTATGAATTTGAATAATGCGCAGCACACTTTTATTAACAGGTGCTCGCATGGACTT	6949
QY	8919	ATGCGGCTCTGTCGCGGGGAAACCTGATCTGATCTGATCTGCGCAGATGGAGCAGCT	8978
Db	6950	ATGCGGTTTATTAGCGGGTGAACCCCTGATGCTGAATTTAGCACAGATGGAAAAAGCT	7009
QY	8979	GGCTGACGGGGATGAGCGGGCAATAGAGGTGACGCGGACGGTCTGCTCTGCGAGGTCT	9038

Db 7010 ATTTGAAAAAGATGAACGGGCACTGGAGGTGACAGAAACGGTTCTCTGGCTGAAGTGT 7069  
 Qy 9039 ATACAGCTCGCGGAGGATCGGCATCTCTCTGGCGCAAGAGTGGTGAACCTGTCA 9098  
 Db 7070 ATGCTGGTCTGACAGAAAT---AGTTTTCATTTTAAAGATAAAGTGAAGTGTGTCA 7126  
 Qy 9099 GTAAAGGTTGGGCGAGTGGGTTACGAAAGCAACGGAATTACAGATGGATCAACAGCAAC 9158  
 Db 7127 ATGAGGTTGAAGGCGAGTGGGCGACAGCTTAAAGGTTTGAACGTCGAAGGACACAA 7186  
 Qy 9159 TCGAGGCAACCTGAAAGTGGCTGACCTCGGTATCGGATCGGCAACGATTAACCGGTCTCCCTG 9218  
 Db 7187 TGAAGCGAGCTCAAAATTAATCGGATCTGAATATTGCTTACCGATTATCTCTGACCGTTT 7246  
 Qy 9219 GCACCATGAGCGCATCAAAACAAATAGCGTACAGCTCCGCGCGCTGGTCCGCCCTATC 9278  
 Db 7247 GTAATACAGCGGTATCAACAAATCAGTGTGACATTAACCTGCGCTTTTATAGGCGCTTATC 7306  
 Qy 9279 AGGAGTTCGGGCAACTACTAAGTTATGGGCGACACAAATGATGCGGCTTTCAGCG 9338  
 Db 7307 AGGATGTTGGGCAACTACTAAGTTATGGGCGACACAAATGATGCGGCTTTCAGCG 9366  
 Qy 9339 CGTGGCGGTCTCACAGGAATGAACGACAGCGGCAATTCGAATGGAATTCGAATGAC 9398  
 Db 7367 CGATTGGGATCTCATGCGCATGAATGACAGTGGTCAATTCAGATGGAATTCGAATGATG 7426  
 Qy 9399 GCGGTTACCTGCGCTTTCAGGACTTCCAGTTGATGACAGGAGCCCTGACACTGAGCT 9458  
 Db 7427 CCAAGTACCTGCCATTTGAAGGGCTTCTGTGGCGGATACAGGACAAATTAACCCCTCAGT 7486  
 Qy 9459 TCCCGGATGTCGAGCGCAACAAACAGCGGATGCTCTCAGTCTGAGCGACATCATCTGCG 9518  
 Db 7487 TTCCCGGTATCAGTGTAAACAGAAAGCTTATTGCTCAGCTGAGCGATATCATCTGCG 7546  
 Qy 9519 ATATCCGTTACCACTT 9535  
 Db 7547 ATATCCGTTACCACTT 7563

RESULT 7  
 US-10-754-115-13  
 ; Sequence 13, Application US/10754115  
 ; Publication No. US20040208907A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hev, Timothy  
 ; APPLICANT: Schleper, Amanda  
 ; APPLICANT: Bevan, Scott  
 ; APPLICANT: Bintrim, Scott  
 ; APPLICANT: Mitchell, Jon  
 ; APPLICANT: Li, Ze Sheng  
 ; APPLICANT: Ni, Weiting  
 ; APPLICANT: Zhu, Baolong  
 ; APPLICANT: Merlo, Don  
 ; APPLICANT: Apel-Birkhold, Patricia  
 ; APPLICANT: Meade, Thomas  
 ; TITLE OF INVENTION: Mixing and Matching TC Proteins for Pest Control  
 ; FILE REFERENCE: DAS-104Xc1  
 ; CURRENT APPLICATION NUMBER: US/10754,115  
 ; CURRENT FILING DATE: 2004-01-07  
 ; PRIOR APPLICATION NUMBER: US 60/441,723  
 ; PRIOR FILING DATE: 2003-01-21  
 ; NUMBER OF SEQ ID NOS: 64  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 13  
 ; LENGTH: 7569  
 ; TYPE: DNA  
 ; ORGANISM: Xenorhabdus nematophilus  
 US-10-754-115-13

Query Match 7.2%; Score 1364.6; DB 18; Length 7569;  
 Best Local Similarity 52.5%; Pred. No. 0;  
 Matches 3943; Conservative 0; Mismatches 3064; Indels 510; Gaps 23;

Qy 2511 TGACGGATTTATTCTCGCGTTTCTGTTCCGAGGTCAAAAAATCACTGGCGACAGCCTGT 2570  
 Db 65 TGACAAACATTTCTGTTTATGTCTTTAGCGAATTTCTGTCATAGGCAAGTGGAACTCTGA 124  
 Qy 2571 CATGGGAGAGGTCTGCTATCTGTACAGTCAAGCGCAGACGAAAGAAAACCGCG 2630  
 Db 125 CGTGGCGAGAAAACAGACTTTTATATCAACAGGCTCATCAGGAATCAAAACAGAAATAAAC 184  
 Qy 2631 TCACCGAATCCCGTATTCTGCGCGGCGGAATCCCTACTGTTGGAATGCGGTTCCGCTGG 2690  
 Db 185 TTGAAGAACTGCGCATTTTGTCCGCTGCTAATCCAACTGGCTAATACCACTAACTT 244  
 Qy 2691 GAATACGGCAGGCGCGGCGAGTCTGATGACTATGATGCTGTTTGGCTCCCGCGCAGACC 2750  
 Db 245 ATATTACACGCTCAACCCTAACAAATAGTTACAACAGTTGTTTATGGCGGCGCCACC 304  
 Qy 2751 GTTTCGCGCCCGCGGCTCGGTGCGCTCCATGTTCTACCGCGCGGCTATCTGACCGAGC 2810  
 Db 305 GTTTTGTAAAAACCGGATCAATTTGCTTCCATATTTTCCAGCGGCTTATTTAACAGAA 364  
 Qy 2811 TGTACCGTGAAGCGAAGGACCTGCATCCGACACCTGCTGTTCCGCGCTGGACATCCGGC 2870  
 Db 365 TATATCGGGAAGCGAAGATTTTTCCTCTGCAATTTCTCAATATCACTTGAATAAACGAC 424  
 Qy 2871 GTCCCGACCTGCGCGGCTGCGCTTAGCCAGAAATATATGAGCAGCGAGCTCTCCACCC 2930  
 Db 425 GCCCGGACATGTTCTTCACTGGCACTGACACAGAAATATATGATGAAGAAATTTCCAA 484  
 Qy 2931 TGAGCCTGTCCAATGAGCTACTGTATGCGGTTATCGGGGCGAGGAGGCTTGACGAGC 2990  
 Db 485 TATCCCTTATCTAATGAATTAATCTGCTGCTGATAATATTCAGACGTTAGAGAAATGAC 544  
 Qy 2991 ACAGCTGAGGAGCTGCTCGCGGGTATCGCTGACCGGCTGACCCCTATCAGCTGGG 3050  
 Db 545 ACGTGTGAATGAATAATGTTGCTCCACTTACCGGCAAAACCGGCTGACACCTATCATCTGC 604  
 Qy 3051 CGTACGAGGCGCGCGCAAGCAATTTCTGCTGAGGACCGCGCTGATGGGTTCAAGC 3110  
 Db 605 CGTATGAGTCAAGCTGCGGCAATTTTATGAGATAAATAAACCTCAGCGATTTAGCC 664  
 Qy 3111 GTAATCCGATGCGCGCAGCTTATGACCCCTGCTCCATGCTGGCGCAATTAAGCGCGATA 3170  
 Db 665 GTAATACAGACGTAGCGGAATTAATGAGCCCAACATCGCTACTTGGCTTATTAAGACTGATA 724  
 Qy 3171 TTTTACCGGAGCTGTATCAGATACTGCGCGAAGAAATACGACAGACAGTTACGAAACAC 3230  
 Db 725 TATCGCTGAATTTGATCAAACTCTTGTAGAGAAATTTACCGGAAATTTCAACAGAAC 784  
 Qy 3231 TCTGGAGTAAGAATTTTGGTGATATGCTCCCTCCCTCCTGTTATCTTATGATGACACTTG 3290  
 Db 785 TGATGAAGAAAAATTTTCGGTACAGATGATGATGATTTTAAAGATTATGCTTCTTTGG 844  
 Qy 3291 CAACATTTTATGATCTTGATTAACGATGAGCTAACTTCTGTTTATGTCATTAAGCGTGGACT 3350  
 Db 845 CTCGCTACTAGGATTTGCTTATGATGAACCTCAGTTTATTTGTCATCTCTCTTCGGTA 904  
 Qy 3351 TTTCAATCCAAACAAATGAATACTACTATTAATAGTCAATTAAGTGTGCTGAATCTGAATG 3410  
 Db 905 AGAAAAATACAAATCAACAGTATAAGAAATGAGCAACTGATAACATTTGGTCAATGACGGGA 964  
 Qy 3411 AAAGCACTGTTTAACTAATCATCATCATTTTAAAGAACGCTAGGCGGAGACTCACAGC 3470  
 Db 965 ATGATACGGCAACGGCAAGATTGATTAAAGCAACCCGCAAGATTTCTACGATTCACATT 1024  
 Qy 3471 AGATTAAACCTGAGCTTATACCTTATGGGATGGAACATATCTTTTAAATTTTTCAGCGTGG 3530  
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 Qy 3531 TGTCAACGATATCAGAGGATAGTTTCAAACTAGGGTGTGTTAGTTCTTAAACAGTAGCAATC 3590  
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3591 TTTACTCTGGGATTTATCAGCTTCAAAAAGGGGTCGCTATAGCATTTCTGTGTAATAG 3650  
1145 ACCAAGATAAAATTTTCGTCCTCCCATTTGCTATATACCCATTTACAGTATTTCCATTAATTTGA 1204  
3651 ATGAAGAAAGTTTAAATGATGGGATCACATAGGATTTGAGTAGAAA-----G 3698  
1205 CGACAGAGCAATTCACCAACGGTATAACATCTCCGCTTATGCGGAGTTAAACCAAAATCCGT 1264  
3699 GGGGGGATATTAATCAACAGTAAACTTCACTCTGATGTAATGATCTCGGATTTCA 3758  
1265 CGGATCGTATCAATGCGCAATGCATCTTTAAATGATGAGTTTCCCGGTGATATATTC 1324  
3759 TTTCTAAATTAATAAGTTATCCGCTATACAAAGCCACGGCATGACACAGCGCGAAA 3818  
1325 TGTAAAGCTGAATAAAGCGATTCGTTTGTATAAAGCCACAGGCATATCTCCAGAAGATA 1384  
3819 TATATCAAAATCAACCAATATTTCTTAATAACGGTCTCACTTAATGACATGCGGTCTCGAGTA 3878  
1385 TCTGGCAAGTAATAGAAAGTATTTATGATGACTTAACCATTTGACAGCAATGTGTTGGGTA 1444  
3879 AAATCTTCTGGTCCGTACTCTGATGGTCACTATCAGCTTGTATGTTGGCCGCTCACTGA 3938  
1445 AGCTGTTTATGTTCAATATATATGACGACATATAATATATAGCTCAGCGATGCGCTG 1504  
3939 TATTGTCAACGAAACCATCAGTGACACAGCGCTTCAGCGCGGAAACCGGCTGTTCCACCA 3998  
1505 TATTGTCTATTCAGATATCAGCAATATTTCACTAAACAAACCAAGTCATTTTACAA 1564  
3999 CGCTGTTCAACACCCCAACCGCTGAACGGCAGCTGTTTCTGAGATGATACCCCTCG 4058  
1565 TACTGTTCAATACACCGCTATTAATAGGCGCAAGTCTTCTGCTGATATAACCAACTG 1624  
4059 ACTTAGCTCTGAACACCGGAGATGCTTTCGCTCAGCTGACTGAAACGGCATTTTA 4118  
1625 ATTTAAACCCCGGTGAATCAAAAACCAATTTTATTTGGGAATTAATGAACGTCGTTTCA 1684  
4119 ACATCAGCGCTCGGGCTTTCCACGCTCTGGCAGTTGGCCAGCGGTGACAGCAGCGCTG 4178  
1685 GAGTGAATGATCTGAATCTGATACATTTATGGAAGCTGCTATGCGGNAACAATCCAG 1744  
4179 GGTTTAGCTCTCTGTGCAATATCCGCGCATCTTACCGAGTGAACCTCTGGCTGACA 4238  
1745 AATTTATGTTCCATCGAGAACTGCTCTGCTTTATCGCTTATCGCTGCTGCGCAGACA 1804  
4239 TCCACGACCTATCCGCTGGTGAAGCTCAATGTTGCTGCTCCGCTCCCTTCCAGCGGG 4298  
1805 TTTATCATCTGACAGTGAATGAATATCCATGTTGTTGCGGTTCTCCCTATGTGAACA 1864  
4299 TGGCCGCGGCTCGCTGTCGATAATGAGCTGACGCA-----GTTTCTGTACCAGA 4349  
1865 CGAAATTTGCCCTTTTCTGTATACAGCATTAACGCAATTAATCAGCTTTCTGTTCCAT 1924  
4350 CCACCACTGGCTCAACGAGCAGGGGTGACGGTCAAGCATGTTGTTCTGATGCTGACGA 4409  
1925 GCACCCAGTGGCTGACAAACAGAAATGGTCTGCTCAGTGAATGTTTCTGATGAACACGG 1984  
4410 CGCAGTACGTACCTGCTGACCCCGCATTTGAGAACCTGCTCGCTTCCCTCGCAACG 4469  
1985 ATAAATACAGCATGCTCTTACCGCGGATTAATGAACCTTATCAGACACTAAGTAATG 2044  
4470 GACTGTGGGCGCGTGAAGCTTTCCCGGAAACGCTCCCGCGCATGGCGTCTCCCTTTATG 4529  
2045 GATTATCAACACTTTTCACTCGGTGATGACGAACCTGATCCGTGCGAGCTGCCCGCTGATTG 2104  
4530 CCGCGCATGACGTGGAGCCGACGGAATACGGCAAGGCGATGCTGACTTGGCGCGGACC 4589  
2105 CTGCCAGCATTTCAATGGATTTACGCCAAGACAGACAGCAAACTAATTTGCTGTGATTAATC 2164  
4590 AGTTGAAGCAGAGGGGCTGACCTGACCGAATTTATCTTTTGTGATGAATGCGGCC 4649  
2165 AGATAAACCAAGAGCTGACATTTGATGATTTTCATGATTTATGCGGCTAACCGTGATC 2224  
4650 CAAATGACAGCAGCGGGCGCAGATGGCAGGGTTCTGCCAAGCCCTGTGGCAACTGGCAC 4709

2225 GCTCAGAGATGAACACCAACAGCAATGTTGCTTTTGTGAGTACTGGGCAACTTCTC 2284  
4710 TGATCATCCGAGCACCAGCCCTCAGACCGCGGAGCTGACGCTGCTGTGTCAGCAGCCGG 4769  
2285 TGATGTTGCGCAATATTTGACTCAGCGAAACGAACGACTGACCTGTTGGTGACAAAACCGG 2344  
4770 GAGCTTCCGACAGATGGCACCATCTGCCCATGACCTGCGGCGCTTCGCGACATTA 4829  
2345 AGAAATTTCAATCAGAAACCAACAGCACTGCAACATGATCTCCCACTTTTGAAGCCCTGA 2404  
4830 CCGCTTTTCATGCGCTGCTTAAACCGCAGCGCAGCATCCCGGGGAGGTCTCTGACCGCAC 4889  
2405 CCGCTTTCATGCTGTGATCATGCGTTGTGGAAGCTACCGCAGACAGAAATTTTAAACAGCAT 2464  
4890 TTGAGACCGGAGAACTGTCTGTCAGCCCTGCTGCGCGGCGCTGTACAGATGAGCAGG 4949  
2465 TGGAACTAGGAGCGCTGACTGCGCAACATTTGCGGTGCGTTTAAATTTGATGCTCAGG 2524  
4950 ATGTGACCGCGCTTGGCGCAGGTGAGGGGGCGGTGAAACAGGACACAGCGTGTTC 5009  
2525 TTGTGACACAAGCATTTGCAACAGACCGGTTTGGGAGTGAATACC-----TTTA 2572  
5010 CCTCTCTGGGAAGAGGTGGAACAGGCTGACAGCTGCTGACATGAGTGAGACCTCTCCA 5069  
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5070 TTACGCGCATCCCGTCTGCTGACCTGATTTGCGCTTGAAGTACATCAATGTCGATGACA 5129  
2633 TTACCCCGATGCTGCTGCTGACCTATAAAATTAATAATATATCGTGAACCAAGAACCC 2692  
5130 GTGCAACGTTGTACAGCAGTGCAGGTGATCCGCTGCTGTCAGGCGCGGCTGAAA 5189  
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5190 GCAGCCAGAGCTCGGCGCTGACAGATTTATCTGAGAGGGGACACAGCAGCGCTTTGTG 5249  
2753 GTCAACAATCCGACAGCTTCAGGCATGCTGATGAAGCCACGACAGCAGCGCCAGTG 2812  
5250 CGTATTTATCTGCTGATCTGCGCACCGAATGTTATCCGGGCGCGATGACCTCTTCGGGT 5309  
2813 CTCTACTACATAAAATATGTCACCTCAACAGATTAAGAGCGGGATGATTTGTACAGCT 2872  
5310 ATCTGCTGCTGATATCAGGTGTCAGCAAGCTAAACCAACCCGCTTTGCGGAGGCCA 5369  
2873 ATCTGCTGATGATTAACCAAGTTTCTGCCAAGTGAACCAACCCGCTGTGGAGAGCCA 2932  
5370 TCGCGGCATACGCTGTATATCAACCGGCGCTTTAAACGGAATAGAACTCAGCGCCATG 5429  
2933 TTGCCAGCATTCAGTTATATGTCACCGGCGTTGAATAATGTTGAAGGAAAGTATCAA 2992  
5430 CAGAGTGAAGGGCGTCAAGTTTTCATGCTGAGTACGTTCAACAAACGTTACAGCA 5489  
2993 AGCCAGTGAACCCGCTCAGTTCTTCTGCGACTGGGAAACCTTACAAATCGACGATAGCA 3052  
5490 CTTGCGCGGCTCTCAGAGTGTACTATCTCCGAAAACCTACCTCGACCCGAGCGTCC 5549  
3053 CTTGCGCGGCTCTGAGCTGAGCTGAGCTTATCTCCGAAAACCTATCTGACCCCAAGTTTC 3112  
5550 GTATCGGGCAGACCGGCTGATGACACCTCTGCTGAGTCTGTCAAGCCAGAGCAGTATCA 5609  
3113 GTATTGCTCAGACAGTATGATGAACAACCTGTTTACAGCAACTTTCCCAAGTCAAGTTAA 3172  
5610 ACGCGATACCTGGAGGATGCTTTAAACCTATCTGACAGCTTTGAGCAGATTTGCCA 5669  
3173 ATATCGATACCTGTGAAGATAGCTTTTAAATAATTTATCTGACCGCATTTGAAGATGTCGCTA 3232  
5670 ATCTGAACACTGTCAGCGGATATCAGATAACCGCAGCATGACGAGGGGACTTACATGCT 5729  
3233 ACTTGACGCTGATAGCGGATATCATGACAGTATCAATGCTCAATGAGGAGTCACTTAT 3292  
5730 ATGTGGTTCGACGATCAGATCAGACTAATGTTGTTGCGCGAGCGCCAAACAGCA 5789

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Qy 5790 AAATCCAAAGACTCAATGATGCCCGGAAATGCTGCGAGCGGATGACAAAAAATTAAGTGG 5849  
Db 3353 AGTGCCAGCAGCGTCAATTTGCTGCGCAATGCTGGGAGATGAAAAAATTTGAAATAC 3412  
Qy 5850 GAATGAATCCGTGTCAGATCTTGCTGCTCGGTGTTTTTCAACAGTGGCTTTATGTGCG 5909  
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Qy 5910 TCTGGGTGGAAGAGAAATCAGTCTCTGATACGGAGGAGAGACACCAACAGCAGC 5969  
Db 3473 TGTGGCTGGAACAAAAGAGCTGAAAATGAAGTGAAGATGGCAAGATAGATCACTG 3532  
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Db 3533 AT---TATATATTAAGACTGTACATATTGTTATGATGGCAGCTGGAGCTCACCCTTTA 3589  
Qy 6030 CGTTGCGACATTTACCGGCAACATCGATTTCCGG-----AAACGAGGGGATGCGATGTG 6082  
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Qy 6083 ACCTGTAATCCCTGACTGAGCAGCTCTATTGCGGTTTTTACTCCGTACCCAGCAAGCGG 6142  
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Qy 6354 ATTCTAAAACTAAGTACTGTTTTTACTAATGAAGATTCCTCTCTTTTACGCCAGCAGC 6413  
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Qy 6414 TTCATATTAAGCAAAATGTTGCTGTTTTGTTAGTAC-----TG 6452  
Db 4010 ATTTTTCAAAAGGCAATATATATATATGATGAGGTAAATACCTGTTATCGATGATAGAG 4069  
Qy 6453 CTGGCATCGCCACTCAATCTACCATAGAAAAATTCGTTTCAGGCGAGGATAGAAATTTGAGG 6512  
Db 4070 ATGAAACGGTTATTTTATTTGATATGATAGACATGATGAATGCTTGGAAAAGAGAAG 4129  
Qy 6513 AAATTAAT-----TTTTATGAGGCCAGGCCCGCGCGGATTTGACGG 6555  
Db 4130 AAGTTTTTCTATATGAACTTTGGAATTTTATTTTCCATCGATCTTTAAAAATGCGCGAAT 4189  
Qy 6556 ATTTGCGGAGTGGATCTTCTAATTTCAAAGATATACAGGTC-GGAAAAGAGCAGTTG 6614  
Db 4190 ATTTTGAAGTGTAAATGCATCTAAGAACCAAGGAAAAAATTTCTAGAAAAATCAGAAATG 4249  
Qy 6615 GTGTCACTGAAAAATCTTATTCGCTCACTGGCGTTAGTGGTT-----CTGTTGAGTTATT 6669  
Db 4250 GAGTTGGTATAAATATGATTTATGAATCAATGATGCTGAAATTCAACTTGTACTAAACA 4309  
Qy 6670 TATTGATTCATCAAAATAAATCTTACGGGAAATTTTGTTCAGATA---AAATGATAACCGC 6726  
Db 4310 TAGTATTAGATTGGAAGATAAACACAGGAGTATGGCATACTATATGTGATCAATCAATTA 4369  
Qy 6727 TTTAATTTAGCGGAGTACATCAAAAGTAAATTAATGCTGCTCTATTGGCTCTCAAGATTT 6786  
Db 4370 ATGATGTTTCAATCAATTAATGAATGGGAAATATTTGGGCACTGTTCTTCCGCGAGGATC 4429

Qy 6787 TTGAGGTGTAAGTGCCTCATGCGGCACCTTCAGATATATGAATTAATTCGATGATATCAT 6846  
Db 4430 CATGTGTGATTTATTTGTTCAATAGCCACAGATATAAAAATGCTTCACTATGATCGAAC 4489  
Qy 6847 ACTGACATCCGGGTAAATGGGACTGAAATTTAAATCTCTGGCCTT----- 6890  
Db 4490 AGATCCAAAGATAAAAAACATTTAGTTTTTTTATAAAAAATGGCTCTGATATTTCTAGTGGAGT 4549  
Qy 6891 -----CCGCTGAAATGGTATAATGATGAAGTCTGAGTCTGCAATCCGGAAATAT 6937  
Db 4550 TAAATGCTGAAGACCATGTGGCATCTAAACCTTTCACACGAATCTGACCCCTATGTTATG 4609  
Qy 6938 CTTTTCACACCAAAATCGCTGAGTTTTTA----- 6965  
Db 4610 ATTTTAATCAAGTAAAGTTGATATTGAAGCTATGATATTCCTCTGCTGAGCGAGTTTA 4669  
Qy 6966 -----CGTTTAATACCAAGTATGATTTGTTGAA----- 6991  
Db 4670 TTATTAAAGCAACCGGCGGTTTATAACGATATTGTTATTGAATCGCCAATTCATATAA 4729  
Qy 6992 ----- 6991  
Db 4730 AACTAAAAATCCAAAGATAACAAGTATATCACTGCAATAAATGCCATCAGGCACAC 4789  
Qy 6992 ----- 6991  
Db 4790 AATATATGAGATTGGCCCTTACAGAACCCGGTTAAATACTTTTATTTCCAGAAAAATAG 4849  
Qy 6992 ----- 6991  
Db 4850 CTGAAAGAGCAATATTGGTATTGATAAATGTTTTAAGTATGAAAAACGAAAAATTTACCAG 4909  
Qy 6992 -----GATGAGTTTGACGTGACGTTTACGTTTACCGCTGTCGATCA----- 7032  
Db 4910 AGCCGCAATTTAGGTGAAGGGTTTTATGCGACATTTAAGTTTGGCCCTCACTAATAAGAGG 4969  
Qy 7033 -----GAATAACCTGTGCTGGCGCCGCGACGCGCATATTTAACCGTCTATC----- 7079  
Db 4970 AGCATGGTGAAGACGTTGGTTTTAAGATCCATATTGGGAATATTGATGGCAATTTCTGCCA 5029  
Qy 7080 -----GAAACATTAATAATGACACTTC 7101  
Db 5030 GACAACTTATTACGAAGGAATGTTATCTGATATTGAAACCAACAGTAACGCTCTTTGTTTC 5089  
Qy 7102 CGTTATCGCATTAAGTAAATAACGCGTGGCGCGCAGTATATTCTGTTTCTACTCGGGTAA 7161  
Db 5090 CCTATGCTAAAGGATATTACATACGTGAAGGTGTCAGATTTAGGGGTTGGGTACAAAAA 5149  
Qy 7162 CGATGTGGCGCTTATTTCGCTCAACACCTCTTTTCCCGCAACTGTCGA----- 7212  
Db 5150 TTATCTATGACAAATCCTGGGAATCTGCTTTCTTTTATTTTGTATGAGACGAAAAATCAAT 5209  
Qy 7213 -----CCGGCGAATACCGGGATTGACCACTTC----- 7241  
Db 5210 TTATATTTCAATTAATGATGCGATCATGATTCGGGAATGACACAAACGGGATAGTAAAAA 5269  
Qy 7242 TTTCCATGGAGACCCAGAGCTTTACGAAACCCCTCTGGAAGAGGGGAGTGTGTTTA 7301  
Db 5270 ATATCAAAAAATATAAAGGGTTTTTATTCATGTCGTCTGATGAAAAATAACACTGAACCCA 5329  
Qy 7302 TGGACTTCTCGGAGGCAATGCCCCTCTATTTCGCGAGCTGTTCTATTACACGCCGATGA 7361  
Db 5330 TGGATTTCAACGGCGCAATGCATCTATTTCTGGGAATTTGTTCTATTACACGCCCATGA 5389  
Qy 7362 TGTGTTTCCAGCGGTTGTTGCAAGAAACAGCACTTCCCGGAAGCACCCGCTGGCTGCAGT 7421  
Db 5390 TGTGTTTCCAGCGCTTTATTGCAAGAGCAGAAATTTTACCGAAATCGACACGCTGGCTGGCT 5449  
Qy 7422 ATGCTCTGGAACCGCGCGGCGACGTTGTTAAACGGGTGCTGCAAGATTTACCTGGAATG 7481  
Db 5450 ATATCTGGAACCGCGCGGATATTTCGGTTTCAGGGTGAATTCAGGATTTATTACTGGAACG 5509



APPLICANT: Jarrett, Paul  
APPLICANT: Ellis, Deborah  
APPLICANT: Morgan, James  
TITLE OF INVENTION: Pesticidal Agents  
FILE REFERENCE: 0380-PO1838US0  
CURRENT APPLICATION NUMBER: US/10/365,319  
CURRENT FILING DATE: 2003-02-12  
PRIOR APPLICATION NUMBER: US/09/242,843A  
PRIOR FILING DATE: 1997-11-18  
PRIOR APPLICATION NUMBER: PCT/GB97/02284  
PRIOR FILING DATE: 1997-08-27  
PRIOR APPLICATION NUMBER: GB 9618083.1  
PRIOR FILING DATE: 1996-08-29  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 38258  
TYPE: DNA  
ORGANISM: Xenorhabdus  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (35499)...(35519)  
OTHER INFORMATION: n = a or c or g or t  
US-10-365-319-1

Query Match 6.7%; Score 1260.8; DB 15; Length 38258;  
Best Local Similarity 52.0%; Pred. No. 4e-306;  
Matches 3921; Conservative 0; Mismatches 3082; Indels 541; Gaps 27;

QY 2511 TGACGGATATTTCCTCGGTTTCCTCCAGAGTCAAAAATACCTGGCGACAGCTGT 2570  
DB 28349 TGCAACAATTTTCGTTTATGCTTTTCAGCGAATTTCTGTCATAGCAAGTGGAACTCTGA 28290

QY 2571 CATGGGAGAGTCTGCTACTCTGACAGTCAGCGGAGCAGCAGACAGAAAGAAACCGG 2630  
DB 28289 CGTGGCAGAAACAGACTTTTATATCAACAGGCTCATCAGGAATCAAAACAGAAATAAC 28230

QY 2631 TCACCGAATCCCGTATTTCGGCCGGCGGAATCCCTACTGGTGAATCCCGTTCCGCTGG 2690  
DB 28229 TTGAGAACTCGCGATTTTGTCCGCTGCTAATCCACAACTGGCTAATACCTTA 28170

QY 2691 GAATACGGCAGGACCGCGAGTCGACAGTATGATGATGCTGGTTGGCTCCCGCGCAGAC 2750  
DB 28169 ATATTACCGCTCAACCCCTAAACAAATAGTTTACAACAGTTGCTTTTATGGCGCGCCACC 28110

QY 2751 GTTTCGCCCGCCCGCTCGGTGGCTCCATGTTCTCAGCGGCGGTATCTCAGCGAGC 2810  
DB 28109 GTTTTGAACCGGGATCAATTGCTTCCATATTTTCCAGCGGGCTTATTTAACAGAA 28050

QY 2811 TGTACCGTGAGGCGAAGGACTGTCATCCGACACCTCGCTGTTCCGGCTGGACATCCGGC 2870  
DB 28049 TATATCGGGAAGCGAAGATTTTCACTGACAACTTCAATATCACTCAATTAAGCAG 27990

QY 2871 GTCCGACCTGGCGGCGCTGGCCCTTAGCAGAAATATGAGCAGAGCTCTCCACCC 2930  
DB 27989 GCCCGACATTTGCTTCACTGGCAGTACACAGAAATATATGGATGAAGAAATTTCCACAT 27930

QY 2931 TGACCTGTCCATGACTACTGATCGCGGTATCGGGGACGCGGAGGCGTTGACGAGC 2990  
DB 27929 TATCCTTATTAATGAATTAAGTCTGTCATATATTCAGAGCTTAGAGAAATGACTATA 27870

QY 2991 ACAGCGTCAGGAGCTGCTCGCGGGTATCGCTGACCGGCTGACCCCTATCACTGGG 3050  
DB 27869 ACGGTGAATGAAGAAATGTTGTCACCTTACCGGCAACCGGATGACACCTATCACTGC 27810

QY 3051 CGTACGAGCGGCGCCGCAAGCCATTTCTGTGAGGACCCGACGCTGAATGGGTTTCAGCC 3110  
DB 27809 CGTATGAGTCAGCGCGTCAGCAATTTTATGCAAGATAAAACCTCACCGCATTTAGCC 27750

QY 3111 GTAATCCGATGTGGCAGCTTATGACCCCTGCTCCATGCTGGCCATTTGAAGCCGATA 3170  
DB 27749 GTAATACAGAGTAGCGGAAATTAATGGAACCAACATCGCTACTGGCTATTTAAGACTGATA 27690

QY 3171 TTTACCGGAGCTGTATCAGATAGTCCCGAAGAAATACGACAGACAGTTACGAAACAC 3230  
DB 27689 TATCGCTGAATTTGTATCAATCTTGTAGAGAAATTACACCGGAAATTTCAACAGAAC 27630

QY 3231 TCTGGAGTGAAGAAATTTTGGTGATATGCTCCCTCCCTCAGCTGTTATCTTATGATGACCTG 3290  
DB 27629 TGATGAAGAAATTTTCCGGTACAGATGATGATCTGATTTTTTAAGAGTTATGCTCTTTGG 27570

QY 3291 CACATTTTATGATCTTGTATACGATGAGCTAATCTTGGTTATTTGTCTTATTAAGGCTGACT 3350  
DB 27569 CTCGCTACTAGATTTGTCTTATGATGAATCTAGTTTATTTGTCAATCTCTCTTCGGTA 27510

QY 3351 TTTCAATCCAAACAATGATACATTAATAGTCAATTAAGTGTGCTGAATCTGAATG 3410  
DB 27509 AGAAATAACAATCAACAGTATAAGNATGAGCAACTGATAACATTTGGTCAATGACGGGA 27450

QY 3411 AAGCACTGTTTAAATAACTATACATCAATTTTAAAGAACGCTAGGCGGAGACTCACAGC 3470  
DB 27449 ATGATACGGCAACGGCAAGATTGATTAAGCGAAACCGCAAGATTTCTACGATTCACATT 27390

QY 3471 AGATTAACCTGAGCTTATACCTTATGGGATGGAACATATCTTTATAATTTTCAGCGTGG 3530  
DB 27389 TAAACTATGACAGAGCTAATTTCCAATCAAGAAATGAATACAATAATAATTTTCAGTGAA 27330

QY 3531 TGTCAACGATATCAGAGGATAGTTTCAAACTAGGGTCTGTTAGGTTCTTAACAGTAGCAATC 3590  
DB 27329 AAAAAACAGAACTGACCACTTGGATTTTCGCTCCAGAAATGAGATAAAGATATATAT 27270

QY 3591 TTTACTCTGGGATATACAGCTTCAAAAAGGGTTCGCTATAGCATTTCTCTGTTGAAATAG 3650  
DB 27269 ACCAAGATAAAATTTTCGTCCTCCATTTGCTAATACCCATTTACAGTATTTCCCATTTAAATTTGA 27210

QY 3651 ATGAAGGAAGTTAAATGATGGATCACAATAGGATGAGTAGAGAA- - - - -GGG 3700  
DB 27209 CGACAGAGAAATCAACCAACGATTAACACTCCGCTTATGGCGAGTTAACCAATCCGTC 27150

QY 3701 GGGGATATTACTCAACAGATAAATTTCACTCTGATTGAATATGATCTCGCATTTTCATT 3760  
DB 27149 GAGTCTATCAATGCCAATGCACACTTTAAATGATGGAGTTCCCGGTGATATATTCCTG 27090

QY 3761 CTTAAATTAATAAGTTTATCCGCTTATCAAGGCCACGGGATGACACCGGCGGAAATA 3820  
DB 27089 TTAAGCTGAATAAAGCGATTCGTTGTATTAAGCCACAGGCATATCTCCAGAAGATATC 27030

QY 3821 TATCAATCACAATATTTCTTAATACGGTCTCACCATTTGACCATCGGGTCTCGAGTAAA 3880  
DB 27029 TGGCAAGTAAAGAAATTTATGATGACTTAACCATTTGACAGCAATGTGTTGGGTAAG 26970

QY 3881 ATCTTCTGCTCGTTTACCTGATCGCTCACTATCAGCTTGAATGCGCCCGTCACTGATA 3940  
DB 26969 CTGTTTATGTTCAATTTATATGACGACTATAATTTAGCTGAGCGATGCGTGGTA 26910

QY 3941 TTGTGCAACGGAAACCATCAGTGACAGGCTTCAGCGGGAACCGGCTGTTTCAACACG 4000  
DB 26909 TTGTGTCATTCAGATATCAGCAATATTCACATTAACCAACACCCAGTCAATTTTACAATG 26850

QY 4001 CTGTTCAACACCCCGCTGACGCGGAGCTGTTTCTGAGATGATATCCCGCTCGAC 4060  
DB 26849 CTGTTCAATACACCGCTATTAATTTGCGCAAGATTTTCTGCTGATATAATCAACAACTGGAT 26790

QY 4061 TTACGCTCTGAAGCAGCGGAGGATGCTTTCCGCTCTCAGGCTACTGAAACCGCATTTAAC 4120  
DB 26789 TTAAACCCCGGTGAATCAAAAACCAATTTTATTTGGGAATATGAACGTTCTTCAGA 26730

QY 4121 ATCAGCGCTCGGGGCTTTCCAGCTCTGCGAGTTGGCCAGCGGTGACAGAGCGTGGG 4180  
DB 26729 GTGAATGATACTGAATGATATACATTTGGAATCTGGCTAAATGGCGGAACAAATCCAGAA 26670

QY 4181 TTTAGCTGCTCTGCTGACATATCGCGCACTCTACCGAGTGAATCTCTGGCTGACATC 4240  
DB 26669 TTTATGTTTCCATCAGAAACCTGCTCTGCTTTATCGGCTTCTGCTGCGAGCATTT 26610

QY 4241 CACGACCTATCCGCTGGTGGAGCTGTCAATGTTTCTGCTGCTCTCCCTCTTTCAGCGGGTG 4300

Db	26609	CATCATCTGACAGTGAATGAATATCCATGTTGTTGTCGGTTCTCCCTATGTGAACAG	26550	Db	25540	ATCTGCTGATTGATAACCAAGTTTCTGCCCAAGTGAACACCAACCCGCTGTGGCAGAACCA	25481
Qy	4301	GCGCGCGGTGCGTGTCCGATATAGCTGAGCGCA-----GTTTCTGTACCAAGCC	4351	Qy	5370	TGCGCGGANTACGGCTGTATATCAACCGGGCCCTTAACGGGAATAGAATCAAGCTCAGCGGCATGG	5429
Db	26549	AAATTTGCCCTTTTCTGATACAGCAATTAACGCAATTAATCAGCTTTCTGTTCCAATGC	26490	Db	25480	TTGCCAGCAATTCAGTTATATGTCAACCGGGCGCTTGAATAATGTTGAAGGAAAGTATCAA	25421
Qy	4352	ACCACCTGGCTCAGGAGCAGGGCTGGACGGTCAGCGATGTGTTCTGTATGTCTGACGACG	4411	Qy	5430	CAGAGGTGAGGGGGCTCAGTTTTTCACTGACTGGGATACGTTCAACAAACGTTACAGCA	5489
Db	26489	ACCAGTGGCTGACAAACAGAAATGGTCTGTGAGTATGTGTTCTGATGACCAAGAT	26430	Db	25420	AGCCAGTGAACAAACCGTCAGTTCTTCTGCGATGGGAAACCTACAAATCGACGGTATAGCA	25361
Qy	4412	CAGTACGGTACCTGCTGACCCCGGACATTTGAGAACCTGCTCGCTTCCCTGGCGCAACGA	4471	Qy	5490	CCTGGCGGGCGCTCTCAGAGCTGGTTTACTATCCGGAACCTACCTCGACCCGAGCGTCC	5549
Db	26429	AATTAACAGACTGTCTTAGCGGATATGAAACCTTATCAGACACATAAGTAATGGA	26370	Db	25360	CCTGGCGGGCGTATCTGAACCTGGCTTATATCCGGAACCTATATCGACCCACGATTC	25301
Qy	4472	CTGTGGGCGGTGAGCTGTTCCGGAAACGCTCCCGGGATGGGCTCCCTTTATPGCC	4531	Qy	5550	GTATCGGGCAGACCCGGCATGATGGACACCTCTGCTGAGTCTGTGACGCGAGCAGTATCA	5609
Db	26369	TTATCAACACTTTCACTCGGTGATGACAACTGATCCGTGCAGCTGCCCGCGTGTGCT	26310	Db	25300	GTATTTGGTCAGACAGGTATGATGAACAACCTGTTACAGCAACTTTCCCAAGTCAGTAA	25241
Qy	4532	GCGCCATCAGCTGACGCCACGGATACGGGAAGCGATGCTGACTTTGGCGGACAG	4591	Qy	5610	ACCGCGATACCGTGGAGGATGCTTTTAAACCTATCTGACCACTGTTTGAGCAGATTGCCA	5669
Db	26309	GCAGCAITTCAAATGATTCAGCAAAACAGCAGAACTATTTGCTGTGGATTAATCAG	26250	Db	25240	ATATCGATACCGTTGAAGTAGCTTTTAAATATCTGACCGCATTTGAGATGTCGTA	25181
Qy	4592	TTGAAGCCAGAGGGGCTGACGTGACGGAAATTTATTTTGTGTGATGAATGCCGCCCA	4651	Qy	5670	ATCTGAACACTGTCTAGCGGATATCAGATAACCCAGCATGACGAGGGGACTACATGT	5729
Db	26249	ATAAACCACAGGACTGACATTCGATGATTTTCATGATTTATGCGGCTAACCGTATCGC	26190	Db	25180	ACTTGCAGGTGATTAGCGGATATCATGACAGTATTAATGTCAATGAGGGGCTCACTATT	25121
Qy	4652	AATGACAGAGCGCGGCAGATGGCAGGGTTCTGCAAGCCCTGTGGCACTGGCACTG	4711	Qy	5730	ATGTGGTCCGACATCAGATCAGACTAATCTGCTACTGCGCGCAGCGCCCAACCAAGCA	5789
Db	26189	TCAGAGAAATGAACACAGCAACATGTTGGCTTTTGTGAGTACTTGGGGCACTTTCTCTG	26130	Db	25120	TAAATTTGGTTATAGCCAGACAGAACCCAGAAATATATTTTGGCGCAATGTCTGATCA	25061
Qy	4712	ATCATCCGAGACCGGCTCAGACCGCGAGCTCAGCTGCTGCTGACGCGGGA	4771	Qy	5790	AAATCCAAGACTCAATGATGCCCGCAATGCCGCGGATGCGATGGACAAAAATTAACCTGC	5849
Db	26129	ATTGTGGCAATATTGGACTCAGCGAAACGAACTGACCTGTTTGTGTGACAAACCGGAG	26070	Db	25060	AGTGCAGCAGCGTCAATTTGCTGCCAATGCCCTGGGGAGATGGAAAAATTTGAATAC	25001
Qy	4772	CGTTCCTCGCACAGATGGCAACATCTGCCCCATGACCTGCCGGCGCTTCGCGACATTAAG	4831	Qy	5850	GAATGAATCCGTTGTCAGATCTTGTGCTCGGTGTTTTTCAACAGTCCGCTTTATGTCG	5909
Db	26069	AAATTCCAATCAGAACACAGCACTGCAACATGATCTCCCACTTTTGAAGCGCTGACC	26010	Db	25000	CCATCAATGTATGGCAGGAAAAATACAGACCTGTTATTATACAAGTCTCTGTTGATTTAC	24941
Qy	4832	CGTTTTCATGCGCTGTTAAACCGCAGCGGAGCCATGCCGGGAGTCTCTGACCGCACTT	4891	Qy	5910	TCGTGGTCCGAGAGAAATCAGTCTGTGATACGGGCGCAGAGCAGCAGCAACCCAGCAG	5969
Db	26009	CGTTCATGCTGTGATCATGCTTGTGAAGTACCGCAGACAGAACTTAAACAGCAATTTGG	25950	Db	24940	TGTGCTGGAAACAAAGAGCTGAAAAATGAAAGTGAAGATGGCAAGATAGATATACATG	24881
Qy	4892	GAGACCGGAGAACTGTCTCAGCCCTGCTGGCCGGCCCTGTCACAG--AATGACAGG	4949	Qy	5970	AGAGCTCACAGCTGAAACTGCTGTTCCGGCGCTACGACGTTACATGAGTTCCTCCGGTGT	6029
Db	25949	AACTTAGAGCGTTGACTGCGGAACAAATTTGGCGGTGGCTTAAATTTTGTATGCTCAGG	25890	Db	24880	AT---TATATATTAACCTGTACATATTCGTTATGATGGCAGCTGGAGCTCACCGTTTA	24824
Qy	4950	ATGTGACCGGCGCTTTGGCGCAGGTGAGGGGGCGGTGAAACAGGACAAACAGCGTGTCA	5009	Qy	6030	CGTTCGACATTAACGGCAACATCGCATTTTCCGG-----AAACGAGGGCATGCAATGTG	6082
Db	25889	TTGTGACACAAAGCATTTGCAACAGACCGGTTTG-----GGAGTGAATACCTTTAC	25841	Db	24823	ATTTTAAATGTGACTGATATAAATAGAAAACTGATCAATAAAAAAGCCAGCATTTGTTATGT	24764
Qy	5010	CCTCTCGGAGAGTGGACAGGCTGAGCAGTGGCTGACATGAGTGAACCTGTCCA	5069	Qy	6083	ACCTGTAACTCCCTGACTGAGCAGCTTATTGCGGTTTTTACTCCGTCAACCAAGCC-	6141
Db	25840	CAACTGGAGAACTTATAGATGTCACTCTGCAATGGCTGATGTCGCTGTACATTTGGGTA	25781	Db	24763	ATTGTTCTTCTGATTATGAAAAAGCGTCATTTATTGTTTATTTCATGAGAAAAAGACA	24704
Qy	5070	TTACGGCATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	5129	Qy	6142	-----GGACTTTGATAACGCTCAGCTGATTTCTGTGGATATATGATATGACGC	6188
Db	25780	TTACCCCGGATGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	25721	Db	24703	ATTATTTCTTTTAAATAGTCTCTCTGCAAGAGAGGATGACCATTAACCTGATATGACAT	24644
Qy	5130	GTGACCGTTGTATACGCCAGTGGCAGGTGTATCCGGTCTGCTGCTGCTGCTGCTGCTGCTG	5189	Qy	6189	TAAATGTCTATCTCAGATA-----TAGGGATTTTTTAAGAGCGTCAAGTATTTA	6239
Db	25720	CGATGCCAACATTTGATGATTGGCAAGCCCGCAGTACTTTGTTGACGGCGGACTGAAAC	25661	Db	24643	TATCCATTTCTCAGAAAAATGATTAGACGCCCATTTGTTAAGAGCACATTTATCAGAACTTG	24584
Qy	5190	GCAGCAGAGCTCGGCTGACAGTATCTGAGGAGGGGACACAGCGGCTTTG	5249	Qy	6240	ATACAGGACACTG---AGAAATTTTAAATATGTTTTTTTTCAGACCTTCCGCTAAATAT	6296
Db	25660	GTCAACAACTCCGACAGCTTCAGGCATGCTGATGAAGCCACGACGACAGCGGCGCAGTG	25601	Db	24583	ATACAGGACAGAAATCAAAATCAATCAATTTGCTACAGATTTATTTGGCGGATATA	24524
Qy	5250	CGTATTATCTGCTAATCTGGACCGAAACATGATATCCGGGCGGATGACCTCTTCGGGT	5309	Qy	6297	TTGTGAGTGCACAGATTAAATTTGA---TGATGTTATCCACAGCGATTTCTCACTCTTA	6353
Db	25600	CTTACTACATCAAAATGGTGACCTCAACAGATTAAGAGCGGGATGATGTCAGCT	25541	Db	24523	AGGAATCTATAACCCAAAAATAAATTAGCCAGTTTTTACCAGAAAAATTTTTTGATCTCT	24464
Qy	5310	ATCTGCTGTGGATTAATCAGGTGTACGCCAAGGTAAAAACCAACCCGATTTGGGAGGCCA	5369	Qy	6354	ATTCTAAACTACAAGTACTGTTTTTACTAAATGAAGATTCCTCTCTTTTGAAGCCAGAGC	6413
				Db	24463	CGTATATATCACCAGGAAATGGTCATATTTAAATTTTAACTCAATCCTTCAATGGAAATTA	24404



Qy 6414 TTCATATTACAGCAAAATGTTTCGTGTTTGTAGTA-----CTG 6452  
Db 24403 ATTTTCAAAGGCAATATATAATGATGAGGTTAAATATACCTGTTATCGATGGTAGAAG 24344  
Qy 6453 CTGGCATCGGCACCTCAATCTACCATAGAAAATTCGTTTCAGGCGAGGATAGAAATTTGAGG 6512  
Db 24343 ATGAAACGGTATTTTATTTGATGATAGACATGATGAATGCTTTGGAAAAGAGAAG 24284  
Qy 6513 AAATTAAT-----TTTTATGAGGCGAGCGCGCGCGCGGATTTGACGG 6555  
Db 24283 AGTTTTTTCATATGGAACCTTTGATTTTATTTCCATCGATCTTAAATAATGCCGAAT 24224  
Qy 6556 ATTTGTCGGAGTGGATGTTTCTAATTCAAAAGTATACAGGTC--GHAAGAAAGACAGTTG 6614  
Db 24223 ATTTTAGAGTGTAAATGCACTAAGAACCAAGGAAGAAAATTCCTAGAAAATCAGAAATTG 24164  
Qy 6615 GTGTCACCTAGAAAATCTTNTTCGTCCTACTGGCGTTAGTGTT-----CTGTTGAGTTATT 6669  
Db 24163 GAGTTGGTATAAAATTTATGATTTATGAATTCAGATGCTGAATTCAAACTTTGATACTAACA 24104  
Qy 6670 TATTGATTCATCAATAAATACTTCAGCGGAATTTTGTTCAGATA--AAATGATAACCGC 6726  
Db 24103 TAGTATTAGATTGGAAGAGATAACACAGAGATGCGCATCTATATGTAATCATTTACTA 24044  
Qy 6727 TTTAATTAGCGGCAGTAGTACATCAAAAGTTAATTACGTGTCGTCTATTGGCTCTCAAGATTT 6786  
Db 24043 ATGATGTTTCAATCAITTAATAACATGGAATAATTGCGGCACCTTCCTTCGCGAGATC 23984  
Qy 6787 TTGAGTGTAAAGTCGCTCATGTCGGCAC--TTCAGATATATGAATTAATTCGATGATATC 6844  
Db 23983 CATGGGTGTATTTATGTTCAACGAGCCACAGATAATAAAACTTGTCTCATCTATGATCGA 23924  
Qy 6845 ATCTGACATCCGCGGTAATGGAATGGAATGGAATTAATTAATCCTGGCTTCGGCTGATGTT 6904  
Db 23923 ACAGATCCAAGATAAAACATAGTTTATTTTAAATAAATGGCTCTGATAT--TCTAGTGG 23865  
Qy 6905 AATGATAAGCTGAGTCTGCAATCGGGAATAATCTTTTCAACCAAACTCGCTGAGTTTT 6964  
Db 23864 AGTTAAATGCTGAAGACCATGTGCATCTAAACCTTCACACGAATCTGACCTATGGTAT 23805  
Qy 6965 ACGGTTAATACAGTGTATA--TTGTTGAAGATGATTTGAGTGAGCTTTACGTTTACACCG 7022  
Db 23804 ATGATTTTAATCAAGTAAAGTTGATATTGAAGCTATGATATTCTCTGCTGGTGAAGGAGT 23745  
Qy 7023 CTGTCGATCAGATAACGTGCTGTCGCCCGCGGAGCCATATTAAACGTCATT----- 7078  
Db 23744 TTATTATTAAAGCAACCGGCGGGTTTAAACGATATTGTTATTGAATCGCCAAATTCATA 23685  
Qy 7079 -----CGAAACATTAATAATGACACTTTCGTTATCGCATTACGTAAATAATACGCTGGCG 7133  
Db 23684 TAAAACTAAATCCAAAGATACAAGTAAACGTTATATCACTGCATATAAATGCCATCAGCA 23625  
Qy 7134 CGCAGTATATTGTTTTCAGTCGGGGTAAACGATGTGGCGTTATTGCGCTCAACACCCCTCT 7193  
Db 23624 CACAATATATGCAAGATTGGCCCTTACA-----GAAACCGGTTAAATACTTTAT 23577  
Qy 7194 TTCGCCCAACTGTCGACCGGGGGAATACCGGATTTGACACCATTTCTTCCATGGAGA 7253  
Db 23576 TTTCCAGAAATTAGCTGAAAGAGCCAAATATTGGTATTGATAATGTTTAAAGTATGAAA 23517  
Qy 7254 CCCAGAGGCTTACGAAACCGCCCTTGAAGAGGGAGTGTGTTTATGGACTTCTC-- 7311  
Db 23516 CGCAAAATTTACAGAGCCGCAATTAGGTGAAGGTTTATGCAACATTTAAGTTGCCCC 23457  
Qy 7312 ----- 7311  
Db 23456 CCTACAATAAAGAGGAGCATGGTGTATGAACGTTGGTTTAAAGATCCATATTGGGAATATTG 23397  
Qy 7312 ----- 7311  
Db 23396 ATGGCAATTCGCCAGACAACCTTATTAAGGAAGAAATGTTTATCTGATATTGAACACCAAG 23337

Qy 7312 ----- 7311  
Db 23336 TAACGCTCTTTGTTCCCTATGCTAAAGGATATTACATACGTGAAGGTGTGATAGGGG 23277  
Qy 7312 ----- 7311  
Db 23276 TTGGGTACAAAAAATTTATCTATGACAAAATCCTGGGAATCTGCTTTCTTTTATTTGATG 23217  
Qy 7312 ----- 7311  
Db 23216 AGACGAAAAATCAATTTTATTTCACTAATGATGCCGATCATGATTCGGGAATGACACAAC 23157  
Qy 7312 ----- 7311  
Db 23156 AGGGGATAGTAAAAAATATCAAAAAATATAAAAAAGGGTATTCAAGTCGTGTCATGAAAAA 23097  
Qy 7312 -----CGAGCAATGCCCCTCTATTTTCTGGAGCTGTTCT 7346  
Db 23096 TAACTGAACCCATGGATTTTCAACCGCGGCCAATGCAATCTATTTCTTGGGATTTGTTCT 23037  
Qy 7347 ATTAC--ACGCGGATGATGTTTCCAGCGGTTGTCAGGAACAGACACTTTCCTGGAGCC 7405  
Db 23036 ATTACAACGCCCATGATGTTTCCAGCGCTTATTGCAAGAGCAGATTTTACCAG--ATCG 22978  
Qy 7406 ACCCGTGGCTGAGTATGTCGGAACCCGCGCGGCACTGCTGTAACCGGGTGTCTGAG 7465  
Db 22977 ACAGCTGGCTGGCTATATCT--GAACCCGACCGGATATTGCGTTCAGGGTGAATGCGAG 22919  
Qy 7466 AATTACACCTGGAATGTCGCTCGCTGGAGGAGGACACCGGGTGGAAACGACTCGCGCTG 7525  
Db 22918 GATTATTACTGGAACTGCGGCCCATTTGGAGGAAGATACGTCCTGGAATGCCAATCCGCTG 22859  
Qy 7526 GACTCATTGACCCCGCATGCAATAGCCAGTACGCCCAATGCAATGCAATTTACAGGTGCGCAC 7585  
Db 22858 GATTCGGTCGATCCGAGCGCGTTGCCAGCATGATCCGATGCACTATAAAGTGGCTTACC 22799  
Qy 7586 TTTATGCTGCTACCTCGACCTGCTGATTGCGCGGTGATGCGCGCTACCGCTACCGCTGCTGAG 7645  
Db 22798 TTTATGAAATGCTGATTTGTTGATTACCGCGGAGATAGCGCCTATCGCCAGCTGAA 22739  
Qy 7646 CGGGAACCTTTAACAGAGCCCGGATGTTGTTAGCTCAGGCTCTGAACTTTCTGGGGCAG 7705  
Db 22738 CGTGATACCTTAAACGAACTAAAAATGTTGATGTACAGCGCTCACTTTTATTTGGGTGAT 22679  
Qy 7706 GAGCCCTATATTCTTTTACGCCGCTGCTGGCGTTGACCTCTGGGTGACGAGCCAGC 7765  
Db 22678 GAGCCTTATTTTTCATTGATTAACGATTTGTCAGAGCCAGCGCTGGAAGAAGCTGCCAGC 22619  
Qy 7766 GAGGTGACGCGCGCATTACCAGAGGCGCTGCTGCGCGGTGCGCGGTTGGTCCCGCT 7825  
Db 22618 CAAACAATGGGCATCATTTATCAACATAAAATGCTGCAACTGCTGAGCGCTGCATTATTA 22559  
Qy 7826 CCGGAGACAGGAGCGGAA--TTCCTCTGAGCGGCACTGTTCTCTCCCGGAGCAGAACGAGGT 7884  
Db 22558 CCCACGAAACGTAACGCAAAATTTGTTAAACCGCATTTGTTCTCCCTCAAAATTAATAAAA 22499  
Qy 7885 GCTCAAAGGCTACTGCAAAACCTTGGCAGCGGCTTCACTAACTCGGCCACACCTCTC 7944  
Db 22498 ACTGCAAGGTTACTGCGAGCATTTGACGCAACGCCCTCTATACTTAACGCTAACCTGAC 22439  
Qy 7945 CATTTGACGCGCGCCCTTTCCCTGTCCTGCTACGCGAGCGCTCGGAAACCGTCCGCGCT 8004  
Db 22438 AATCGAGCTCAGCCTCATTTCTCTATGCGACCGCGGAGATCCGTTCCATGTT 22379  
Qy 8005 GCAGAGTGGCTGCTCAACAGCGCGCAGGGTGTGTCAGCACTGCGCGCGCGGTGATGCC 8064  
Db 22378 ACTCAGTGTGCTCATCTGCTTCAAGCGCGCGGCGGATTTTACCTCATGCACTGATGCC 22319  
Qy 8065 GCTTTACGTTTCCCGTTCATGCTGGAGAACCGCCCGGGGATGTTGAGCTCTGACCGG 8124  
Db 22318 GATGTACCGGTTTTCGGTGAATTTCTGGAAAATGCCAAGTGGGGGTGAAGCAGTTGATACA 22259  
Qy 8125 GTTCGGCAACACACTGCTCGGTATTATACCGAGCGTCAGGATGCGGAGCGCTGGCCAAACT 8184



Qy	9898	GGTAGGTGCTGCTGCGGCACTCACGGCTGCTGCGCACCCAAAGACAGCGCAGGCCACC	9957	Db	1375	CTGATGGATATTAAACGCTGACGGCAACTGGACTGGTGATTAACGGCGCGGCTAAAG	1434
Db	301	GGTGAAGTGTGGTCGTAGCATTAATGAGCGAGTCAAGCTGATATCCGACGTGAATCC	360	Qy	11035	GGGATGTATGATCGCAACCCCGCGCGGACTGGTTGATTTACACCCCTGTGACGCTTG	11094
Qy	9958	TCACTACTGGGGATAAACCCAGCGGGAAGCTTCAACGTTGAGTTTACCGTTTACGTAACGTAACG	10017	Db	1435	GGCTATACACAGCCAAACACCGGATGGCAGTTGACGCGTTTACGCGCATACATGCGCCCTG	1494
Db	361	TCATTGACGGGCATCAATTTGGGTGACCTTCAACCGTTACCTGTTATGCTGCCGCTA	420	Qy	11095	CCCGTAGAATATGCGCATCCAAAGCAGTCTCGCGATATCTCGGGGCTGGTTAAACG	11154
Qy	10018	GAGGGTAGTCTCAGCCCGCTTGAGCGTTGGCTGCCCGCGACGAGACAGAAACGGAAATTT	10077	Db	1495	CCGATAGAAATATTTCTCATCTCGGCTCAACTTTCGCAATTAATGGAGCCGGCTGTCC	1554
Db	421	GAAGCCACTTTAAACCGGTTGGAATACTGGCAACCCCAACACCGCGCAACCGATTTT	480	Qy	11155	GACATGGTGCTTATCGGGCGCGCAGTGTTCGCTCTTATTCGGGCAAAAACGATGTTGG	11214
Qy	10078	TGGGTGTTATATACCCCTGACGACAGTGGCTCTGCTGGGCCGAAATGGCGAGGCTCGC	10137	Db	1555	GATTTAGTGTCTAATTTGGTCCCAAAAGTGTGGCTTATATGTCAATAACCGTGTGTTTT	1614
Db	481	TGGCTGATATACAGCCCGACGACAGTCCATTTACTGGGCAAAAATCTCAGGCACGT	540	Qy	11215	AATAAGGGGAGACCGTGCAGCAAAACGGAAGACTCATCTGCGGTCCTCGGGGGTTGAC	11274
Qy	10138	ATCAGCAACCCACAGCCCAACACACAGCGCGGTTTGGCTGATGAGTCTCTCGGTATCA	10197	Db	1615	ACCGAAGGGCGGATGTGGTGCAATCCGGTGATATCACCTGCGCTACCGGGCGCGAT	1674
Db	541	ATCAGCAATCCACTCAATGTTAAACCAACAGCGCAATGGCTGTTGGAAGCCTCGATATCA	600	Qy	11275	CCACGTACCTCGTGGCGTTTCACTGATATGGCTGGCAGTGGAGACAGCAGCATTTGACGGAG	11334
Qy	10198	CTTACCGCGCAACAGATGTTATTCAATACCGTGGCAAGATGATGACGGTGTGACGAG	10257	Db	1675	GCCCGTAGTTAGTGGCATTTAGTACTGCTGCTGAGTTCAGGCCAGCAGCATCTGTTGAA	1734
Db	601	TCCACAGCGAAGAGATTAATCAATATCGCGCTGAAGATGAAGCAGGTTTGTGAACC	660	Qy	11335	GTGCGTCTAAATGGAGTACGTTTACTGCCCAAACTTGGGCAACGCTCGTTTCGGTCAGCCG	11394
Qy	10258	GCGAGCGCGACGCGCACCCCGAGCGCGGCCCAACGTTTATCGGTGGCGGCTCTGGTAT	10317	Db	1735	GTTAGTGCAACTCAAGTCACTGCTGCGCGCAATCTGGGCAATGCGCGTTTGGTCAGCCA	1794
Db	661	GACGAGCTAGCAGCCCAACCCAGCGCAACCGTTTCAGCGCTACCTGCAACAGTACATTAC	720	Qy	11395	GTGCAATATTCGCGGTTTACGACAGTCACTAGTCTGCTGCTGATGATGATGATGATGATG	11454
Qy	10318	GGTAACCGTCAGGGGCTCGGACGCTACCGCGCT---GGTGTGACCAACATCAATGGAT	10374	Db	1795	ATCGTATTCGCGGATTCAGCCAACTGCGCGCAGTTTAACTCTGATCAGTTCATCTG	1854
Db	721	GGGAACCTGACCGCAGCGAGCTTTTCTTACACTAAACGAGATGACCCACTTAATCT	780	Qy	11455	GCCGATACCGAGCGTTCCGCTACCGAGCTGATTTATGCGATGATGATGATGATGATGATG	11514
Qy	10375	AGCTGGCTGTTATCTGCTGTTGATTATGTTGAGGTAGTCTGCTGCTGCTGAGCG	10434	Db	1855	GCCGATTTGATGGAGCGGCTGCGGATTTGATTTATGTTTATGTTTATGTTTATGTTTATG	1914
Db	781	GGCTGGATGTTCTGTTAGTATTGACTAGCGGCGCAAAACAGCTTATCTGAAATG	840	Qy	11515	ATTTATTTCAACACAGATGGTAAATTTTTCGCGAGCCGATACGCTGCTTCTTTCGCCAAA	11574
Qy	10435	CCGCGCTGGCAAAACACAGGAAGTGGGAGTGGCTGTGCTGCTCAGGATTTGTTTTCGGG	10494	Db	1915	ATTTTCAGCAATGAAAGTGGCAACGCTTTTTCGCAAAACCATTCACACTCTCTTCTTCTGAC	1974
Db	841	CCGCTGTTAAAGCCACAGCA-----ATTGGCTTTGCCGAAAGACCGTTTTCGGT	894	Qy	11575	GGTGTGCGGTATGATCGCACTGCGAGTCTGCAAGTGGCGGATATCAGGGGCTGGGGGTG	11634
Qy	10495	TATGAGTTTGGTTTAACTGCGGACTGCGCGCTGTCGCGTCAAGTTTGTGTTTTCAT	10554	Db	1975	GGCTCGGTTTGTGATGATACCTGCGCAGTTGCAAGTAGCCGATGTACAAGGTTTAGCGCT	2034
Db	895	TATGAGTACGGTTTGAATTTGCTGCTACCTGCGCGCTTATGCGGCCAAATCTGATGTTTCA	954	Qy	11635	CCTAGCCTGTTACTGACGCTCCCGCATGTCGCGCTCATCAGTGGGTGTCGCAATTTATCG	11694
Qy	10555	TACCTAGTGTCTGGCGGGAGTTCCGGAGCGAATGATGCGCAGCATTTGTTCTCGC	10614	Db	2035	GTACGCTGATCTTAAGCGTACCGCAATATGGGCCCACTATTGGCGCTCGCATCTGACC	2094
Db	955	CGTCTCAAAACCTTATCTGGTCAGGCAAGGGGATGATGAACCTGCGTAGTGTGCGGT	1014	Qy	11695	GCACAGAAACCCCTGGTTGTTGATGGCATGAACAACAATATGGGGGCCCGGCAATGCACTG	11754
Qy	10615	CTGTTGCTGACTACAGGAAAGTCTTCACTCAGTCTGCTCGAGAACGTGCAACCAAGTG	10674	Db	2095	AACGCGAAACCGTGGTTACTCAGTGAAACGAAACAATATGGGGCCCAATCACACCTTG	2154
Db	1015	CTGATCTGGATTATGACGAAACCGCATGGTCAGTACGCTCGTTTCTGTCGCGCGGTA	1074	Qy	11755	CACATTCGAGTTTCGGTTCAGTTCTGGCTGGATGAGAAAGCCGAGGACCTGGCGGAGGC	11814
Qy	10675	GCTTATGAGTCGAGCGGAGCTCTTGTGCTTGGCTGCGGCACTGCGATTTGGGGTGGCAACC	10734	Db	2155	CATTACCGTAGCTCTGTCCAGTTCTGGCTGGATGAAAGAGCTCGCGCATTTGGCTACCGGA	2214
Db	1075	GGCCATGAGGACAAACACGGTTTACCGCTGCGCCTGCAACCTGGAACCTGGGCTATCAGCCT	1134	Qy	11815	AGTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	11874
Qy	10735	TTTACCCCGCGCATTTGTCGCAATGTCAGACGGCTGACGATATGGCAAGTTGAGTTTG	10794	Db	2215	CAAAACCGGTCTGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2274
Db	1135	TTTGAGCCAGAACAAACCGCACTTGGCAATCAATGATGATGATGATGATGATGATGATGATG	11194	Qy	11875	GATGAGATCACCGGTAAACCGTCTGGTCAGCGAGCTGCTTTTATCGCCACCGCGCTCTGGGAC	11934
Qy	10795	CTTCAACCTTATCAGCTTGTAGACTTTAAACGGGCAAGTGTGGTATCTCTGTATCAG	10854	Db	2275	GATGAAATCAGCGCAATAAGTTAGTGACCACTTACGTTATGCTCAGCGCGCTTGGGAT	2334
Db	1195	ATTCAGCGCTGGCAACTGCTTGACCTGAAGGAGAGCGGTGCGCGCACTTCTCTATCAG	1254	Qy	11935	GGGACAGAACCGGAGTTTCGGGGGTTTGGTTTGTGAGATCAGGAGATACCGATACCTTG	11994
Qy	10855	GACAGCGGTGCTGGTGGTACCGTGAAACCGGTACCGCAGTGGGGGATGATCCGGATGCT	10914	Db	2335	GGACGTGAACGGGAATTTGCTGGCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	2394
Db	1255	GATAGAAATGGCTGGTGTATCGATCTGCCCAACGTCAGCGCGGGGAAGAGATGAATGCG	1314	Qy	11995	GCAAGCCAGGTTACCGGACGAGGACTGATGCTCTGTTGAGCCGAGCTGATGCTGCTGCTG	12054
Qy	10915	GTGACCTGGGGGGGCTGCGGCTCGGACATGCGGCTTGTGATACAGCGGCATC	10974	Db	2395	GC---TCAAGGCAATGCGCGGAACTACACACCGGCACTTCAACAAAGCTGTTGATGCC	2451
Db	1315	GTACCTGGGGGAAATGCAACTCTTCCCATCACACGCTGTGTCAGGATACGCTCA	1374	Qy	12055	ACCGGGTACCGGCACTAGACGAGCTGCTGCGGAGACGTTATTTGGCAAAACGATGCGGCC	12114
Qy	10975	CTGCGGATCTTAATGGGATGGTGGCTGGAGTGGGTGCTTACCGGCCCGCGTGGCG	11034				

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 Db 2512 GCTTTCCGCGTTTACGCCACGCTTTTACTCTCTGGAAGAGGGCAAGATGTCACCTG 2571  
 Qy 12175 ACTCCG---GACACAGCAGACATTTCTGGTTGACGAGCCCTGAAAGGCATCTGCTG 12231  
 Db 2572 ACACCGGAAGATGACCATATCTATATCTGTTAAACCGGGCGCTAAAGGTGAGCCACTG 2631  
 Qy 12232 CGCAGTGAGTTATACCGTGCAGTGCAGCAGCAGCGCGATATCCCTTACAGCGTCACT 12291  
 Db 2632 CGTAGTGAATCTACCGGCTGGATGGCAGCGCACACAGATCCCTTATACAGTACT 2691  
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 Db 2692 GAATCCCGTCCACAGGTGGCCAAATACAAAGTGGCGCCACCGTTTCCCGGCTGCTCTGG 2751  
 Qy 12349 CCGATGGCGGGAAGCGGTACGTCTAGTTTATGAACGGTACCAATATCTCAATGC 12408  
 Db 2752 GCCTAGTCTGGAAAGCGGTAGTTATCACTACGAACGTATATCAGTATCCCGAGTGC 2811  
 Qy 12409 CAACAGCAGCGGTACTCTCTCAGTGATGAATACGGTTTCCCACTGCGTCAAGTCTGTC 12468  
 Db 2812 AATCAGGATATACGTTGTCAGTGACCTATTTCGGGCAACCACTGAAACAGGTTTCCGTA 2871  
 Qy 12469 AATTATCCAGACGCCCTCGTCCGGCGGACAAATCCATATCCGGCGTCTTTACCGGAGC 12528  
 Db 2872 CAATATCCCGCGGCAACAAACCAATCCGTATCCCGATACCCCTACCGGATACG 2931  
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 Db 2932 CTGTTGCCAGCAGTTATGACGATCAACACACTATTGGGATTAACCTGCCGACATCC 2991  
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 Qy 12709 GAACACCTGTTGGCGCCGGAAGCCTGCTCCGATAGTCAGGTCTCGGTACGCTGGCGGGT 12768  
 Db 3106 GAACCTGTGCTGAAATAGCCTGATTGCGGATGAATAACCTCGGAACTCAAT 3165  
 Qy 12769 CAGCAGCAAGTCTGGTATCTGATATCAAGAAGTGGCCACCGTCTCGGCCACTC 12828  
 Db 3166 CAGCAACGAACGTTCTATACCGCAGGGAAGAAACCAACACCGCTGAAACACCGCACGCA 3225  
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 Db 3226 CAAGCGTTAATCGCTTTTACGAAACGGCGGTATTAACGGAATCTCTGTTATCCGCGTTT 3285  
 Qy 12889 GCTGCTTACATTGTGATGA-----ACATCTCAGCAAGCCGTTTACCGGCAA 12936  
 Db 3286 GATGGCGGTATTACGCCAGCAAGATTACCGGGAATCTGACACAGCGCGGATACCAACAA 3345  
 Qy 12937 TCCGGATACCTTTTCCCTCAGGAGGGAAGCAGAACAGGCATTTGGACCCAGTGTGAG 12996  
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 Db 3400 GGCTATACGATTACGGGAGCGGAAGCAATTTTGGGCTCTGTGGCAACAGTAAACAGC 3459  
 Qy 13057 ATGTTGACCGGCCAGTTTACCGTGACCGGTGACCGGTACGACTCGGTCACTACGAGTGG 13116  
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 Qy 13117 CAGGATCCGAGGATTTGACCAACAGCGCATATGACTGGGCTTCTGAGCGCCGCTC 13176  
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Qy 13177 CCGGTGACGGACCCCAATGATTAATCTGCAGTCCGTCACCTCTGGATGCTCTGGCCGGGTG 13236  
 Db 3580 CAACTGACTGACATCAACAGTAATGTGCATCTCATCCTTTGGATGCTCTGGGACGCCCT 3639  
 Qy 13237 ACCACCTTCGAGTTCTGGGGCAGCAGAAATGATTTGACACCGGTTCACAGT----- 13287  
 Db 3640 GTACGCAACGTTTCTGGGGATCGAAAGCGGTGGCAACAGGTTACTTTCATCAGAA 3699  
 Qy 13288 GATGCCACGTTTCTCGGTTCCGGAACCGCAGCAGCGCTCTGGGCTTGAACGGCGCCCTA 13347  
 Db 3700 GAAAAACCATTTCTCCCAACAAAGATATCGATACCGCTATTAAATCTAAACGGAACCATC 3759  
 Qy 13348 CAGTAGACAGTCTCTGGTATGTCACGACAGTGG----- 13386  
 Db 3760 CCTGTGCACAGTGTCTGGTCTATGACCGGACAGTTGGATGCCACTATTTCAGTCAAGAA 3819  
 Qy 13387 ----- 13386  
 Db 3820 ACCITCAACACATTAACGAGGAAGCAGGAGACGCTGCGTGTATTCAGTATTATCAG 3879  
 Qy 13387 -----GGAGATGACGACAATGAGAAA----- 13408  
 Db 3880 GAAAGATTGGCGTATTGCGCACTGACTCGCGCGCTTGCTACAAAGTCAAAAGATCAGT 3939  
 Qy 13409 -----TGCCCCCGCACGTCGTCGTCG 13431  
 Db 3940 ACACCATAGTTAAACTGTTAAACACAGCATTTGTTTACTTCCCAATACCTTACGCTG 3999  
 Qy 13432 GCTACCGATCGTATGACAGTATACCGGACAGAGGTCGCGCAACAGGTGACATTCAGT 13491  
 Db 4000 ACCACAGACCGTTATGACCGGACTCTGAGCAGCAAAATTCGCCAACAACTGCAATTTAGT 4059  
 Qy 13492 GACGGTTTGGCGGTAGTTGCAATCGCAACCGCGAGCGCGGCAACCGCTGGCAA 13551  
 Db 4060 GATGGTTTGGCGCTCTGCTACAAGCGTCTGTACAGCATGAGGCGAGGCGGAGCTGGCAA 4119  
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 Db 4120 CGTAACCAAGACGGTCTCTGGTGACAAAAGTGA-----GAATACC 4161  
 Qy 13612 AATTTCCGTCGGCGTCAACCGGAGGGCGGATGATGACAAATAAAGGTCTGCTGTCGG 13671  
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RESULT 10  
 US-10-754-115-22  
 ; Sequence 22, Application US/10754115  
 ; Publication No. US20040208907A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hev, Timothy  
 ; APPLICANT: Schleper, Amanda  
 ; APPLICANT: Bevan, Scott  
 ; APPLICANT: Bintrim, Scott  
 ; APPLICANT: Mitchell, Jon  
 ; APPLICANT: Li, Ze Sheng

APPLICANT: Ni, Weiting  
APPLICANT: Zhu, Baolong  
APPLICANT: Merlo, Don  
APPLICANT: Apel-Birkhold, Patricia  
APPLICANT: Meade, Thomas  
TITLE OF INVENTION: Mixing and Matching TC Proteins for Pest Control  
FILE REFERENCE: DAS-104X01  
CURRENT FILING DATE: 2004-01-07  
PRIOR APPLICATION NUMBER: US 60/441,723  
PRIOR FILING DATE: 2003-01-21  
NUMBER OF SEQ ID NOS: 64  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 22  
LENGTH: 4431  
TYPE: DNA  
ORGANISM: Photorhabdus luminescens  
FEATURE:  
NAME/KEY: exon  
LOCATION: (1)..(4431)  
US-10-754-115-22

Query Match 5.9%; Score 1108.8; DB 18; Length 4431;  
Best Local Similarity 56.0%; Pred. No. 2.4e-268;  
Matches 2493; Conservative 0; Mismatches 1732; Indels 225; Gaps 12;

QY 9598 ATGCAGAAATCATCAAGACATGGCCATTACTGCCCCACAGTTGCCCTCCGGGGGGGGTGGC 9657  
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QY 9658 GTCAACCGGGTCAAGGGTGATATCGCGCGCGCAGGGCGGATGGTGGGGACCCCTGAGT 9717  
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QY 9718 ATTCCCTTGGGGTATAGCCCGTGGGGTTACGCCCCCACTGGGGGACATTAATATAC 9777  
DB 121 CTGCAATATACCAATTTCCGCGGGCGTGTATACGACCCCTCGCTCACTCTGAATTAACA 180

QY 9778 AGCCGGTGGGGAACGCCCTTTGGCATTTGGCTGGGGGTATCGCGGGTGTGGTGTCCAG 9837  
DB 181 AGTGGAAACCGGTAAACGCCATTTGGTCTCGTTGGGACTGCGCGGTCAATTCGT 240

QY 9838 CGTGTACGGCGCAACCGGAGCACCTTACCTACGATGATATCTGATGAATTCACCGGTCCGGAC 9897  
DB 241 CGTCGACACAGTACCGCGGTACCGAATTAACGATGAACCGGATCTTTCTGGGGCCGAA 300

QY 9898 GTGAGTGTGTGGTGGCGGACTCAACCGCTGTGGGACCCCAAGAACACCGGAGGCCACC 9957  
DB 301 GGTGAAGTGTGTGGTGTAGCATTAATGAAGCAGGTCAAGCTGATATCCCGCAGTGAATCC 360

QY 9958 TCACCTACTGGGATAAACCAGCGGAAGCTTCAACGTTACGTTTACCGTTTACGTTACG 10017  
DB 361 TCATTGAGGGCATCAATTTGGGTGGCACTTCAACGTTTACGTTTACGTTTACGTTTAC 420

QY 10018 GAGGGTGTCTACGCGCGCTTGAGCTGTGGCTGGCGCGGACGAGACAGAAACGGAATTT 10077  
DB 421 GAAAGCCATTATACCGGTGGATATCTGGCAACCCCAACACCGCGGCAACCGATTT 480

QY 10078 TGGGTGTATATACCCCTGACGACAGTGGCTCTGCTGGGCGGAATGCGCAGGCTCGC 10137  
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QY 10258 GCGGAGCGGACGCGGACCCCGGCGGCGGCAAGCTTATCCGTTGCGGTGCGGTCTGAT 10317  
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12769 GAGCAGCAAGTCTGGTATCTGATTCACAAAGCTTGCACCGTCCGCTCGCTCGGCACCTC 12828  
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Db  
3226 CAAAGCTTAATCGCCTTTACCGAAACGGCGGTATTAAACGGAATCTCTGTTATCCGCGTTT 3285  
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12889 GCTGCTACATTTGTGATGA-----ACATCTCGAAGAACCGGTTTACCGGCAA 12936  
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3286 GATGGCGTATTACGCCAGACGAATTAACCGGAATACTGACACAGCGCGGATACCAACAA 3345  
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12937 TCGGATACCTTTTCCCTCGAGGAGGGAAGCAGACAGGCATTTGGACCCAGTGTGAC 12996  
Db  
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QY  
12997 GGATATGTTACCTATGCTCGCGCGCAGAGCAATTTCTGGCTACCGCTATCTTTTGGGACAGT 13056  
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3400 GGCATATCCGATTAACGGGACGAACAAATTTGGCGTCTCTGTCGCAACAGTAACAGC 3459  
QY  
13057 ATGTTGACCGGCGCCAGTTTACCGTGACGGGTGACGGTACGATGCGGTCTATCAGCAGTGG 13116  
Db  
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QY  
13117 CAGGATCGCAGGAGTTGTCACACAGCCGACTATGCTGGCGCTTCTCTGACGCCGCTC 13176  
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3520 CAAGATGCTGCGCGCTCACGCTCTCAGCAATTAATGACTGGCGTTTCTCACCAACG 3579  
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13177 CCGGTGACGAGCCCAATGATTAATCTGCAAGTCCGTCACCTCTGATGCTCTGGCGCGGCTG 13236  
Db  
3580 CAACTGACTGACATCAACGATAATGTGATCTCATCACCTTGGATGCTCTGGGACGCCCT 3639  
QY  
13237 ACCACCTGGGATTTCTGGGGCAGGAGATGATTTGCCACCGGTTACAGT----- 13287  
Db  
3640 GTCCGCAACAGTTTCTGGGGATCGAAAGCGGTGGCAACAGGTACTCTTTTCATCAGAA 3699  
QY  
13288 GATGCCAGTTCTCGCTTCCGACGCGCAGCAGCGCTCTGCGTTGACGCGGCCCTA 13347  
Db  
3700 GAAAAACCAATCTCTCCACCAACGATATCGATACCGCTATTAAATCTAACCGGACCACTC 3759  
QY  
13348 CCAGTAGCAGCTGTGTTGTTATGTCAGCGACAGTTGG----- 13386  
Db  
3760 CTTGTGCGACAGTGTCTGTCTATGACCGGACAGTTGGATGCCACTATTTCAGTCAAGAA 3819  
QY  
13387 ----- 13386  
Db  
3820 ACCTTCAACACATTAACGCGAAGAGCAGGAGACGCTGCTGATTCAGTATTATCAGC 3879  
QY  
13387 -----GGAGATGACGACAATGAGAAA----- 13408  
Db  
3880 GAAGATTGGCGTATTTTGGCACTGACTCGCCGCGGTTGGCTACAAAGTCAAAAGTCACT 3939  
QY  
13409 -----TGCCCCCGACAGTGGTCTGCTG 13431  
| | | | |





1198 ATTGAGCGTGGCAACTGCTTGACCTGAAAGGAGAGGGCTGCCGGCAATCTCTATCAG 1257  
10855 GACAGCGGTGCTGGTGGTACCGTGAAACCGGTGACGCAAGTGGGGGATGATCCGATGCT 10914  
1258 GATAGAAATGGCTGGTGGTATCGATCTGCCCAACGTCAGCGCGGGGAGAGATGAATGCG 1317  
10915 GTGACCTGGGGGCGCTGGCGGCTGCCGACAAATGCCCGCTTGTGATACACGCGCATC 10974  
1318 GTCACTGGGGGAAATGCAACTCTTCCCATCACACCAAGCTGTGCAGGATAACGCTCA 1377  
10975 CTGGCGGATCTTAATGGGGATGGTGGCTGGAGTGGGTGGTTACCGCCCCCGGTGGGG 11034  
1378 CTGATGGAATTAACCGTGACGGGCAACTGGACTGGGTGATTAACCGGGCGGGGCTAAGG 1437  
11035 GGGATGATGATCGCACCCCGCGCGCACTGGTGTGCAATTTACACCCCTGTGACGCTTG 11094  
1438 GGGTATCACAGCGCAACACCGGATGGCAGTTGGACGCGTTTACGCCAATTAACATGCCCTG 1497  
11095 CCGGTAGATATCGGATCCAAAGCAGTGTCTCGGCTCTATTTCGGGCAAAACAGATGTTGG 11154  
1498 CCGATAGATATTTCTCATCTCGCGCTCAACTTGGCGATTTAATGGGAGCCGGGCTGTCC 1557  
11155 GACATGGTCTATCGGCGCGCAGTGTTCGGCTCTATTTCGGGCAAAACAGATGTTGG 11214  
1558 GATTAGTGTAAATGGTCCCAAGTGTGGCTTAATATGTCAATAACCGGTGATGTTT 1617  
11215 AATAAGGGAGACCGTGACGAAACCGAAAGACTCACTCTGCGGTCCCGGGGTGAC 11274  
1618 ACCGAAGGCGGATGTGGTCAATCCGGTGTATCACCTGCGCTACCGGCGCGCAT 1677  
11275 CCAGTACCTCGTGGCTTCAGTGATATGGCTGGCAGTGGACAGCAGATTTGACGGAG 11334  
1678 GCCGTGAAGTAGTGCAATTTAGTGACGTAAGTGGTTCAGGCGCAAGCACAATCTGGTTGAA 1737  
11335 GTGCGTGTAAATGGAGTACGTTACTGGCCAAACCTGGGCGACGCTGTTTCGGTACGCG 11394  
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11395 GTGAATATTCGGGTTTTAGCCAGTCAGTACGTTTAAACCTGACCAAGATATTTGCTG 11454  
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11455 GCGGATACCGAGGTTCCGCTACCGACCGACCTGATTTATGCGATGATGACCGGTTAGTC 11514  
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11515 ATTTATTTCAACAGAGTGGTAATTTATTTTCGCGAGCCGATACGCTGCTTTCGCCGAAA 11574  
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1978 GGCCTCGGTTTTGATGATACCTGCCAGTTGCAAGTAGCCGATGTACAAGGGTTAGGCGTT 2037  
11635 CTTAGCCTGTACTGACGTTCCCAATGTGCGGCTCATCATCTGGGTGTCGATTTATCG 11694  
2038 GTGAGCCTGATCTTAAGCGTACCGCATATGGCGCCACATCATTTGGCGCTGCGATCTGACC 2097  
11695 GCAGACAAACCTGGTGTGTAATGGCATGAACAATAATGGGGCGCGGATGCACCTG 11754  
2098 AACGCGAACCCTGGTTACTCAGTGAAACGAAACAAATATGGGGGCCAATCACACTTG 2157  
11755 CACTATCGAGTTCCGTGAGTTCTGGCTGGATGAGAAAGCCGAGCACTGGCGGAGGC 11814  
2158 CATTACCGTAGTCTCTCGAGTCTGGCTGGATGAAAGCTGCGGCAATTTGGCTACCGGA 2217  
11815 AGTTCCTCTGCTTACCTGCAATTTAATTGCAATACCTGTGGGTTCCGTGGTGGCAG 11874  
2218 CAAACACCGGTCTGTTACCTGGCCCTTCCCGGTTCCATACCTTTGGGCAACAGAAACCGAG 2277  
11875 GATGAGATCACCGGTAACCGTCTGGTCAGCGACGCTGCTTTATGCGCCACCGGCTCTGGGAC 11934

2278 GATGAAATCAGCGGCAATAAGTTAGTGACCACTGTTAGTCTCACGCGCTTGGGAT 2337  
11935 GGGCAGGAAACGCAAGTTTCGGGGGTTTGGTTTGTGATCAGGATATCCGATACCTTG 11994  
2338 GGACGCTGAACCGGAAATTCGTGGCTTTGGTTATGTTAGCAGACAGACGCAATCAACTC 2397  
11995 GCAAGCCAGGATACCGGACGAACTGAGTATGCCCTTCTGTGAGCCGGAATGTTGATGCC 12054  
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12055 ACCGGGTACCGGCAAGTAGCAGAGCTCTGCCGAGACGATATTGGCAAAACGATGCCGC 12114  
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12175 ACTCG---GACGACAGCAGACATCTGTTTGCAGCGAGCCCTGAAAGGCACTCTGCTG 12231  
2575 ACACCGGAAGATGACCAATAATCTATCTGTTTAAACCGGGCGCTTAAAGGTGAGCCACTG 2634  
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2635 CGTAGTGAATCTTAAGGCTGATGGCAGCGCAGCAGCAACAGATCCCCTATACAGTACT 2694  
12292 GAGTCTGCGCCGAGGTACGGCTAGTGTGAAGCGAATG---GAGACTACCCGCTGGTGTGG 12348  
2695 GAATCCCGTCCACAGGTGGCGCAATTAACAAGATGGCGCACCGTTTCCCGGCTGCTCTGG 2754  
12349 CCGATGGGCGGAAAGCGTACGTTTATGAAACCGTACCAACATGATCCTCAATGC 12408  
2755 GCTCAGTCTGGAAGCGTATGATCACTACGAACTGATTTATCAGTATCCCCAGTGC 2814  
12409 CAACAGCAGCGGTACTCTCAGTGTGAATACGCTTTCCCACTGCTGCTGAGTCAAGTGC 12468  
2815 AATCAGGATATCAGTGTTCAGTGACCTATTTCGGGCAACCACTGAAACAGTTCCTGTA 2874  
12469 AATTTACACGACGCGCTCCGTGGCGGACAAATTCATATCCGCGGTCTTTACCGGCGAG 12528  
2875 CAATATCCCGCGCAACAAACCAACCAATCCGTATCCCGATACCCCTACCGGATAGC 2934  
12529 CTGTTGCGCAACAGTTATGACGAGCAGCAGAGATATTACGCTGGGTTGCAACAGAGC 12588  
2935 CTGTTTGGCAGCAGTTATGACGATCAACAAACAGCTATTTCGATTAACCTGCGCAATCC 2994  
12589 AGTGACATCACTTTGTTTCACTGTCTGAGGGGCATTTGGTTTGGGGTTGGCGAGGCG 12648  
2995 AGTTGGCACCATCTTATT-----GGTAATGAGCTAAGAGTGTGGGATTACCGGATGCG 3048  
12649 TCGCGGAGCAGTATTCAGTATCTCTGCGGACAACTGTCGCGGAAAGGGGCTGTGACGCTG 12708  
3049 ACACGAGTATGCTCTTACTTACGATGCCAAACAGTACCTGTGATGGCTTAAATCTG 3108  
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3109 GAAACCTGTTGGTGAATAATAGCTGATTTGCCGATGATAAAACCTGCGGAATACCTCAAT 3168  
12769 CAGCAGCAAGTCTGGTATCTGATTTCAAAAGACGTTGCGCCGCTGCTCTCGGCGACCTC 12828  
3169 CAGCAACGAACTTTATACCGACGGGAAACCAACACACCTGAAACACCGACACGA 3228  
12829 CCCCCCAAGGTAGCTTTTATCGAAACGCGCGCTGCTGGATGAGGGTATGTTGATGTTTAC 12888  
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12889 GCTGCTCATATGTTGATGA-----ACATCTCGAGCAAGCCGTTTACCGGCAA 12936  
3289 GATGGCGTATTTACGCCAGACGAATTAACGGGAATTAAGACAGCGCGGATACCAACAA 3348  
12937 TCCGGATACCTTTTCCCTCGAGGAGGAGCAGAACAGGCAATTTGGAGCCCAAGTGTCTAG 12996  
3349 GAGCCTTATCTGTTTCCACGCAACCGCGGAAACAA-----AGTTTGGGTAGCGCTCAA 3402



Db	643	GATGAATAATTACGCACCAATTTACAGGCTACAGCCCAACGTTATTTACACATCGTGTATTAC	702
Qy	10318	GGTAACCGTTCAGGCGGCTCGGACGCTACCGGCGCTGGTGTGCA---CACCATCAATGGAT	10374
Db	703	GGCAACCGTACAGCAGCGAAACATTACCCGGTCTCGGATGGCAGCGCCCATCACAGCA	762
Qy	10375	AGCTGGCTGTTTATCTGGTGTGTTGATATATGTTGACGCTAGCTCGGTGCTCTGAAGCG	10434
Db	763	GACTGGTGTGTTCTATCTGGTATTGATATACGGCGAACGCGATAACAACTGAAAAACGCCA	822
Qy	10435	CCGGCCCTGGCAAAACACCCAGGAAGTGGGGAGTGGCTGTGCTGTCAGGATGTTTTCCTGGG	10494
Db	823	CCAGCATTTTCGACTACAGTAG-----CTGGCTTTCGGCTCAGGACCGGTTTTCCTGGT	876
Qy	10495	TATGAGTTTCGGTTTTAACCTGCGGACTGCGCGGCTGTGCGGCTAGGTTTGTGATGTTCCAT	10554
Db	877	TATGAATATGGCTTTGAGATTCGTACCCGCGCTTATGCGCTCAGGTATTTGATGTACCAT	936
Qy	10555	TACCTAGTGTCTTGGCGGGAGTTCGGGAGCGAATGATGCCCGCAGCATTTGATTTCTGCG	10614
Db	937	CACCTCGAACACTGGATAGTAGTAAGATAACAGAACACACGACCAACGCTGGTTTCACGC	996
Qy	10615	CTGTGCTGGACTACAGGGAAAGTCTCTTCACTCAGTCTCTCTCGAAGAACGTGACCAAGGTG	10674
Db	997	CTGATACTCAATTACAGCAAGAACGCGATAGCCAGCACGCTAGTATTCTGTCGCCGAGTG	1056
Qy	10675	GCATTAGTTCGGACGGGAGCTCTTGTGCTTTCGCGGCACTGGCATTTGGGGTGGCAACC	10734
Db	1057	GGACACAGCAAGATGGTAAATGTCGTACCCCTGCGCCCATTAAGAAATTTGGCATATCAGGAT	1116
Qy	10735	TTTTACCCCGCGCATTTGTCGGCATGGCAGACGCGTGACGATATGGGCAAGTTGAGTTTG	10794
Db	1117	TTTTACCGCGACATCAGCGCTCACTGGCAACCAATCGATGTACTGGCAACTTCAATGCC	1176
Qy	10795	CTTCAACCCCTATCAGCTTTGATAGCTTAACGGCGAAGGTGGTGGGTATCTGTATCAG	10854
Db	1177	ATTTCAGCGCTGGCAGCTAGTTCGATCTCTAAAGGCGAAGGATTTACCCGCGCTGTTATATCAG	1236
Qy	10855	GACAGCGTGCCTGGTGTACCGTGAACCGGTACGCGAGTACGCGGAGTATCCCGATGCT	10914
Db	1237	GATAAAGCGCTTGGTGTACCGCTCGGCACACGCTCTGGCGGAATTTGGCTCAGATGCC	1296
Qy	10915	GTGACTTGGGGGCGGCTGCGGCCCTCGCGAACAATGCCCGTTTGTGATAACAGCGGCATC	10974
Db	1297	GTCACTTGGGAAAGATGCAACCTTTATCGTTTATCTCTTTGCAAAAGTAATGCTCTG	1356
Qy	10975	CTGCGCATCTTAATGGGATGTGCGGTGGAGTGGTCTGTACCGCCCCCGGTGTGGG	11034
Db	1357	TTGGTGATATCAATGGAGACGGCAACTTGAATGGGTATCACCGGACCGGATTTACGG	1416
Qy	11035	GGGATGTATGATCGCACCCCGCGCGCACTGGTTGCATTTTACCCCGCTGTGAGCTTTG	11094
Db	1417	GGATATCATAGTCAACGCCCGGATGGCAGTTGGACACGTTTTTACCCCATCAACGCTCTG	1476
Qy	11095	CCCGTAGAATATGGGATCCAAAGCAGTGTCTCGCCGATATCTTGGGGCTGGTTAAG	11154
Db	1477	CCGGTGAATACACCCATCCACGCGCGCAACTCCGAGATTTAATTTGGGAGCCGGGCTATCC	1536
Qy	11155	GACATGCTGTATTCGGGCGCGCAGTGTTCGCTCTATTTCGGGCAAAAACGATGTTGG	11214
Db	1537	GATTTGGTGTGATCGGCCCTTAAGACGCTGGTTTATATGCCAATACCCGCAAGCGCTTT	1596
Qy	11215	AATTAAGGGGAGACCGTGACGAAAAACGGAAGAATCACTCTGCGGCTCCCGGGGTGAC	11274
Db	1597	GCCAAAGGAAAAAGATGTGGTGCAATCCGGTGTATCACACTGCGCGTGGCGGCGCCGAT	1656
Qy	11275	CCAGTACCTCTGTCGGGTTTCAGTGATATGGCTGGCAGTGGGACAGCAGCATTTTGCGGAG	11334
Db	1657	CCAGTAAGTTTGGTGGGTTTGTGTATGTATTTGGGTTTCAGGTCAAGCCCATCTGGTTGAA	1716
Qy	11335	GTGCGTCTAATGGAGTACGTTTACTGGCCAAACCTTGGGGCAGCGTCTGTTTCGGTCAAGCG	11394
Db	1717	GTAAGCCGACTAAAGTCACTGCTGGCTTAATCTTGGGGCGGGAGGTTTGGTCAAGCC	1776
Qy	11395	GTGAATATTCGGGTTTTTACGAGTCACTGCTTTAAACCCCTGACCAAGATATTGCTG	11454
Db	1777	ATTACCTTTACGGGANTTCAGCCAGCAACCGAGTTTAAACCCGCTCAAGTTTATCTG	1836
Qy	11455	GCCGATACCAACCGTTCGGGTACCGGACTCATTTTATGCGATAGTGACCGGTTAGTC	11514
Db	1837	GCCGATCTGATGCGAGCGGTCCACGGATCTGATTTATGTTTCATACAAACCGTCTGGAT	1896
Qy	11515	ATTTATTTTCAACAGAGTGGTAAATTTTTCGCGAGCCGCGATACGCTGCTTTGCCGAAA	11574
Db	1897	ATCTTCTGAAACAAAAGTGGCAATGGCTTTGCTGAAACCAAGTGCATTAACGTTTCCCGAA	1956
Qy	11575	GGTGTGCGCTATGATCGCACTGCAGTCTGCAAGTGGCGGATATCCAGGGGCTGGGGGTG	11634
Db	1957	GGTCTGCGTTTGTATCATACCTGTCAAGTTTACAAATGGCGGATGTACAAGGATTTAGCGGTC	2016
Qy	11635	CCTAGCCCTGTACTGACGGTCCGCCATGTGCGCCCTCATCATCTGGGTGTGCCATTTATCG	11694
Db	2017	GCCAGCTGATACTGAGCGTGGCCATATGTCTCCCCCATCACTGGCGCTGCGATCTGACC	2076
Qy	11695	GCAGACAAAACCTGGTTTGAATGGCATGAAACAAATATGGGGGCGCGGCHATGCACTG	11754
Db	2077	AACATGAAGCGGTGGTTACTCAATGAAATGAAACAATATGGGGTCCCATCAACCTTG	2136
Qy	11755	CACATATCGAGTTTCGGTGCAGTTCTGCTGGATGAGAAAGCCGAGACACTTGGCGGAGCG	11814
Db	2137	CGTTACCGCAGTTCTCCCAATTTCTGGCTGGATGAAAGAGCCGCGGCTGACTACCGGA	2196
Qy	11815	AGTTCCCTGCTGCTACCTGCCATTTACATTCGATACCCCTGTGGGTTGGGTGGCAG	11874
Db	2197	CAAAACACCGTTTGTCTATCTCCCTTCCCGATCCACACCTATGGCAAAACGAAACAGAA	2256
Qy	11875	GATGAGATCACCGGTAAACGCTGTGTCAGCGAGCTGTTTATCGCACCGCGTCTGGGAC	11934
Db	2257	GATGAATTCAGCGGCAACAAATAGTACAAACACTTCGTTATGCTCGTGGCGCATGGGAC	2316
Qy	11935	GGGCAGGAAACCGAGTTTCGGGGGTTTGGTTTGTGAGATCAGGAGTACCGATACCTTG	11994
Db	2317	GGACCGCAGCGGAAATTTCCGGATTTGGTTATGTAGAGCAGACAGACGCACTCAACTG	2376
Qy	11995	GCAAGCAGGGTACGGCGACGGAACTGAGTATGCTTCTGTGAGCCGGAACCTGATATGCC	12054
Db	2377	GC---TCAAGGCAACGCGCCAGAACGTACGCCACCGCGCTGACCAAAACCTGGTATGCC	2433
Qy	12055	ACCGGGTACCGGCAGTACGACGAGCGTCTGCCGAGACGTTATTTGGCAAAACGATGCCGCC	12114
Db	2434	ACCGGACTGCGCGGTAGATAGCAATATCAACAGGATTTGGCGTGTATCAGGCT	2493
Qy	12115	GCTTTTCCGATTTTCGACCCCGTTTCTGTCGTTTCAGGAGAGGATGAGACAGACATAT	12174
Db			

12472	Qy	TATCCAGCAGCGCCCTCGGTGGGGAGCAATCATATATCCGGCGTCTTATCCCGCGCAGCGCTG	12533
2854	Db	TACCCGCGCGCCGAGCAGCGCAATCAATCTGTATCTCTGTATACATATTCCTTGATAAGTTG	2913
12532	Qy	TTCCGCAACAGTTTATGACGAGCAGCAGCAGATATTACGCTCGGGTGTGCAACAGAGCAGT	12591
2914	Db	TTAGCCAAACAGCTATGATGACCAACACGCCAATTTACGGCTCACCTATCAACATCCAGT	2973
12592	Qy	GCACATCACCTTGTGTTTCACTGTCTGAGGGGCAATGGTGTGTGGGTTTGGCGGAGCGTCG	12651
2974	Db	TGGCATCACCTGACCAACAATACCG-----TTCCAGTATTGGGATTACCGGATAGTATACC	3027
12652	Qy	CGGGACGATGTTATTCACGTTCTCTCGGACACGTCGCCGAGGGGTCTGACGCTGGAA	12711
3028	Db	CGCAGTGATCTTTTACTTATGCGCGCTGAAAATGTCTGCTGTGGTGTGTTTAAATCTGGAA	3087
12712	Qy	CACCTGTGGCGCCCGAAAGCCTGTGTCGAGTAGTCAAGTCGGTACGTCGGCGGTGAG	12771
3088	Db	CTTCTGAGTGATAAANAATAGCTGATCGCGGACGATAAACACAGTGAATACCTCGGTGAG	3147
12772	Qy	CAGCAAGTCGTGTATCTGGAATTCACAAGACGTTGCCACCGTCTGCTCCGCCACTCCCC	12831
3148	Db	CAAAAAACCGCTTATACCGCATGGACAAAAATACAACCGCTTGCAAAACCAACACGGCAA	3207
12832	Qy	CCCAAGGTAGCTTTTATCAAAACGCCGTCGTGGATGAGGGTATGGTCAGTTTCACTGGCT	12891
3208	Db	GCCTGATTGCTCTTATACCGAAAACAACGCTTATCAACCAAGTCACATTTATCAGCGTTTAAAC	3267
12892	Qy	GCCTACATTTGTGATGAACA-----TCTCGAGCAAGCGGTACCGGCAATGCC	12939
3268	Db	GGNAGCATCCGTCCTCGATAAATATCAACGACGCTGGAGCAAGCTTGGATATACGCAACA	3327
12940	Qy	GGATACCTTTTCCCTCGAGCGAGGGAAGCAGAACAGGCATTTGTGGACCGCAGTGTCAAGGA	12999
3328	Db	AATTATCTATTCCTCGCACTGGAGAAG-----ATAAAGTTTGGTAGCCCATCAACGCGC	3381
13000	Qy	TATGTTTACCTATGCGCGCGCAGACATTTCTGGCTACCGCTATCCTTTCCGGGACAGTATG	13059
3382	Db	TATACCGATTATGGTACAGCGGCAAGTTCTGGCGCCGCAAAAAACAGAGCAACACCCAA	3441
13060	Qy	TTGACCGGCCAGTTTACCGTGAACGCGTACGCGTACGACTGCGTCTATCACGCAAGTGGCAG	13119
3442	Db	CTCACCGGTAAATCACCTCTATCTGGATGCAAACTATTGGCTTGTGGTACAAACCGCG	3501
13120	Qy	GATGCGCAGGGAATGTCTACCAACGCGACTATGACTGCGGCTTCTTCAACGCCGTCGCG	13179
3502	Db	GATGCTGCTGGACTGACAACCTCAGCAAAATATGACTGCGGTTTTCTGACCCCGGTGCAA	3561
13180	Qy	GTGACGGACCCCAATGATTAATCTGCAAGTCCTGCTCTGATGCTCTGGCGCGGGTGAAC	13239
3562	Db	CTCACCGATATCAATGACAATCAGACACCTTATCACACTGGATGCAATGGGCGGACCAATC	3621
13240	Qy	ACCCTCGGATTTCTGGGGCAGGAGATGGTATTGCCACCGGTGA-----CAGTGAAT	13290
3622	Db	ACATTCGCTTTTGGGGAATGAAAACGGCAGATGACAGGTTATTCCTCACCGGAATAA	3681
13291	Qy	GCCACGTTGTCCGTTCCGGACGGCGCAGCAGCGCTCTGGCGTTTGACGGCGCCCTACCA	13350
3682	Db	GCATCATTTTCTCCACCATCCGATGTTAATGCGCTATTGAGTTTAAAAAACCCTCCCT	3741
13351	Qy	GTAGCACAGTGTCTGTGTATGTACGGACAGTCTGGGAGATGACGACAATGAGAAAA	13408
3742	Db	GTAGCACAGTGTCAAGTGTACGCACACAGAAAGCTGGATCCAGTATTAAAGTCAGAAA	3799

RESULT 13

RESOLUTION 13  
US-10-609-113-43

US-10-003-113-43 ; Sequence 43, Application US/10609113

; Publication No. US20040110184A1

GENERAL INFORMATION:

; APPLICANT: Bintrim, Scott

APPLICANT: Bevan, Scott

; APPLICANT: Zhu, Baolong

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; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: Pesticidally Active Proteins and Polynucleotides Obtainable from
; FILE REFERENCE: Paenibacillus Species
; FILE REFERENCE: DAS-101XC2
; CURRENT APPLICATION NUMBER: US/10/609,113
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US 60/392,633
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/441,647
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 4425
; TYPE: DNA
; ORGANISM: Photorhabdus strain w14
; US-10-609-113-43

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Query Match 5.5%; Score 1046.4; DB 17; Length 4425;  
Best Local Similarity 56.4%; Pred. No. 1.4e-252;  
Matches 2166; Conservative 0; Mismatches 1606; Indels 66; Gaps 9;

Qy	9598	ATCGAAATCATCAAGACATGGCCATTACTGCCCCCAAGTGGCTTCGCGGGCGGTGGC	9657
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Qy	9658	GTCAACGGGCTCAAGGGTGATATCGGGGGCAGGGCCGGATGGTGGCGGACCTGTAGT	9717
Db	61	ATCAGCGGAATGGTGAAAGATTTAAACCCCACTGGACCGGATGGTATGGCCGCGCTATCT	120
Qy	9718	ATTCCCTTGCGGTTAGCCCCCGGTTCAGCCCCCACTGGGGGCACTTAATTTATCAC	9777
Db	121	CTACCATTTGCTATTTCGCGGGCGGGTATGCTCCCGCATTCACCTCTGNAATTACAAC	180
Qy	9778	AGCGGTGCGGGGAAACGGCCCCCTTTTGGCATTTGGCTCGGGGTATCGGCGGTGCTGCTGCAG	9837
Db	181	AGCGGGCGCGTAACAGTCCATTTGGTCTCGGGTTGGGATTCGAACGTTATGACTATCCGC	240
Qy	9838	CGTGTACGGCAACGGAGCACTCACTACGATGATACTGATGAATTACACGGTCCCGAC	9897
Db	241	CGCGCACCCATTTTGGCGTCCCCCAATTATGACGAAACGGATACCTTTTGGGGCCAGAA	300
Qy	9898	GGTGAGGTGTGGTTCGGCACTCAACGGCTGTGGCACCCCAAGAAAGCACGGCAGGCCACC	9957
Db	301	GGCGAAGTGTGGTG-----GTAGCGGATCAACCTCGCGACGAATCC	342
Qy	9958	TCACTACTGGGGAATAAACCGAGCGGAAGCTTCAACGTTTCAGGTTTACGTTACGTACG	10017
Db	343	ACATTACAGGGTATCAATTTAGCGCGCACCTTTTACCGTTACCGGTACCGTTCCCGTCTG	402
Qy	10018	GAGGGTAGTCTCAGCGCCTTCAGCGTTGGCTGCCCGCGACGACAGAAACGGAATTT	10077
Db	403	GAAAGCCATTTACGCCGATGGAAATTTGGCAACCCAAACAAACAGGTAAACAGATTTT	462
Qy	10078	TGGGTGTATATACCCCTGACGGACAGGTGGCTCTGTCTGGGCGGAAATGCGCAGGCTCGC	10137
Db	463	TGTTGATATATAGCCAGATGGCAGGTGCATCTACTGGGTAAATCACCGAAGCGGG	522
Qy	10138	ATCAGCAACCCACAGCCCCAACACAGACGGCGGTTTGGCTGTATGGAGTCTCTCGGTATCA	10197
Db	523	ATCAGCAACCCATCCCAACAGCACAAACAGCACAATGGCTGCTGGAAAGCCTCTGTATCA	582
Qy	10198	CTTACGGCGGAACAGATGTTATTACCAATACCGTGGGAGATGATGACGGTTGTGACGAG	10257
Db	583	TCACGTGGCGGAACAAATTTATTCAATATCGCGCGAAGATGACACAGGTTGGGAAGCA	642
Qy	10258	GCAGGCGGACGCGCACCCGAGGCGCGGCCCAACGTTATCCCGTGGCGGTCTGGTAT	10317
Db	643	GATGAATTTACGCACCATTTACGGCTACAGGCGCAACGTTATTTACACATCGTGTATTAC	702
Qy	10318	GGTAAACCGTCAGCGGCTCGGACGCTACCGGCGCTGGTGTGCA---CACCATCAATGAT	10374
Db	703	GGCAACCGGTACAGCCAGCGAAACATTATCCGCTCTGGATGGCAGCGGCCCATCAAGCA	762



[illegible]

## RESULT 14

RESOL 14  
US-10-754-115-44

US-10-734-113-14 ; Sequence 44, Application US/10754115

Sequence 44, Application US/1071071, Publication No. US20040208907A1

; GENERAL INFORMATION:

; APPLICANT: Hey, Timothy

APPLICANT: Schleper, Amanda

APPLICANT: Bevan, Scott

APPLICANT: Bintrim, Scott

APPLICANT: Mitchell, Jon

; APPLICANT: Li, Ze sheng

APPLICANT: Ni, Weiting

APPLICANT: Zhu, Baolong

```

; APPLICANT: Merlo, Don
; APPLICANT: Apel-Birkhold, Patricia
; APPLICANT: Meade, Thomas
; TITLE OF INVENTION: Mixing and Matching TC Proteins for Pest Control
; FILE REFERENCE: DAS-104XC1
; CURRENT APPLICATION NUMBER: US/10/754,115
; CURRENT FILING DATE: 2004-01-07/754,115
; PRIOR APPLICATION NUMBER: US 60/441,723
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44
; LENGTH: 4425
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) . (4422)
; US-10-754-115-44

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Query Match 5.5%; Score 1046.4; DB 18; Length 4425;  
Best Local Similarity 56.4%; Pred. No. 1.4e-252;  
Matches 2166; Conservative 0; Mismatches 1506; Indels 66; Cons 9.

Qy	9598	ATGCAAAATCATCAAGACATAGCCATATTATGCCCCCAGATGTGCTTCCGGGGCGGTGCG	9655
Db	1	ATGCAAAATTCACAAGATTTTAGTATTACGGAATCTGTCACTGCCCCAAAGGGGGGGCGCT	60
Qy	9658	GTACACGGGCTCAAGGTTGATATCGGGGGCAGGCGCGGATGTTGCGGCGACCCCTGAGT	9717
Db	61	ATCACGGGAATGGTGAAGCATTTAAACCCACATGGACCGGATGGTATGGCCGCGCTATCT	120
Qy	9718	ATTCCCTTGCCTGTAGCCCCGGTTCAGCCCCACCTAGCGGCGACTTAATATTAC	9777
Db	121	CTACCATTGCCTATTCTTCGCGGGCGGGTTATGCTCCCGCATTTCACTCTGANTTACAAC	180
Qy	9778	AGCCGTTGGGGAAACGGCCCCCTTTTGGCATTTGGCTCGGGGTATCGCGGGTGTGCTGCCAG	9837
Db	181	AGCGGGCGCGGTAAACAGTCCATTTGGTCTGGGTGGGATTTGCAACGTATTGATATCCGC	240
Qy	9838	GGTGTACGGCAACGGAGCACCTACTACGATGATCTGTAGAAATTTACCCGTCGGCAC	9897
Db	241	CGCCGCAACCATTTTGGCGTCCCCATATTAGCAAAACCGATACCTTTTGGGGCCAGAA	300
Qy	9898	GGTGAGTGTGTTGCTGGCGCACTCACGGTGTCTGGCACCCAGAAGCACGGCAGGCCACC	9957
Db	301	GGCGAAGTGTGTGTG-----GTAGCGGATCAACCTCGCAGCAATCC	342
Qy	9958	TCACTACTGGGATAAACCCAGCGGAAGTTCAACGTTTCAAGTTTACCGTTTCACTGTAAG	1001
Db	343	ACATTACAGGGTATCAATTTAGCGGCCACCTTTACCGTTTACCGGCTACCGTCCCGTCTG	402
Qy	10018	GAGGTTAGTCTACGCGCCTTGAGCGTTGGCTGCCCGCCGACGACGACAGAAACGGAAATTT	1007
Db	403	GAAGGCCATTTACGCGGATTGGAAATATTGGCAACCCCAAACAACAGGTAAAAAGATTTT	462
Qy	10078	TGGTGTATTATACCCTGTACGGACAGGTGGCTCTGCTGGCGCGAAATCGCAGGTCGC	1013
Db	463	TGTTGTATATAGCCAGNATGGCGAGTGTGATCTACTGGTAAATTCACCGCAAGCGCGG	522
Qy	10138	ATCAGCAACCCACAGCCCCAACACAGACGGCGGTTTGGCTGTATGAGTCTCTCGGTATCA	1019
Db	523	ATCAGCAACCCATCCCAACAGCACAAACAGCAACAATGGCTGTGGAAGCCTCTGTATCA	582
Qy	10198	CTTACCGCGAAACAGATGTATTACCAATACCGTGGCGAAGATGATCAACGGTGTGACGAG	1025
Db	583	TCACGTGGCGAAACAAATTTATTATCAATATCGCGCCGAAAGTACACAGGTCGCAAGCA	642
Qy	10258	GGCAGCGCAGCGCACCCGACCGCAGGCGGGCGGCCAACGTTATCCGGTGGCGGTCTGGTAT	1031
Db	643	GATGAATTTACGCACCATTTTACAGGCTACAGCGCAACGTTATTTTACATCTGTTATTAC	702
Qy	10318	GGTAAACCGTCAGCGCGCTCGGACCGCTACCGGCGCTGGTGTGCA---CACCATCAATGGAT	1037

Db 703 GGCACCGTACAGCCAGCGAAACATTACCGGCTCTGGATGGCAGCGCCCATCACAGCA 762  
QY 10375 AGCTGCTGTTTATCTCTGTTGTTGATTATGTTGAGCTGAGCTCGGTGCTGTCTGAAGCG 10434  
Db 763 GACTGGTGTCTTATCTGGTATTTGATTATCGGCGAAACGAGTAAACACCTGAAACGCCCA 822  
QY 10435 CCGGCTGGCAACACACAGGAAGTGGGAGTGGCTGTGCTCAGGATTGTTTTCGGG 10494  
Db 823 CAGCAATTTGACTACAGTAG-----CTGGCTTTGGCGTCAGGACCGTTTTCCTCCGT 876  
QY 10495 TATGAGTTTGGTTTAACTCGGACTCGCGGCTGTGCGGCTGAGGTTTGTGATGTTCCAT 10554  
Db 877 TATGAATATGGCTTTGAGATTCGTACCGCGCTTATGCGCTCAGGTATTGAIGTACCAT 936  
QY 10555 TACTAGGTGTTCTGGGGGAGTTCCGGAGCGAATGATGCGGCAGCATGATTTCTCGC 10614  
Db 937 CACCTGCAAGCACTGGATAGTAGATAACAGAAACACAGGACCAACGCTGGTTTTCACGC 996  
QY 10615 CTGTTCTGGACTACAGGGAAGTCTTCACTCAGTCTCTCGAGAACGTGCACAGGTG 10674  
Db 997 CTGATACTCAATTACGACGAAGCGGATAGCAGCACGCTAGTATTCTGTTCCGCGAGTG 1056  
QY 10675 GCTTATGAGTCGACGGGACGCTCTGTGCTTCCCGGCACTGGCAATGGGGTGGCAACC 10734  
Db 1057 GGACACGACGAGATGGTAAATGTCGTACCCCTGCGCCATTAGAAATGGCATATCAGGAT 1116  
QY 10735 TTTACCGCGGACATTTGCGGATGGCAGACGCTGAGATATGGGCAAGTTGAGTTTG 10794  
Db 1117 TTTTACCGCGCATCACGCTCACTGGCAACCAATGATGATCTGCGCAAACTTCAATGCG 1176  
QY 10795 CTTCAACCTTACAGCTTGTAGACCTTAACGGCGAAGTGTGGTGGTATCTGTATCAG 10854  
Db 1177 ATTACGCGCTGGCAGCTAGTCGATCTAAAGGGAAGGATTAACCGGCTGTTATATCAG 1236  
QY 10855 GACAGCGTGCTGTGTGTACCGTGAACCGGTACGCGCAGTCGGGGGATGATCCGATGCT 10914  
Db 1237 GATAAAGCGCTTGGTGTGTACCGCTCCGACACGCTCTGGCGAAATGGCTCAGATGCC 1296  
QY 10915 GTGACCTGGGGCGCGTGGGCGCTTCGCGCAATCCCGCTTTGTGATTAACAGCGCATC 10974  
Db 1297 GTCACTTGGGAAAGATGCAACCTTTATCGGTTATTCTCTTTGCAAAAGTAATGCTCG 1356  
QY 10975 CTGGCGGATCTTAATGEGGATGTGCGTGGAGTGGTGTACCCGCCCGGCTGGGCG 11034  
Db 1357 TTGGTGGATATCAATGGAGCGCCCACTTGACTGGGTTATACCCGACCGGATTAACGG 1416  
QY 11035 GGGATGTATGATCGCACCCCGCGCGAGCTGGTTGCAATTTCAACCCCTGTGAGCCTTG 11094  
Db 1417 GGATATCATAGTCAACCGCGGATGGCAGTTGGACACGTTTTACCCCACTCAACGCTCTG 1476  
QY 11095 CCGGTAGATATCGCATCAAAAGCAGTGTCTCGCGATATCTCGGGGCTGGTTAAAG 11154  
Db 1477 CCGGTGGAATACACCCATCCACGCGGCAACTCGCAGATTTAATGGGAGCCGGCTATCC 1536  
QY 11155 GACATGCTGTTATCGGCGCGCAGTGTTCGCTCTATTCCGCGCAAAACGATGTTGG 11214  
Db 1537 GATTGGTGTGATCGGCTTAAGAGCGTGGTTTATATGCCAATACCCGCGACGCGCTT 1596  
QY 11215 AATAAAGGGGAGACCGTCGAGCAAAACGAAAGACTCACTCTGCGGTCGCGGGTTGAC 11274  
Db 1597 GCCAAAGGAAAGATGTGGTGCAATCCGGTGATATCACACTGCGGTGCGGGCGCGAT 1656  
QY 11275 CACGTACCTCTGTGGGTTTCAATGATATGGCTGGCAGTGGAGCAGCAGATTTGACGGAG 11334  
Db 1657 CCACGTAAAGTTGGTGGCTTTAGTGATGATTGGGTTTCAGGTCAAGCCCATCTGGTTGAA 1716  
QY 11335 GTGCGTCTAAATGGAGTACGTTACTGCGCAAACTCGGCGCAGTGTGTTTCGCTCAGCG 11394  
Db 1717 GTAAGCGCACTAAAGTACCTGCTGCGCTTAATCTGGGGCGGAGCTTTGGTCAACCC 1776  
QY 11395 GTGAATATTCCCGGTTTATAGCCAGTCACTACGTTTAAACCTGACCCAGATATTGCTG 11454

Db 1777 ATTACCTTACCGGATTCAGCCAGCCAGCAACCGAGTTTAAACCCGGCTCAAGTTTATCTG 1836  
QY 11455 GCGGATACCGACGGTTCGGTACCAGGACCTGATTTATGCGATGAGTACCGGTTAGTC 11514  
Db 1837 GCGGATCTGGATGGCAGCGGTCGAACGGATCTGATTTATGTTTATCAAAACCGTCTGGAT 1896  
QY 11515 ATTATTATCAACACAGAGTGGTAAATTTTCGCGGAGCCGATACGCTGCTTTCGCGAAA 11574  
Db 1897 ATCTTCCTGAACAAAGTGGCAATGGCTTTGTGTAACAGTACATTAGCTTTCGCGAA 1956  
QY 11575 GGTGTGCGTATATGATGCACTCTGCAAGTCTGCAAGTGGCGGATATCCAGGGGCTGGGGTG 11634  
Db 1957 GGTCTGGCTTTTGTATCATACCTGTCAAGTTTACAAATGGCGGATGTACAAGGATTTAGCGTC 2016  
QY 11635 CTTAGCTGTTTACTGACGGTCCCGCATGTGCGGCTCATCACTGGGTGTGCCATTTATCG 11694  
Db 2017 GCGAGCTGATATGAGCGTGGCGCATATGTCTCCCATCATCTGGCGCTGCGATCTGACC 2076  
QY 11695 GCAGCAAAACCTGGTTGTTGAATGGCATGAACAACAATATGGGSCCGCGCATGCACATG 11754  
Db 2077 AACATGAAGCCGTGTTACTCAATGAATGAACAACAATATGGGGTCCATCACACCTTG 2136  
QY 11755 CACTATCGCAGTTCGGTTCAGTTCGGCTGGATGAGAAAGCGGAGCACTGGCGGCGAGC 11814  
Db 2137 CGTTACCGCAGTTCCTCCCAATTCGGCTGGATGAAAAGCGCGGCTGACTACCGGA 2196  
QY 11815 AGTTCCTGCTGCTACTCTGCTGATCAATTTACATTCGATACCTGTGGGTTCGGTGGTGAG 11874  
Db 2197 CAAACACCGGTTTGTCTATCTCCCTTCCGATCCACCTATGGCAACGGAACAGAA 2256  
QY 11875 GATGAGATCACCGGTAACCGTCTGCTGACGACGCTGTTTATCGCCACGCGCTCTGGGAC 11934  
Db 2257 GATGAATCAGCGGCAACAAATAGTCAACACTTGTGTTATGCTGCTGGCGCATGGGAC 2316  
QY 11935 GGGCAGGAAACGCGAGTTTCGGGGGTTTGGTTTTGTGAGATCAGGGATACCGATACCTTG 11994  
Db 2317 GCACGCGAGCGGAAATTCGCGGATTTGGTTATGTAGACGACAGACAGCATCACTG 2376  
QY 11995 GCAAGCAGGGTACGGGACGGAACGTAGTATGCTTCTGTGAGCGGAACTGTGATGCC 12054  
Db 2377 GC---TCAAGGCAACCGCGCAGACGTACGCCACCGGCTGACCAAAACTGGTATGCC 2433  
QY 12055 ACCGGGTACCGGAGTAGACAGCGTCTGCGGAGACGTTATGGCAAAACGATCGCGC 12114  
Db 2434 ACCGACTCCCGTGTATGATTAACGATTAACGCGATTTGGCTGATGATCAGGT 2493  
QY 12115 GCTTTTGGCGATTTCCGACCGCTTTCTACTGTGCTTCCAGGAGATGAGCAGATAT 12174  
Db 2494 TTTTGGCGTTTCTACCGGCTTTTACGACTTGGCAAGATAACAAGATGTCCCGTTAAACA 2553  
QY 12175 ACTCCGAGCAGCAGCAGACATTTCTGGTTGAGCGAGCCCTGAAAGGATCTGTGCGC 12234  
Db 2554 CCGGAAGATGATAACAGCTGTTACTGGTTTCAACCGCGGTTTGAAGGTTCACTGTACGT 2613  
QY 12235 AGTGAAGTTATACGGTGGGATGGCAGCAGCGCGGATATCCCTTACAGCGTCACTGAG 12294  
Db 2614 AGTGAATCTGATCGGATGGAGATGATGATCAAAATAAACAGTTCCCTATCTGCTGAA 2673  
QY 12295 TCTCCCGCAGGTACCGG---TAGTTGAAGCGAATGGAGACTACCCGGTGGTGGCGC 12351  
Db 2674 TTTTGGTTACAGTACGTGATTAACAGATACCGCAGCGGATACCTGTACTTTGGTCA 2733  
QY 12352 ATGGGCGGGAAGCGGTACGTGATTTATGAACGATGATCAATGATCTCAATGCCAA 12411  
Db 2734 TCTGTAGTTGAAGCGCAACTATCATACGAACGATTCGCCAGCGACCCGAATGCACT 2793  
QY 12412 CAGCAGGCGGTACTCTCAGTATGAATACCGTTTCCCACTGCTGCTCAGTCACTGCAAT 12471  
Db 2794 CAAATATTACGCTATCCAGTATGATTTGGTTCAGCGCTTAAACAGCTTTCGGTACAG 2853  
QY 12472 TATCCAGCAGCCCTCCGTCGGCGGCAATCAATATCCGGCGTCTTACCGGCGAGCTG 12531  
Db 2854 TACCGCGCGCGCAGCAGCGCAATCAATCTGTATCTGTATACATTTGCTGATAGTTG 2913



QY 12532 TTCCCAACAGTTATGACGACGACGACGATATTACGCTGGGTTGCAACAGAGCAGT 12591  
 DB 2914 TTAGCCCAACAGTATGATGACCAACACGCAATTAACGGCTACCTATCAACATCCAGT 2973  
 QY 12592 GCACATCACCTTTTTCACCTGTCTGAGGGGCAATGTTGTTGGGTTGGCGAGGGCTGC 12651  
 DB 2974 TGGCATCACCTTATACCAACATACCG-----TTCCGAGTATTGGGATTACCGGATAGTACC 3027  
 QY 12652 CGGACGATGATTTCAGTACTCTGCGGCAACAGTCCGGAAGGGGTCTGACGCTGGAA 12711  
 DB 3028 CGAGTGATATCTTATGCGGCTGAAATATGTCCTCTGTTGTTTAAATCTGGAA 3087  
 QY 12712 CACTGTGTGGCCCGAAGCCTGGTCTCGGATAGTCAGTCTGCTGCGGTACGCTGGCGGGTCAG 12771  
 DB 3088 CTTCGAGTGATAAATAGCCTGATCGCGGACGATAAACACGTAACCTCGGTCCAG 3147  
 QY 12772 CAGCAAGTCTGTGATCTGATGATTCAGAGAGTTCAGAGAGTTCGCGTCTGCGCACTCC 12831  
 DB 3148 CAAAAAACCCCTTATACCGATGACAAATACAAACGCGTTGCAAAACACCAACACGCA 3207  
 QY 12832 CCAAGGTAGCTTTTATCGAAGCGGCTGCTGATGAGGTATGTCAGTTCACCTGGCT 12891  
 DB 3208 GCCTGATTCCTTACCGAACAACGATTAACACGATCCACATTTATCAGCGTTTAA 3267  
 QY 12892 GCCTACATTTGGATGAACA-----TCTGAGCAAGCGGTTACCGGCAATCC 12939  
 DB 3268 GGAAGCATCCGTCGTAATTAATATCAACACGCTGGAGCAAGCTGATATCAGCAACA 3327  
 QY 12940 GATACCTTTTCCCTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 12999  
 DB 3328 AATTATCTATCTCCCTCGCACTGGAGAAG-----ATAAAGTTTGGGTAGCCATCAGCG 3381  
 QY 13000 TATGTTACCTATCGCGGCGAGAGCATTTCTGGCTACCGTATCCTTTCCGGACAGTATG 13059  
 DB 3382 TATACCGATTTGTTACAGCGGCACAGTCTCGCGCCCGCAAAACAGAGCAACACCCAA 3441  
 QY 13060 TTGACCGGCGGAGTACCGTACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 13119  
 DB 3442 CTCACCGGTAATACCTCATCTGGAGTGAACATTAATGCTGTTGGTACAAACCCGG 3501  
 QY 13120 GATGCGCGAGGATTTGACCAACGCGGAGTATGACTGGCGTCTCTGACGCGCGCTCCGG 13179  
 DB 3502 GATGCTGCTGAGTACCAACCTCAGCAAAATATGACTGGGCTTTCTGACCCCGGTGCA 3561  
 QY 13180 GTACGCGACCGGATGATATCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 13239  
 DB 3562 CTCACCGATATCAATGACAAATCAGCACTTATCAGATGATGATGATGATGATGATGAT 3621  
 QY 13240 ACCTGCGATTTGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 13290  
 DB 3622 ACATGCGCTTTTGGGAACTGAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3681  
 QY 13291 GCCAGTGTGCTGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 13350  
 DB 3682 GCATCTTTTCTCCACCATCCGATGTTAATGCGCTATTGAGTTAAATAACCGCTCCCT 3741  
 QY 13351 GTAGCAGAGTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 13408  
 DB 3742 GTAGCAGAGTCTGAGGTTCTACGACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3799

RESULT 15

US-10-242-056-31

; Sequence 31, Application US/10242056

; Publication No. US20030113323A1

; GENERAL INFORMATION:

; APPLICANT: Ensign, Gerald C

; APPLICANT: Bowen, David J

; APPLICANT: Petell, James

; APPLICANT: Fatig, Raymond

; APPLICANT: Schoonover, Sue

; APPLICANT: ffrench-Constant, Richard

; APPLICANT: Orr, Gregory L  
 ; APPLICANT: Merlo, Donald J  
 ; APPLICANT: Roberts, Jean L  
 ; APPLICANT: Rocheleau, Thomas A  
 ; TITLE OF INVENTION: Insecticidal Protein Toxins from  
 ; TITLE OF INVENTION: Photorhabdus  
 ; NUMBER OF SEQUENCES: 88  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Dowelanco  
 ; STREET: 9330 Zionsville Road  
 ; CITY: Indianapolis  
 ; STATE: IN  
 ; COUNTRY: US  
 ; ZIP: 46268  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/242,056  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/063,615  
 ; FILING DATE: 18-MAY-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/395,497  
 ; FILING DATE: 28-FEB-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/007,255  
 ; FILING DATE: 06-NOV-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/608,423  
 ; FILING DATE: 28-FEB-1996  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/705,484  
 ; FILING DATE: 28-AUG-1996  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/743,699  
 ; FILING DATE: 06-NOV-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Borucki, Andrea T.  
 ; REGISTRATION NUMBER: 33651  
 ; REFERENCE/DOCKET NUMBER: 50301E  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 317-337-4846  
 ; TELEFAX: 317-337-4847  
 ; INFORMATION FOR SEQ ID NO: 31:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4458 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 1..4458  
 ; US-10-242-056-31

Query Match 5.1%; Score 969.8; DB 15; Length 4458;

Best Local Similarity 53.8%; Pred. No. 3.3e-233;

Matches 2395; Conservative 0; Mismatches 1857; Indels 201; Gaps 11;

QY 9598 ATGCAAAATCATCAAGACATGCGCATTTACTGCCCCCACCACGTTGCTTTCCGGGGCGGTGCG 9657

DB 1 ATGCGAGATTCCACCAGAGTATCGATTACACGCTGCTACTTCCCAAGAGTGGCGGTGCT 60

QY 9658 GTCACCGGCTCAAGGTTGATATCGCGGCGGAGGCCGAGTGGTCCGGGAGCCCTGAGT 9717

DB 61 ATCAATGGCATGGGAGAGCACTGAATGTCGCGGCCCTGATGGAATGGCCTTATCT 120

QY 9718 ATTCCCTTCCGGTTAGCCCCCGGTGCGGGGTAGCCCCCAGCTGGGGCACTTAATTATCAC 9777

121 CTGCCATTACCTCTTCGACCGCAGAGGACCGCTCCTGGATTATCGCTGATTACAGC 180  
9778 AGCCGGTCGGGGAACCGCCCTTTGGCATTTGGCTGGGGTATCGCGGGTGTCTGTGCCAG 9837  
181 AACAGTGCAGGTAATGGGCTTTTCGGCATCGGCTGCAATGGTGTATGTCCATTAGC 240  
9838 GGTGCTACGCGCAACCGGACACCTACTACGATGATATGATGAATTCACCGGTCCGGAC 9897  
241 CGACGCAACCAACATGGCATTCACAATACGGTAATGACGACACGTTCTCTATCCCCACAA 300  
9898 GGTGAGGTGTGCTGCGGCACCTCAGCGTGTGGCACCCCAAGAACGACGCGAGGCC--- 9954  
301 GCGAGGTATGATATCGCCCTGAATGACCAAGGCAACCTGATTCGTCAAGAGTT 360  
9955 ACCTCACTACTGGGGATAAACCCAGCGGGAAGCTTCAAGTTACGTTTACCGTTTACCGT 10014  
361 AAAACGCTGCAAGGCGTTACTTGGCAATTTCCATATACCGTACCGCTATCAAGCCCGC 420  
10015 ACGGAGGTAGTCTCAGCGCCTTGAGCGTTGGCTGCCGCCGACGAGACAGAAACG--- 10071  
421 CAGATCCTGGAATTCAGTAAATTCGAATACTGGCAACCTGCTCCCGTCAAGAGGACGC 480  
10072 GAATTTTGGGTGTATATACCTCTGACGACAGGTGGCTCTGCTGGGCCGAAATGCGCAG 10131  
481 GCTTTCTGGCTGATATCGACACCGGACGGGCATCTACACATCTTAGGGAACCGCGCAG 540  
10132 GCTCGCATCAGAACCCCAAGCCCAACACAGACGCGGGTTGGTGTGATGAGTCTCTCG 10191  
541 GCTTGTCTGGCAATCCGCAAAATGACCAAAATCGCCAGTGGTGTCTGGAAGAACT 600  
10192 GTATCACTTACCGGCAACAGATGTATTACCAATACCGTCCGGAAGATGACGGTTGT 10251  
601 GTACCCGACCGCGTGAACATGTCAGCTATCAATATCGAGCGGAAGATGAAGCCCAATGT 660  
10252 GACGAGCGGAGCGCAGCGCACCGCGAGCGGCCGCCCAACGTTATCCGTGGCGGTC 10311  
661 GACGACAAATGMAAAACCGCTCATCCCAATGTTACCGCACAGCGCTATCTGGTACAGTG 720  
10312 TGGTATGTGTAACCGTCAAGGGGTCGGAGCTACCGCGCGCTG---TGTGCAACATCA 10369  
721 AACTACGGCAACATCAAAACCAAGCCAGCGCTTCTGTATGATATACGCACTCCCGCA 780  
10369 ATGATAGTGGCTGTTTATCTGTTGTTGATGATGAGTGGTGTGCTGCTGCTCT 10428  
781 CCGAAGAGTGGCTGTTTATCTGGTCTTTCACCGGTGAGCGCATCCTCAGCTCAT 840  
10429 GAAGCCCGGCTTGGCAAAACACAGGAAGTGGGGAAGTGGTGTCTGTCAGGATTTGTTT 10488  
841 ACGTGCCAAACATGGGA---TGCAGGTACAGCGCAATGTTCTGTACGCCGGATATCTTC 897  
10489 TCGGGTATGAGTTTGGTTTAACTTGGGACCTGCGCGCTGTGCGGTCAAGTTTGTATG 10548  
898 TCTCGTATGAATATGGTTTGAAGTGGCTACTCGCGCTTATGTCAAAAGTGTGTATG 957  
10549 TTCCATTACTAGTGTCTGCGGGGAGTTGGGAGCAATGATCGCCAGCATTTGATT 10608  
958 TTTACCGGACCCGCTCATGGCCGGAGAGCGAGTACCATAAGCCCCCGGAATGEGTT 1017  
10609 TCTCGCGTGTGCTGACTACAGGGAAGTCTTCACTCAGTGTCTGCGAGAACGTGCAAC 10668  
1018 GGACGCTTAATCTGGAATATGACAAAACGCCAGCGTCACCAAGTTGATTACCATCCGT 1077  
10669 CAGGTGGCTATGAGTCGGAACGGACGTCTTGTGCTTCCGGCATCTGGCATTTGGGGTGG 10728  
1078 CAATTAAGCCCATGAATCGACGGGAGCGCAGTCACCCAGCCACCATAGAACTAGCCCTGG 1137  
10729 CAAACCTTTACCCCGCGCATTTGTCGGATGCGACGCGTACGATATGCGCAAGTTG 10788  
1138 CAAAGTGTGATCTGAGAAAATCCCGCATAGGCAACGCTTTGACGCATAGATAATTTT 1197  
10789 AGTTTCCTTCAACCCCTATCAGCTTGTAGACCTTTAACCGGGAAGGTGTGGGTATCTCTG 10848

1198 AACTCGCAGCAACGTTATCAACTGGTTGATCTCGGGGAGAAGGTTGCCAGTATGCTG 1257  
10849 TATCAGGACAGCGGTCTGTGGTACCGTGAACCGGTATAGCCAGTGGGGGATGATCCG 10908  
1258 TATCAAGATCGAGGGCGCTTGGTGTATAAAGCTCCGCAACGTCAGGAAGACGAGACAGC 1317  
10909 GATGCTGTACCTGGGGGGCGCTCGGCGCTCCGACAAATGCGCGCTTTGCAATACAGC 10968  
1318 AATGCGGTCACTTACGACAAAATTCGCCCCACCTACCTACCCAAATTTGCAGGATAAT 1377  
10969 GGCATCTCGCGGATCTTAATGGGATGGTCCGGCTGGAGTGGTCTGTATACCGCCCCCGT 11028  
1378 GCTCATTTGATGGATATCAACGAGACGCGCAACTGGATTGGTTGTTTACCGCTCCGT 1437  
11029 GTGGGGGATGTATGATCGCACCCCGCCCGGACTGTGTTGCAATTTCAACCCCTGTCA 11088  
1438 ATTCGCGATACCATAGTCAGCAACCCGATGGAAGTGCAGCACTTTACGCAATCAAT 1497  
11089 GCTTTCGCGTATAGATATCGCATCCAAAGCAGTGTCTCGCGATATCTGGGGGCTGG 11148  
1498 GCTTTCGCGTATAGATATTTTATCCAGCATCCAGTTCGCTGACCTTACCGGGCAGGC 1557  
11149 TTAACGGAATGCTTATCGGGCGCGCAGTGTTCGCTCTTATTCGCGCAAAACGAT 11208  
1558 TATCTGATTTAGTGTGATCGGGCGGAAAGCGTGGCTATATGCGCAACGAGCAAC 1617  
11209 GGTGGAATAAAGGGGAGACCGTGCAGCAAAACGGAAGACTCATCTGCGGTCCCGGG 11268  
1618 GGTGCGGTAAAGGAGATGTCCCCCAATCCACAGGTATCACCTGCTGTCTCAGG 1677  
11269 GTTGACCAACGATACCTCTGCGCTTCACTGATATGGCTGGCAGTGGACAGCAGCATTTG 11328  
1678 ACGGATGCCCGAAACTGGTGGCTTTCAGTGAATGCTCGGTCCGCTCAACAACTCTG 1737  
11329 ACGGAGTGGTGTCTTAATGGAGTACGTTACTGCGCAAACTGGGGCAGCGTGTTCGCT 11388  
1738 GTGGAATCAAGGTAATCGCGTCACTGTTGCGCAATCTAGGSCATGCGCTTTCGCT 1797  
11389 CAGCGGTGAATATTCGCGGTTTTCAGCAGTCACTGAGTCACTGTTTAACTGACCAATA 11448  
1798 CAACCACTAATCTCTCAGGATTTAGCCAGCCCGAAATAGCTTCAATCCGAAACGGCTG 1857  
11449 TTTGTCGGCGATACAGCGGTTCCGCTACCGGACCTGATTTATGCGATGAGTACCGG 11508  
1858 TTTTCGCGGATATCGACGCTCCGCGACCCGACCTTATCTATGCGCAATCCGCTCT 1917  
11509 TTAGTCAATTTTCAACACAGAGTGTAAATTTTTCGCGAGCCGCGATACGCTGTCTTG 11568  
1918 TTTGCTCATTTATCTCAACCAAGTGGTAATCAGTTTGTATGTCGCCCTTACATTAGCGTTG 1977  
11569 CCGAAAGGTGTCGGTATGATCGCACTGCACTGCTGCAAGTGGCGGATATCCAGGGCTG 11628  
1978 CCGAAGGCGTAAATTTGACAACTTTCGCAACTTCAAGTCCCGATATTCAGGGAATTA 2037  
11629 GGGGTGCTTAGCTGTACTGACGCTCCCGCATGTCCGCGCTCATCAGTGGTGTGCCAT 11688  
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11689 TTAGTGGCAGCAAAACCTTGGTTGTAATGGCATGAACAAATATGGGGGCCCGCAT 11748  
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11749 GCATGCACTATCGCAGTTCGGTGCAGTTCGCTGGATGAGAAAGCCGAGCAGCTGGCG 11808  
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2278 ATTCAGGATGAATCAGCGGCAACCGGCTCACAGTGAAGTCAACTACAGCCACGCGCTC 2337

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DB 3109 ATTTCCCTTGAATCTTGCTGAAAGATGATGGCTCTGACAGATGAAAGCGCGCTT 3168  
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DB 4009 ATCACCAGTCTGCTGATGATGAGCTATCGGCAACAGCAGCAGCAACAGAGCGTGAGCTTT 4068  
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DB 4429 GAAACGATACAG 4441

Search completed: January 27, 2005, 10:24:46  
Job time : 9352 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 26, 2005, 06:08:43 ; Search time 50294 Seconds

(without alignments)

13720.507 Million cell updates/sec

Title: US-10-070-489A-1

Perfect score: 18937

Sequence: 1 ggatccgagtggaaggaatca.....cgtgccacggagcatggc 18937

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1.\*

2: gb\_est2.\*

3: gb\_hic.\*

4: gb\_est3.\*

5: gb\_est4.\*

6: gb\_est5.\*

7: gb\_est6.\*

8: gb\_gss1.\*

9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	385.6	2.0	1023	9	CNS01EVJ
C 2	296	1.6	983	9	CNS01GGB
C 3	256.8	1.4	654	8	AQ991360 Rfc02280
C 4	241.4	1.3	672	8	AQ990989 Rfc01839
C 5	223.6	1.2	749	8	AQ991727 Rfc00357F
C 6	216.8	1.1	685	8	AQ990831 Rfc01661
C 7	216.6	1.1	748	8	AQ991760 Rfc00753F
C 8	214.6	1.1	605	8	AQ990411 Rfc01179
C 9	197.6	1.0	881	9	CNS01R9G
C 10	192	1.0	617	8	AQ990217 Rfc00949
C 11	188.6	1.0	602	8	AQ991038 Rfc01893
C 12	188.2	1.0	604	6	CB065346 EST645027
C 13	178	0.9	735	8	AQ991741 Rfc00508F
C 14	158	0.8	765	8	AQ991783 Rfc02280F
C 15	154.8	0.8	594	8	AQ990688 Rfc01498
C 16	144.8	0.8	603	9	CNS01LYT
C 17	141.6	0.7	683	9	AL150262 Anopheles
C 18	139.6	0.7	693	9	AL157024 Anopheles
C 19	133.2	0.7	733	2	AW901477 RCO-NN101
C 20	125.6	0.7	312	8	AQ990147 Rfc00989
C 21	125.6	0.7	547	8	AQ990013 Rfc00707
C 22	119.2	0.6	494	8	AQ991400 Rfc02327
C 23	118	0.6	548	8	AQ989849 Rfc00508
C 24	117.4	0.6	567	8	AQ990696 Rfc01508

25	105.8	0.6	660	8	AQ991527	AQ991527 Rfc02507
26	105.2	0.6	406	8	AQ990055	AQ990055 Rfc00763
27	100	0.5	460	8	AQ991476	AQ991476 Rfc02418
C 28	92.4	0.5	819	8	AQ991798	AQ991798 Rfc02474F
C 29	86.2	0.5	479	8	AF175370	AF175370 AF175370
C 30	85.4	0.5	710	8	AQ989937	AQ989937 Rfc00617
31	84	0.4	422	8	AQ991079	AQ991079 Rfc01939
32	81.6	0.4	1101	9	CNS00EVL	AL0619706 Drosophil
C 33	81.4	0.4	1101	9	CNS0021J	AL061936 Drosophil
C 34	80.4	0.4	1139	8	AQ897537	AQ897537 HS_3153 A
C 35	79.2	0.4	1101	9	CNS0039G	AL063921 Drosophil
C 36	79	0.4	781	8	AQ991625	AQ991625 Rfc01183F
C 37	77.6	0.4	477	9	CNS07FW3	AL0608997 Anopheles
C 38	76.8	0.4	1896	9	CG753083	CG753083 P048-1-C0
C 39	76.2	0.4	1127	9	CL128786	CL128786 ISB1-95C2
C 40	75.6	0.4	1101	9	CNS00EVL	AL0609706 Drosophil
C 41	75.2	0.4	802	9	CNS0124I	AL011000 Drosophil
42	75	0.4	1029	9	CNS01ZGM	ALI174271 Tetradon
43	74.8	0.4	585	9	CNS01NVV	ALI152748 Anopheles
44	72.8	0.4	720	8	AQ990621	AQ990621 Rfc01421
C 45	71.6	0.4	1592	9	CG750135	CG750135 P044-3-D0

## ALIGNMENTS

RESULT 1  
CNS01EVJ/c

LOCUS  
DEFINITION

CNS01EVJ 1023 bp DNA linear GSS 30-MAY-2001  
Anopheles gambiae GSS SP6 end of clone 03B12 of NotreDamel library  
from strain PEST of Anopheles gambiae (African malaria mosquito),  
genomic survey sequence.

ACCESSION

AL141056

VERSION

AL141056.1 GI:6999174

KEYWORDS

GSS.

SOURCE

Anopheles gambiae (African malaria mosquito)

ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;

Anopheles.

REFERENCE

1 (bases 1 to 1023)

Genoscope.

AUTHORS

Submitted (16-FEB-2000)

TITLE

Submitted (16-FEB-2000)

JOURNAL

Submitted (16-FEB-2000)

COMMENT

This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut Pasteur.

FEATURES

source

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Best Local Similarity 76.7%; Pred. No. 2.2e-90;  
Matches 517; Conservative 4; Mismatches 123; Indels 30; Gaps 3;

QY 18268 ACTGGTACGATCGGTGCCAGGAACCTTTCATCAGCACCGCGGCGGTTTCG 18327  
|||||  
Db 1023 ACTGGTACGGTTCGTACGAGAACCCCTTTCATCAGCACCGCGGCGGACGTTTG 964

Laboratory of Biochem. and Biol. Molec. of Insects, Institut Pasteur.	
FEATURES	Location/Qualifiers
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Matches 397; Conservative 2; Mismatches 52; Indels 31; Gaps 4;	
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QY	18387 TCGGTTGGCCAGAAACCATAGTAACGACCACTTTAAATCCCGTGCAGGATATGGC 18446
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QY	18447 TGACGTAACGCTGCAGATCTCTCTCGCTGATTTTCCTGGGCTTTGTCTGCTGCTATC 18506
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QY	18567 CCACCGCGCGCGCTTCAGGTACCGCGCCAGGTATTTCACTGCGCCAGGCGCCCGCGG 18626
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QY	18627 TCTTTTGGCAAAATTCATCTTCCAGGGCGCGGTATTTGCGCATACAGG- 18677
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QY	18678 -----TCTTCGTTGCGGATATGCGCAGACCGCGCGGCGCCAGGATTGATG- 18725
Db	
QY	18726 -----CGCAGCAGGTGAACACCGGCATTTGCGCCAGATGGCTTCACCTCTCTTTT 18777
Db	
QY	18778 TAAAGAACAGCTCCGCCAGACGTGTGTTTGAAGTCAAGACCGCGCGGTAAACGGAGA 18837
Db	
QY	18838 CGTGATATGCGGATGTCATTTGAGCTGCGCGCTTAGTGTTGAGCGCGCAAAAATGC 18897
Db	
QY	18898 CGGCTTCGATGCCC 18911
Db	
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CNS01GGB/c	
LOCUS	
DEFINITION	
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VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

MEDLINE  
PUBMED  
COMMENT

20378633  
10919786  
Contact: ffrrench-Constant RH  
Department of Biology and Biochemistry  
University of Bath  
South Building, Bath BA2 7AY, UK  
Tel: (44) 1225 826621  
Fax: (44) 1225 826779  
Email: bssrfc@bath.ac.uk  
This is one of 2,122 random reads from the M13 library. For  
annotation of identified clones (BLASTX, BLASTN and mapping to E.  
coli K12 genome) please see ffrrench-Constant et al. 2000, Nucleic  
Acids Res.  
Seq primer: M13 Forward  
Class: shotgun.

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library"  
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Matches 407; Conservative 0; Mismatches 236; Indels 1; Gaps 1;

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DB 8 CCGGGCTTACACGGCAGTTTCAGCATCCCGTCTGGCGCGTGGCGGCTGATCTGTC 67

QY 8445 CCAATATTTACGGGCTGGCGCTGGCGCTATGGGCGCACTATTTAAAGCCACCG 8504  
DB 68 CTAACATCTTGGCTTGGCGTGGCGAGCGTGGGGGCTATCGTGGCGACAG 127

QY 8505 CCATCGGCATCCAGGTGCTCTCGATGCCACCGCATATCAGCGGACAAATCAGCCAGT 8564  
DB 128 GTTATGTGATGGAATCTCCGCGAATGTTATGAACACCGAAGCGGATAAATATAGCCAAT 187

QY 8565 CGGAGTGTACCGCGTGGCGGAGGTGGGAATCCAGCGTGTAGTGGCGAGTCTG 8624  
DB 188 CTGAAACCTACCGTGGCGGTCAGAGTGGGAGATCCAGCGGAATAATGCCGAAGCGG 247

QY 8625 ACGTGGCGCAGATTGATCCAGTGGCGGCCATGGCAGTGGCGGGAAGGGCTGAGC 8684  
DB 248 AATTGAAGCAATCGATGCTCAGCTCAATCAGTCTGCTGATCGCGGGAAGCGCGGTAT 307

QY 8685 TGCAGAAACTTACCTTTAGACCCAGCAGACCCAGGACAGGCGCAGTTGGCAATCTCTGC 8744  
DB 308 TGCAGAAACCAAGTCTGAAACCCCAACAAGAACAGACCCCAATCTCAATTGSCCTTCTGC 367

QY 8745 AGAGTAAGTTCAACAATACGGCTCTGTACAGTGGCTGGCGGCGAGGTTGTCGCCCAATT 8804  
DB 368 AACGTAAAGTTACGAATCAGGCGGTTATACAATGGCTGGCTGGCTGCGACTGGCGCGGATTT 427

QY 8805 ATTACCAAGTTCTATGACCTGGCAGTATCCCGCTGGCTGATGGCGCAACAGCCCTGGCAGT 8864  
DB 428 ACTTTCAGTTCTACGATTTGGCGGTGGCGGTGGCTGATGGC-AGCAAGCTTACCGTT 486

QY 8865 GGGATAAAATTCGAGACTAGTTCGTTTATCCAGCGCGGGGCGCTGATGGGGGCAAAATGCCG 8924  
DB 487 GGGAACTCATGATGACNTGCGCTTATTAACCGGGCGCTGGCAGGGAACCTATGCGG 546

QY 8925 GTCTGCTGGCGGGGAAACCTGATGCTGAATCTGGCGGAGATGGAGCAGGCTGGCTGA 8984  
DB 547 GTCTGCTTGCAGGTGAAACCTTGTATGCTGAGTCTGGACAAATGGAAGACGCTCATTTTGA 606

QY 8985 CGGGGGATGAGCGGGCAATAGAGGTGACCGGACGCTGCTGCTG 9028  
DB 607 AACCGGATAAACCCCAATTTANAGTTGAACGACAGTATCCTTG 650

RESULT 4  
AQ990989/c  
LOCUS  
DEFINITION  
Photorhabdus luminescens strain W14 M13 library  
Photorhabdus luminescens genomic clone PLG01839, genomic survey  
sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Photorhabdus luminescens  
Photorhabdus luminescens  
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
Enterobacteriaceae; Photorhabdus.  
REFERENCE  
AUTHORS  
1 (bases 1 to 672)  
ffrench-Constant R.H., Waterfield N., Burland V., Perna N.T.,  
Daborn P.J., Bowen D. and Blattner F.R.  
A genomic sample sequence of the entomopathogenic bacterium  
Photorhabdus luminescens W14: potential implications for virulence  
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)  
MEDLINE  
PUBMED  
COMMENT  
Contact: ffrrench-Constant RH  
Department of Biology and Biochemistry  
University of Bath  
South Building, Bath BA2 7AY, UK  
Tel: (44) 1225 826621  
Fax: (44) 1225 826779  
Email: bssrfc@bath.ac.uk  
This is one of 2,122 random reads from the M13 library. For  
annotation of identified clones (BLASTX, BLASTN and mapping to E.  
coli K12 genome) please see ffrrench-Constant et al. 2000, Nucleic  
Acids Res.  
Seq primer: M13 Forward  
Class: shotgun.

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library"  
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kb) and then cloned into M13 Janus."

ORIGIN

Query Match 1.3%; Score 241.4; DB 8; Length 672;  
Best Local Similarity 62.8%; Pred. No. 5.6e-52;  
Matches 390; Conservative 0; Mismatches 228; Indels 3; Gaps 1;

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QY 5369 ATCGCGGCATACGGCTGATATCAACCGGCGCTTAAACGGAATAGAACTCAGCGCCATG 5428  
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QY 5429 GCAGAGGTGAGGGGGCGGTTCAGTTTTTTTCACTGACTGGGATACGTTCAACAAACGTTACAGC 5488  
DB 555 TCGGGGTTATCAGCGCCCAATTTCTTTATCGACTGGGACAAATACAATAAACGCTACAGC 496

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Db 220 GATGCTGTAGCCCAAGATGATCCGATGCACTACAAGTGGCTACCTTATGCGGACGTTG 161  
 QY 7601 GACCTGCTGATGCGCGCGGTGATGCGGCTACCGGCTGCTCGAGCGGAGACCCCTTAAC 7660  
 Db 160 GATCTGCTAATGCGCCGCTGCTGATGCTGCTTACCGCCAGTTAGAGCGTGATACGTTGGCT 101  
 QY 7661 GAGCGCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7710  
 Db 100 GAAGCTAATAATGGGTATATACAGAGCGCTTAATCTGTGGGTGATGAGCC 51

RESULT 8  
 AQ990411  
 LOCUS  
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 Photorhabdus luminescens genomic clone PLG01179, genomic survey  
 sequence.

ACCESSION AQ990411.1 GI:9649005

VERSION  
 KEYWORDS  
 SOURCE

ORGANISM

Photorhabdus luminescens  
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 Enterobacteriaceae; Photorhabdus.

REFERENCE 1 (bases 1 to 605)

AUTHORS ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,  
 Daborn, P.J., Bowen, D. and Blattner, F.R.

TITLE A genomic sample sequence of the entomopathogenic bacterium  
 Photorhabdus luminescens W14: potential implications for virulence

JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

MEDLINE 20378633

PUBMED 10919786

COMMENT Contact: ffrench-Constant RH

Department of Biology and Biochemistry

University of Bath

South Building, Bath BA2 7AY, UK

Tel: (44) 1225 826621

Fax: (44) 1225 826779

Email: bssr@bath.ac.uk

This is one of 2,122 random reads from the M13 library. For  
 annotation of identified clones (BLASTX, BLASTN and mapping to E.  
 coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic  
 Acids Res.

Seq primer: M13 Forward

Class: shotgun.

Location/Qualifiers

1..605

/organism="Photorhabdus luminescens"

/mol\_type="genomic DNA"

/strain="W14"

/db\_xref="taxon:29488"

/clone="PLG01179"

/dev\_stage="primary phase variant"

/clone\_lib="Photorhabdus luminescens strain W14 M13  
 library"

/notes="Genomic DNA from strain W14 was size selected (1-2  
 kb) and then cloned into M13 Janus."

ORIGIN

Query Match 1..11; Score 214.6; DB 8; Length 605;

Best Local Similarity 62.3%; Pred. No. 7.6e-45;

Matches 351; Conservative 0; Mismatches 211; Indels 1; Gaps 1;

QY 14967 TTACGGAAACGCTTGTGATCGCTGGCAATACCGATCGCGAGAGATTTCTCAATCTGGCTG 15026

Db 1 TGACAGAGCGCTTATCTGCGCTGGGAATACAACTCGGAGAAAGATTAACCTCTCG 60

QY 15027 GCCAGTGTCTAGTATTACGATACCGCGGACTGTGTCAGACGACGATCGCCCTGA 15086

Db 61 GTCTGTGTATACCCACTACGACACAGCGGAGTGACCCGGTTGATGAGTCACTGCTGG 120

QY 15087 GCGCGCTGCGCTGCGCGCTGACGCGGAGTTGCTGCCCGACGCGGGGGGCAACTGGA 15146

Db 121 CGGGGCGCATGCTATCCCAATCTCACCATTCTGCGGGAAGGCGAGGGTAACTGGA 180  
 QY 15147 TGGGTGAGGATCCCTCGGCTTGGAAATGACCTCTCTGATGGGAGAGCTTTCTTCCACCAGA 15206  
 Db 181 GCGGTGACGACGAAACTGTCTGGCAGGGAATCTGGCAAGTCTGAGGTCTATACGACACAAA 240  
 QY 15207 CCACGCTGATCGACCGGCGGCTCTTGAGCATCACGATGCAAAAGTAATCTGCAGC 15266  
 Db 241 GTACCACCTAATCCATCGGGGCTTTACTGACCCAAACCGATCGAAAGGCAATATTTCAGC 300  
 QY 15267 GTGTGGCATATGATGTGGCTGGCTGCTATCGGCGAGTTGTTGACGCTGAAGGACGGCA 15326  
 Db 301 GTCTGGCTTATGACATTCGCGTCAAGTTAAAGGAGAGTTGGTTGACGTTGAAGGCCAGA 360  
 QY 15327 CGGAGCAGGTATCTGCTGGCTCCCTGAGCTACTCGGCGCGCGGAAAAAGTTGCGTGAAG 15386  
 Db 361 GTGAACAGGTGATTGTTAAGTCCCTGAGCTGCTGAGCCGCGAGTCTATAAATTGCGTGAAG 420  
 QY 15387 AACACGGCAACGCGCTGTTAAGTCTGTTATTTACGAG-CCGGAACACAGCGCTGAGC 15445  
 Db 421 AGCACGCTAACGCGCTGTTACCGAGTACAGTTATGAGCCCGGAACTCAACGCTCTGATA 480  
 QY 15446 GGGATTAAAAACGAAACGCTCGCTCGGCACGTTGCCGGAGCAAAAGTGTGCGAGGACCTG 15505  
 Db 481 GGTATACACACCGCGCTGCCAANGAGTCAATCANGAGCCAGAAAGTATTGCGAGTCTA 540  
 QY 15506 CGCTATACGTATGACCCGCTAGG 15528  
 Db 541 CGCTATAAGTATGATCCCGTGG 563

RESULT 9

CNS01R9G/c

LOCUS

DEFINITION

Anopheles gambiae GSS T7 end of clone 32J18 of Notredamei library  
 from strain PEST of Anopheles gambiae (African malaria mosquito),  
 genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Anopheles gambiae (African malaria mosquito)  
 Anopheles gambiae  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;  
 Anopheles.

REFERENCE 1 (bases 1 to 881)

Genoscope.

Direct Submission

Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

2 (bases 1 to 881)

Direct Submission

Submitted (16-FEB-2000) BMI, Institut Pasteur, 25, rue du Dr.

Roux, Paris 75015, France

This clone is from an A. gambiae BAC library provided by F.H.  
 Collins and sequenced by Genoscope in collaboration with the  
 Laboratory of Biochem. and Biol. Molec. of Insects, Institut  
 Pasteur.

FEATURES

source

1..881

/organism="Anopheles gambiae"

/mol\_type="genomic DNA"

/strain="PEST"

/db\_xref="taxon:7165"

/clone="32J18"

/clone\_lib="Notredamei"

/note="end : T7"

ORIGIN

Query Match 1.0%; Score 197.6; DB 9; Length 881;

Best Local Similarity 83.0%; Pred. No. 3e-40;  
Matches 244; Conservative 8; Mismatches 27; Indels 15; Gaps 2;

QY 18446 CTGACGTAAACGCTGACGATCTCTCTGCTGATTTTCTGGGTTTGTGCTGCTGTA 18505  
DB 881 CTGACGTAAACGCTGACGATCTCTCTGCTGATTTTCTGGGTTTGTGCTGCTG 822

QY 18506 CGGTGATCGTAATCTGATGACACACGCGCCCGCGGTAGTGGCTAGCTGAGAAGCC 18565  
DB 821 CGGTGATCGTAATCTGATGACACACGCGCCCGCGGTAGTGGCTAGCTGAGAAGCG 762

QY 18566 GCACCGCGCGGCGCTTCAGGTACCGGCGCAGGTATTTTCAGCTGCGCCACGCGCGCG 18625  
DB 761 GCACCGCGCGGCGCTTCAGGTACCGGCGCAGGTATTTTCAGCTGCGCCACGCGCGCG 702

QY 18626 GTCTTTTGGCAAAATTCATTTTC-CAGGCGCGCGGTATTTGCGCATGCG- 18675  
DB 701 GTCTTTTGGMAAAATATACATTTTCAGGCGCGCGGTATTTGCGCATGMAAGTAAGGTG 642

QY 18676 -----GGTCTTCGTTGCGGATATGCGGACCGCGCGCGCGCGCGCGCGCGCG 18724  
DB 641 MMACAGATMTTATGAGTATGACMGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 588

RESULT 10  
AQ990217  
LOCUS  
DEFINITION  
Photobacterium luminescens strain W14 M13 library  
Photobacterium luminescens genomic clone PLG00949, genomic survey  
sequence.

ACCESSION  
AQ990217  
VERSION  
AQ990217.1  
KEYWORDS  
GSS.  
SOURCE  
Photobacterium luminescens  
Photobacterium luminescens  
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
Enterobacteriaceae; Photobacterium.

REFERENCE  
AUTHORS  
1 (bases 1 to 617)  
ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,  
Daborn, P.J., Bowen, D. and Blattner, F.R.  
A genomic sample sequence of the entomopathogenic bacterium  
Photobacterium luminescens W14: potential implications for virulence  
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

JOURNAL  
MEDLINE  
PUBMED  
20378633

COMMENT  
10919786  
Contact: ffrench-Constant RH  
Department of Biology and Biochemistry  
University of Bath  
South Building, Bath BA2 7AY, UK  
Tel: (44) 1225 826621  
Fax: (44) 1225 826779  
Email: bsrfc@bath.ac.uk  
This is one of 2,122 random reads from the M13 library. For  
annotation of identified clones (BLASTX, BLASTN and mapping to E.  
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic  
Acids Res.  
Seq primer: M13 Forward  
Class: shotgun

FEATURES  
source  
1. .617  
/organisms="Photobacterium luminescens"  
/mol\_type="genomic DNA"  
/strain="W14"  
/db\_xref="taxon:29408"  
/clone="PLG00949"  
/dev\_stage="primary phase variant"  
/clone\_lib="Photobacterium luminescens strain W14 M13  
library"  
/note="Genomic DNA from strain W14 was size selected (1-2  
kb) and then cloned into M13 Janus."

ORIGIN  
Query Match 1.0%; Score 192; DB 8; Length 617;

Best Local Similarity 60.8%; Pred. No. 8.1e-39;  
Matches 355; Conservative 0; Mismatches 225; Indels 4; Gaps 3;

QY 8410 GCTCTTTTGGCGGCGCGCGCGATATGTCGCCAATATTTAGCGGCTGCCCTCGG 8469  
DB 18 GNCOCGTATGGCGGCGCGCGGTGATATGNNCCAAATATCTTCGGCTGGCTGATGG 77

QY 8470 GGGCTCCCTCTATGGGGCACTATTTAAAGCCACCGCATCGGCATCGCTGCTCCGA 8529  
DB 78 CGGNATGCANTATGGNGCTATTGNCATATGCCATCGCTGACGGTATGAGTTGAGTCTTC 137

QY 8530 TGCCACCCGCATATCAGCGGACAAATCAGCCAGTTCGGAAGTGTACCGCGTCCCGGGA 8589  
DB 138 TGCCAAAGATGGTGTGATGCGGAGAAAGTTGCTCAGTCGGAATATATATCGCGCTGCA 137

QY 8590 GAGGTGGGAAATCCACGCGGTAGTGGCGAGTCTGAGTGGCGCAGATTGATGCCAGCT 8649  
DB 198 AGAATGGAAATTTACGCTGACACGCAACGCGGAGATTAAACAGTTAAACGCGCACT 257

QY 8650 GCGCGCATGCGCGCGCGCGCGCGCTGAGCTGCGAGAAACCTTACCTTGAGACCCA 8709  
DB 258 GGAATCAGTGTCTATTGCGCGGTGAAGCCGCTGAATGCAAAAGAGTACTGAAACCCA 317

QY 8710 GCAGACCCAGGCAAGCGCGCATTTGCGCATTCCTGCGAGATTAAGTTCAA-CAATACGGCTC 8768  
DB 318 GCAAGCTCAGCGCGCGCGCAACTTACTTTCTTAAGAAGCAAAATTCAGTAAATCAAGCGT 377

QY 8769 TGTACAGCTGCGTGGCGCGCGCGGTGTCGCCCATTTTATACAGTTCTATGACCTCG-CA 8827  
DB 378 TATATAGTTGGTTTACCGCGCGGTGTCAGGTATTTATTTCCAGTTCTATGACTTGGCCC 437

QY 8828 GTATCCCGCTGCTGATGCGCAACAGCGCTGCGAGTGGGATAAAATTCGAGACTAGGTG 8887  
DB 438 GTATCAGTTGCTGATGCGAGNACATCTCATGGAAGCTAATGATAATTNCATT 497

QY 8888 TTTATCCAGCGCGCGCTGGAATGGGGGCAATGCGGTCTGCTGCGCGGGGAAACCTTG 8947  
DB 498 ACTTTGCAACCGGTGATGCGCAAGGAACCTTA--CCCGGCTTATTGTGGAAGAGCTTTG 555

QY 8948 ATGCTGAATCTGCGCGAGATGCGAGCGCTGCTGACGGGGA 8991  
DB 556 ATACAAATCTGGCAAAATGGAAGCATATCTGAAATGGGA 599

RESULT 11  
AQ991038  
LOCUS  
DEFINITION  
Photobacterium luminescens strain W14 M13 library  
Photobacterium luminescens genomic clone PLG01893, genomic survey  
sequence.

ACCESSION  
AQ991038  
VERSION  
AQ991038.1  
KEYWORDS  
GSS.  
SOURCE  
Photobacterium luminescens  
Photobacterium luminescens  
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
Enterobacteriaceae; Photobacterium.

REFERENCE  
AUTHORS  
1 (bases 1 to 602)  
ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,  
Daborn, P.J., Bowen, D. and Blattner, F.R.  
A genomic sample sequence of the entomopathogenic bacterium  
Photobacterium luminescens W14: potential implications for virulence  
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

JOURNAL  
MEDLINE  
PUBMED  
20378633

COMMENT  
10919786  
Contact: ffrench-Constant RH  
Department of Biology and Biochemistry  
University of Bath  
South Building, Bath BA2 7AY, UK  
Tel: (44) 1225 826621  
Fax: (44) 1225 826779  
Email: bsrfc@bath.ac.uk  
This is one of 2,122 random reads from the M13 library. For

annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.  
Seq primer: M13 Forward  
Class: shotgun.

# FEATURES

source  
1. .602  
/organism="Photorhabdus luminescens"  
/mol\_type="genomic DNA"  
/strain="W14"  
/db\_xref="taxon:29488"  
/clone="PLG01893"  
/dev\_stage="primary phase variant"  
/clone\_lib="Photorhabdus luminescens strain W14 M13 library"  
/notes="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

## ORIGIN

Query Match 1.0%; Score 188.6; DB 8; Length 602;  
Best Local Similarity 62.1%; Pred. No. 6.5e-38;  
Matches 332; Conservative 0; Mismatches 199; Indels 4; Gaps 2;  
QY 8509 CGGCATCCAGGTGCTCCGATGCCACCGCATATCAGCGGACAAAATCAGCCAGTCGGA 8568  
Db |||||  
QY 48 CGGTATTGAGTTCAGTCTTCCCAAGATGGTTGATCGGAGAAAGTTGCTCAGTCGA 107  
Db |||||  
QY 8569 AGTGTACGCCGTCGCGGGAGAGTGGGAAATCCAGCGTGATAGTGCAGTCTGACGT 8628  
Db |||||  
QY 108 AATATATCGCGTCGCGCTCAGAAATGGAATTCAGCGTGACACGACCAAGCGGAGAT 167  
QY 8629 GCGCGAGATGATGCCAGTCGCGCATGGCAGTGCCTCGGGAGGGCTGAGTCGA 8688  
Db |||||  
QY 168 TAACCAAGTTAAACGCCCACTGGAATCCTGTTCTATTCGCGGGAAGCGCTGAAATGCA 227  
QY 8689 GAAACCTTACCTTTGAGACCCAGCAGACCCAGGCGCAGTTGGCATCTTCTGCGAGAG 8748  
Db |||||  
QY 228 AAAAGAGTACCTGAAACCCAGCAAGCTCAGGCGCAGGCACACTTACTTTCTTAAGAG 287  
QY 8749 TAAGTTCAACATACACGCTCTGTACAGCTGGCTGCGGGGAGGTTGTCGCCATTATTA 8808  
Db |||||  
QY 288 CAAATTCAGTAATCAACAGCGTTATATAGTTGGTTTACGAGGCGCTTGTCTCAGTATTATTT 347  
QY 8809 CAGATTCTATGACCTGCGAGTATCCCGCTGCTGATGGCGCACAGCGCTGCGAGTGGCA 8868  
Db |||||  
QY 348 CAGTTTCTATGACTTGGCGGTATCACGTTGCTGTATGGCAGAGCAATCTCTCAATGGGA 407  
QY 8869 ---TAAATTCGAGACTAGGTGCTTTATCCAGCGGGGGCTGGATGGGGGCAAAATGCCGG 8925  
Db |||||  
QY 408 AGCTAATGATAATTCCTATTAGCTTTTGTCAACCGGGTGATGGCAAGGAATTCAGCCGG 467  
QY 8926 TCTGCTGGCGGGGAAACCTGATGTGATCTGGCGCAGATGGAGCAGCGCTGGCTGAC 8985  
Db |||||  
QY 468 CTTATTGTGTGGAGAGCTTTGATACAAATCTGGC-CAAATGGAAGAGGCATATCTGAA 526  
QY 8986 GGGGGATGAGCGGGCAATAGAGTGTACGCGAGGCTCTGCTCTCGAGGTTCTAT 9040  
Db |||||  
QY 527 ATGGGAATCTCGCGCTTTTGAAGTAGAACGACGCGGTTCAATTTGAGTGGGTTAT 581

RESULT 12  
CB065346  
LOCUS  
DEFINITION  
EST845027 HOGA Medicago truncatula CDNA clone HOGA-2E7, mRNA  
sequence.  
ACCESSION  
VERSION  
CB065346.1 GI:27810924  
KEYWORDS  
EST.  
SOURCE  
Medicago truncatula (barrel medic)  
ORGANISM  
Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;

## REFERENCE

AUTHORS  
Hahn,M.G., Ojanen-Reuhs,T., Samac,D., Town,C.D., Van Aken,S.,  
Utterback,T., Cho,J. and Fraser,C.M.  
TITLE  
ESTs from roots of Medicago truncatula treated with  
oligogalacturonides of Dp 6-20  
JOURNAL  
Unpublished (2001)

## COMMENT

Contact: Michael G. Hahn  
Complex Carbohydrate Research Center  
University of Georgia  
220 Riverbend Road, Athens, GA 30602-4712, USA  
Tel: 706-542-4457  
Fax: 706-542-4412  
Email: hahn@ccrc.uga.edu  
TIGR sequence name: MTMAE28TK  
More information is available at: www.medicago.org  
Seq primer: SKnod (CTA gAA CTA gtg gAT CC).

## FEATURES

source

1. .604  
/organism="Medicago truncatula"  
/mol\_type="mRNA"  
/cultivar="A17"  
/db\_xref="taxon:3880"  
/clone="HOGA-2E7"  
/tissue\_type="3 day old seedling roots"  
/dev\_stage="24 hours after treatment in the dark at 26 C  
with 0.5 mg/ml oligogalacturonides (DP 6-20) in the  
presence of 100 ug/ml Gentamicin"  
/lab\_host="XLOLR"  
/clone\_lib="HOGA"  
/note="Vector: pBluescript SK-; Site1: EcoRI; Site 2:  
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA  
was directionally ligated into the Unizap XR vector from  
Stratagene and packaged using Gigapack III Gold packaging  
extracts. Plasmids containing cDNA inserts were excised  
from the recombinant lambda-Zap phage using Ex-assist  
helper phage and propagated in SOLR cells."

## ORIGIN

Query Match 1.0%; Score 188.2; DB 6; Length 604;  
Best Local Similarity 61.6%; Pred. No. 8.3e-38;  
Matches 301; Conservative 0; Mismatches 188; Indels 0; Gaps 0;  
QY 7274 GCCCTGGAGAGGGAGTGATGTGTTATGACCTTCCTCGGAGCCAAATGCCCTCTATTTC 7333  
Db |||||  
QY 12 GTCATGCCACGCGAGGCGCGGTGCCGATGCACTTCACCGCGCAACCGCGTGTATTTC 71  
QY 7334 TGGGAGCTGTTCTATTACACGCCGATGATGTGTTCCAGCGGTTGTTGCGAGGAACGAC 7393  
Db |||||  
QY 72 TGGGAGCTGTTCTACTACGCCCGATGATGTGATGCGAGCGTTCTCCAGGAAGAGCGC 131  
QY 7394 TTCGCGGAAGCACCCGCTGGCTGCAGTATGTCTGGAACCCCGGCGGGACGCTGGTAAAC 7453  
Db |||||  
QY 132 TACGACCAACGCTGAACAATGGCTCGTTTATATCTTCAACCCCTTTGGGGTATGGCGATGG 191  
QY 7454 GGGGTGCTGCAGAAATTACCTGGAAATGCTCGTCCGCTGGAGGAGGACACCGGCTGGAC 7513  
Db |||||  
QY 192 GCTGGGACGCTTCGCGCTTGTGGAACGTAACGCCCTCTGGAAGAGGACAGTTCTGGGAAC 251  
QY 7514 GACTCGCGCTGGACTCCCAATGACCCCGATGCAATAGCCCACTAGACCCCATGCAATTAC 7573  
Db |||||  
QY 252 GATGAGCGCTGCGTTCGCTGACCCCGATGCGCTGGCCGAGAACGACCCCATGCACTAC 311  
QY 7574 AAGTCGCGCACTTTTATGTCGTACCTCGACCTGTGATTGCCCGGGGTGATGCGCGCTAC 7633  
Db |||||  
QY 312 AAGCTCAATGCAATTCATCGCGCTGTGATATCAACATCGGTCTGTGGCGATGCGCGCTTAT 371  
QY 7634 CGGCTGCTCGAGCGGACACCTTAAACGAGCCCGGATGTGTACGTCCAGGCCCTGAC 7693  
Db |||||  
QY 372 CGCAACTGGACGAGATAGCTTCGCGCAGGCGCAAGATGTGTATCAGCGCGCCCTGGAG 431  
QY 7694 CTTCTGGCGCAGAGCCCTATATTTCTTTTGAACGCCGACTGCTGCGCGCTTGACCCCTGGGT 7753  
Db |||||

Db 432 CTGTTGGGGAGCGGCCCTGGACTCCCGCGGCAACCGGTTGGAAAGAGCACTGCTGGGG 491

QY 7754 GAGCAGCC 7762

Db 492 CAACTGGCC 500

RESULT 13

LOCUS AQ991741

DEFINITION Rf00508F Photorhabdus luminescens strain W14 M13 library

Photorhabdus luminescens genomic clone PLG00508F, genomic survey

sequence.

ACCESSION AQ991741

VERSION AQ991741.1 GI:9650237

KEYWORDS GSS.

SOURCE Photorhabdus luminescens

ORGANISM Photorhabdus luminescens

REFERENCE 1 (bases 1 to 735)

AUTHORS ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T., Daborn,P.J., Bowen,D. and Blattner,F.R.

TITLE A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence

JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

MEDLINE 20378633

PUBMED 10919786

COMMENT Contact: ffrench-Constant RH  
Department of Biology and Biochemistry  
University of Bath  
South Building, Bath BA2 7AY, UK  
Tel: (44) 1225 826621  
Fax: (44) 1225 826779  
Email: bssrfc@bath.ac.uk  
This is one of a selected subset of flipped clones from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.  
Seq primer: M13 Reverse  
Class: shotgun.

FEATURES

source

1..735

/organism="Photorhabdus luminescens"

/mol\_type="genomic DNA"

/strain="W14"

/db\_xref="taxon:29488"

/clone="PLG00508F"

/dev\_stage="primary phase variant"

/clone\_lib="Photorhabdus luminescens strain W14 M13 library"

/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN

Query Match 0.9%; Score 178; DB 8; Length 735;

Best Local Similarity 62.7%; Pred. No. 4.7e-35;

Matches 277; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

QY 7370 CAGCGGTTGTCAGGAAACAGCACTCCCGGAAGCCACCGCTGGCTGCAGTATGCTGG 7429

Db 32 CAGCGCTGCTACACGAACAACACTTCGATGAAGCAACCGTTGGTTGAAATATATCTGG 91

QY 7430 AACCGCGCGGACGCTGGTAAACGGGGTCTGCAGAAATTACACCTGGAATGCGGTCG 7489

Db 92 AATCCATCTGTTATATTGACGATGGTCAGATTACAGCACTACCGCTGGAATGCGGCCA 151

QY 7490 CTGAGGAGGACACCGCTGGAACGACTCGCGCTGGACTCCATTGACCCCGATGCAATA 7549

Db 152 TTATTGGAAGATATCAGTTTGAACAGATGATCCACTGAATTCAGTCGATCCCGATGCCATA 211

QY 7550 GCCCAGTACACCCCATGCAATTACAGGTGCGCCACCTTTATGTCGTAACCTCGACCTGCTG 7609

Db 212 GCACAATATGATCCAAATGCACTATATAAGTCGTTACTTTTATGCGCACCCCTTGATCTGTTG 271

QY 7610 ATTGCCCGCGGTGATCCCGCTACCGCTGCTCGAGCGGACACCCCTTAACGAGGCGCCGG 7669

Db 272 CTGGACCGTGGAGATTACCGCTATCGTCAGTTAGAACGGGACACGCTTAATGAAGCTAAG 331

QY 7670 ATGTGTACGTCCAGGCCCTGAACCTTCTGGGCGACGAGCCCTATATTTCTTTGACGCC 7729

Db 332 ATGTGTATATGCAACGACTGCATCTGTTAGGCGATAAACCTCATCTATCTTTCAAGTTCA 391

QY 7730 GACTGTGCGGCTTGACCTGGTGACGACGAGCGAGGTGACGCGGATACCGATTACAG 7789

Db 392 ACGTGGCGTAAACCGAGTTTGGTGACCTGCGCAACCGGAAAAACAGGAGGAACAAGCC 451

QY 7790 GAGGCCCTGCTGGCGCTGGGCC 7811

Db 452 CATGCAATGACTGCCCTCGGAC 473

RESULT 14

LOCUS AQ991783/c

DEFINITION Rf02280F Photorhabdus luminescens strain W14 M13 library

Photorhabdus luminescens genomic clone PLG02280F, genomic survey

sequence.

ACCESSION AQ991783

VERSION AQ991783.1 GI:9650377

KEYWORDS GSS.

SOURCE Photorhabdus luminescens

ORGANISM Photorhabdus luminescens

REFERENCE 1 (bases 1 to 765)

AUTHORS ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T., Daborn,P.J., Bowen,D. and Blattner,F.R.

TITLE A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence

JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

MEDLINE 20378633

PUBMED 10919786

COMMENT Contact: ffrench-Constant RH  
Department of Biology and Biochemistry  
University of Bath  
South Building, Bath BA2 7AY, UK  
Tel: (44) 1225 826621  
Fax: (44) 1225 826779  
Email: bssrfc@bath.ac.uk  
This is one of a selected subset of flipped clones from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.  
Seq primer: M13 Reverse  
Class: shotgun.

FEATURES

Location/Qualifiers

1..765

/organism="Photorhabdus luminescens"

/mol\_type="genomic DNA"

/strain="W14"

/db\_xref="taxon:29488"

/clone="PLG02280F"

/dev\_stage="primary phase variant"

/clone\_lib="Photorhabdus luminescens strain W14 M13 library"

/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN

Query Match 0.8%; Score 158; DB 8; Length 765;

Best Local Similarity 56.8%; Pred. No. 1e-29;

Matches 366; Conservative 0; Mismatches 260; Indels 18; Gaps 4;

QY 9343 GCGCGTCTCACGCGAATGAACACACGCGCAATTCCAACTGGATTTCAATGACCCGCG 9402

